

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 5, 2006, 17:01:34 ; Search time 118.845 Seconds
(without alignments) updates/sec
2085.165 Million cell

Title: US-10-691-079-1
Perfect score: 2863
Sequence: 1 MGSNKSXPKDASQRRRLSEP.....AFLEDYFTSTSPYQPGENL 542

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*

- 1: Geneseqp19808:*
- 2: Geneseqp19008:*
- 3: Geneseqp20008:*
- 4: Geneseqp20018:*
- 5: Geneseqp20028:*
- 6: Geneseqp20038:*
- 7: Geneseqp20048:*
- 8: Geneseqp20058:*
- 9: Geneseqp20068:*
- 10: Geneseqp20078:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	2863	100.0	542	5	ABB97339 Novel hum
2	2863	100.0	542	8	ADY84075 Human Src
3	2821	98.5	536	2	AAR39706 Human pp6
4	2821	98.5	536	5	ABG95123 Human V-8
5	2821	98.5	536	5	AaU78678 Human SH2
6	2821	98.5	536	6	ABP57260 Human src
7	2821	98.5	536	7	AD120072 Human C-S
8	2821	98.5	536	8	AD122904 Human MP2
9	2821	98.5	536	8	ADQ88400 Human wil
10	2821	98.5	536	8	ADQ97772 Human can
11	2821	98.5	536	8	ADU04517 Protein t
12	2821	98.5	536	8	ADY84076 Human Src
13	2821	98.5	536	9	ADY94834 Human wil
14	2821	98.5	536	9	AEA35914 Human Src
15	2821	98.5	541	8	ADY84080 Human Src
16	2820.5	98.5	541	8	ABP57261 Mouse Src
17	2820.5	98.5	541	8	ADY84077 Murine Src
18	2816	98.4	535	7	ADF45087 Human kin
19	2816	98.4	535	8	ADP21154 Human non
20	2788	97.4	530	8	ADQ88402 Human mut
21	2788	97.4	530	3	ADY94836 Human mut
22	2650.5	92.6	533	3	AAY44447 Wild-type
23	2650.5	92.6	533	4	AAH84661 Amino aci

24	2650.5	92.6	533	9	ABE07192 Chicken c
25	2645.5	92.4	533	3	AAY44449 Mutant ch
26	2645.5	92.4	533	2	AAR39705 Chicken p
27	2644.5	92.4	533	3	AAY44451 Mutant ch
28	2469	86.2	523	9	ABE07190 Rous sarc
29	2396.5	83.7	565	4	ABG23778 Novel hum
30	2230	77.9	423	8	ADQ97769 Mouse can
31	2110.5	73.7	543	4	AAH84663 Amino aci
32	2110.5	73.7	543	6	ABG10302 Novel hum
33	2110.5	73.7	543	4	ADA00843 Human Src
34	2110.5	73.7	543	7	ADP45099 Human kin
35	2110.5	73.7	543	8	ADL22913 Human MP2
36	2110.5	73.7	543	8	ADQ19329 Human PRO
37	2110.5	73.7	543	8	ADQ19331 Human PRO
38	2110.5	73.7	543	8	ADQ26047 v-yes-1 y
39	2110.5	73.7	543	8	ADU06318 Novel bro
40	2110.5	73.7	543	9	ADW78761 Human Yam
41	2110.5	73.7	543	9	ADY19868 PRO polyP
42	2110.5	73.7	543	9	AEA35915 Human PRO
43	2110.5	73.7	543	9	ABE01122 Human c-y
44	2110.5	73.7	543	9	ADU74614 Perinucle
45	2104.5	73.5	541	5	AAU74614 Perinucle

ALIGNMENTS

RESULT 1
ABB97339 standard; protein; 542 AA.

27-JUN-2002 (first entry)
Novel human protein SEQ ID NO: 607
Human; antianaemic; vulnary; antiinflammatory; immunomodulator;
antifertility; cerebroprotective; cytosolic; rheumatic; gene therapy;
neuroprotective; antiparkinsonian; protein therapy; EST;
expressed sequence tag.

OS Homo sapiens.

XX MO200222660-A2.

XX 21-MAR-2002.

XX 10-SEP-2001; 2001MO-US026015.

XX 11-SEP-2000; 2000US-00659671.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Zhou P, Auendi V, Zhang J, Zhao QA, Ren F;
PI Yang Y, Wehrman T, Dirmann RT;

XX WPI: 2002-292408/33.

XX N-PSDB: ABN32525.

XX An isolated polynucleotide for treating diseases associated with its
encoded polypeptide such as cancer and multiple sclerosis.

XX Example 2; SEQ ID NO 607; 509pp; English.

CC The present invention provides the protein and coding sequences of 444
CC novel human proteins. These were isolated from expressed sequences tags
CC (ESTs). They can be used to stimulate cell growth, to regulate
CC haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth
CC e.g. in burn treatment, to regulate the immune system e.g. to treat
CC multiple sclerosis, to regulate activin or inhibin e.g. to treat
CC infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke
CC and cancer, to screen for drugs, to treat inflammatory conditions e.g.

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CC rheumatoid arthritis, and to treat nervous system disorders e.g.
 XX Parkinson's disease. The present sequence is a protein of the invention
 SQ Sequence 542 AA;

Query Match 100.0%; Score 2863; DB 5; Length 542;
 Best Local Similarity 100.0%; Pred. No. 1.5e-245;
 Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSNKSXPXKASQRRRLSEPAENVHAGGAFPAQSPSPKASADGHRGPSAFAAPAAE 60
 DB 1 MGSNKSXPXKASQRRRLSEPAENVHAGGAFPAQSPSPKASADGHRGPSAFAAPAAE 60
 QY 61 PKLFGGNSSDVTTSPPQAGPLAGVTTFVALYDSESTEDLSFKKGBRLQIVNNTKRY 120
 DB 61 PKLFGGNSSDVTTSPPQAGPLAGVTTFVALYDSESTEDLSFKKGBRLQIVNNTKRY 120
 QY 121 DVREBDMWLHSLSTGQGYIPSNVYAPSDSIQAEWYFGKITRRESERLLINANPRGT 180
 DB 121 DVREBDMWLHSLSTGQGYIPSNVYAPSDSIQAEWYFGKITRRESERLLINANPRGT 180
 QY 181 FLVRESSTTGAYCISVSDPDNAKGLNVKHYKIRKLDGSGFYTSRTQFNSIQQLVAYYS 240
 DB 181 FLVRESSTTGAYCISVSDPDNAKGLNVKHYKIRKLDGSGFYTSRTQFNSIQQLVAYYS 240
 QY 241 KHADGLCHRLTYVCTSPKQTOGLAKDAWEIPRESLRLEVLDGCGCFGEVWMTNGTTR 300
 DB 241 KHADGLCHRLTYVCTSPKQTOGLAKDAWEIPRESLRLEVLDGCGCFGEVWMTNGTTR 300
 QY 301 VALKTLKPGTMSPEAFLOEAOVMKKLRHEKLVOLYAVVSEEPYIVTEYMSKSLDPLK 360
 DB 301 VALKTLKPGTMSPEAFLOEAOVMKKLRHEKLVOLYAVVSEEPYIVTEYMSKSLDPLK 360
 QY 361 GETGKTYRLPOLVDMAAQIASGMAVVERMNYVHRDLRAANILVGENLVCAVADFGIARLI 420
 DB 361 GETGKTYRLPOLVDMAAQIASGMAVVERMNYVHRDLRAANILVGENLVCAVADFGIARLI 420
 QY 421 EDNEYTAPOGAKFPIKWTAPPAALYGRFTIKSDVMSFGILLTELTTKGRVYPGMVNRV 480
 DB 421 EDNEYTAPOGAKFPIKWTAPPAALYGRFTIKSDVMSFGILLTELTTKGRVYPGMVNRV 480
 QY 481 LDQVERGYRMPCEPCESLHDLMOCKMRKEPERPFEYLQAFLEDYFTSTEPQYORGE 540
 DB 481 LDQVERGYRMPCEPCESLHDLMOCKMRKEPERPFEYLQAFLEDYFTSTEPQYORGE 540
 QY 541 NL 542
 DB 541 NL 542

RESULT 2
 ADY84075
 ID ADY84075 standard; protein; 542 AA.
 XX ADY84075;
 AC
 XX
 DT 02-JUN-2005 (first entry)
 DE Human Src protein isoform 1 SEQ ID NO.1.
 XX
 XX pharaceutical; Alzheimer's disease; neuroprotective; nootropic;
 KW Src tyrosine kinase.
 XX
 OS Homo sapiens.
 XX
 PN EP1413887-A1.
 PD 28-APR-2004.
 XX
 PF 22-OCT-2002; 2002EP-00292608.
 XX
 PR 22-OCT-2002; 2002EP-00292608.
 XX

PA (AVET) AVENTIS PHARMA SA.
 XX
 XX Wercken L, Zambrano N, Russo T;
 XX
 DR WPI; 2004-332834/31.
 XX

PT Identifying therapeutic compound for treating Alzheimer's disease,
 PT Involves providing Src protein and determining inhibitory effect of
 PT compound on Src activity.
 XX

PS Claim 4; SEQ ID NO 1; 45pp; English.

CC The invention relates to a novel method for identifying (M1) a
 CC therapeutic compound for the treatment of Alzheimer's disease, involving
 CC providing a Src protein and determining the inhibitory effect of a
 CC compound on the Src activity. The method optionally involves providing a
 CC sequence which regulates Src expression and determining if a compound
 CC inhibits the expression of Src protein. A compound of the invention has
 CC neuroprotective and nootropic activity. The compound identified by the
 CC method of the invention is useful for preparing a pharmaceutical for
 CC treating Alzheimer's disease. The present sequence represents isoform 1
 CC of human Src protein.
 XX

SQ Sequence 542 AA;

Query Match 100.0%; Score 2863; DB 8; Length 542;
 Best Local Similarity 100.0%; Pred. No. 1.5e-245;
 Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSNKSXPXKASQRRRLSEPAENVHAGGAFPAQSPSPKASADGHRGPSAFAAPAAE 60
 DB 1 MGSNKSXPXKASQRRRLSEPAENVHAGGAFPAQSPSPKASADGHRGPSAFAAPAAE 60
 QY 61 PKLFGGNSSDVTTSPPQAGPLAGVTTFVALYDSESTEDLSFKKGBRLQIVNNTKRY 120
 DB 61 PKLFGGNSSDVTTSPPQAGPLAGVTTFVALYDSESTEDLSFKKGBRLQIVNNTKRY 120
 QY 121 DVREBDMWLHSLSTGQGYIPSNVYAPSDSIQAEWYFGKITRRESERLLINANPRGT 180
 DB 121 DVREBDMWLHSLSTGQGYIPSNVYAPSDSIQAEWYFGKITRRESERLLINANPRGT 180
 QY 181 FLVRESSTTGAYCISVSDPDNAKGLNVKHYKIRKLDGSGFYTSRTQFNSIQQLVAYYS 240
 DB 181 FLVRESSTTGAYCISVSDPDNAKGLNVKHYKIRKLDGSGFYTSRTQFNSIQQLVAYYS 240
 QY 241 KHADGLCHRLTYVCTSPKQTOGLAKDAWEIPRESLRLEVLDGCGCFGEVWMTNGTTR 300
 DB 241 KHADGLCHRLTYVCTSPKQTOGLAKDAWEIPRESLRLEVLDGCGCFGEVWMTNGTTR 300
 QY 301 VALKTLKPGTMSPEAFLOEAOVMKKLRHEKLVOLYAVVSEEPYIVTEYMSKSLDPLK 360
 DB 301 VALKTLKPGTMSPEAFLOEAOVMKKLRHEKLVOLYAVVSEEPYIVTEYMSKSLDPLK 360
 QY 361 GETGKTYRLPOLVDMAAQIASGMAVVERMNYVHRDLRAANILVGENLVCAVADFGIARLI 420
 DB 361 GETGKTYRLPOLVDMAAQIASGMAVVERMNYVHRDLRAANILVGENLVCAVADFGIARLI 420
 QY 421 EDNEYTAPOGAKFPIKWTAPPAALYGRFTIKSDVMSFGILLTELTTKGRVYPGMVNRV 480
 DB 421 EDNEYTAPOGAKFPIKWTAPPAALYGRFTIKSDVMSFGILLTELTTKGRVYPGMVNRV 480
 QY 481 LDQVERGYRMPCEPCESLHDLMOCKMRKEPERPFEYLQAFLEDYFTSTEPQYORGE 540
 DB 481 LDQVERGYRMPCEPCESLHDLMOCKMRKEPERPFEYLQAFLEDYFTSTEPQYORGE 540
 QY 541 NL 542
 DB 541 NL 542

RESULT 3
 AAR39706
 ID AAR39706 standard; protein; 536 AA.

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CC infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke

CC and cancer, to screen for drugs, to treat inflammatory conditions e.g.

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CC rheumatoid arthritis, and to treat nervous system disorders e.g.
CC Parkinson's disease. The present sequence is a protein of the invention
XX
XX
SQ Sequence 542 AA;

Query Match 100.0%; Score 2863; DB 5; Length 542;
Best Local Similarity 100.0%; Pred. No. 1.5e-245;
Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSNKKPKDASQRRRSLEPAENVHAGGAGFPASQTPSPASADGHRGSAAPAPAAE 60
DB 1 MGSNKKPKDASQRRRSLEPAENVHAGGAGFPASQTPSPASADGHRGSAAPAPAAE 60
QY 61 PKLFGFNSSDVTYSPQAGPLAGVTFVALYDSESTETDLSFKKGERLQIVNTRKY 120
DB 61 PKLFGFNSSDVTYSPQAGPLAGVTFVALYDSESTETDLSFKKGERLQIVNTRKY 120
QY 121 DVREGDMWLAHSLSTGQGYIPSNVYAPSDSIQAEEMFYFKITRRSERLLNAENPRGT 180
DB 121 DVREGDMWLAHSLSTGQGYIPSNVYAPSDSIQAEEMFYFKITRRSERLLNAENPRGT 180
QY 181 FLVRESSETTKGAYCLSVSPDNAGLVNKHKKIRKLDGSGFYITSTRQFNSLQOLVAAYS 240
DB 181 FLVRESSETTKGAYCLSVSPDNAGLVNKHKKIRKLDGSGFYITSTRQFNSLQOLVAAYS 240
QY 241 KHADGLCHRLTTCPTSKPTQGLADAMEIPRESLRLEVKLGQCGFGEVMMGTWGTTR 300
DB 241 KHADGLCHRLTTCPTSKPTQGLADAMEIPRESLRLEVKLGQCGFGEVMMGTWGTTR 300
QY 301 VAIKTLKPGTMSPEAFLOEAQVMKCLRHEKLVOLYAVVSEEPITYITEYMSKSLDPLFK 360
DB 301 VAIKTLKPGTMSPEAFLOEAQVMKCLRHEKLVOLYAVVSEEPITYITEYMSKSLDPLFK 360
QY 361 GETGKYLRLPOLVDMAAQIASGMAYVERMYVHRDLRAANILVGENLVCKVADFGLARLI 420
DB 361 GETGKYLRLPOLVDMAAQIASGMAYVERMYVHRDLRAANILVGENLVCKVADFGLARLI 420
QY 421 EDNEYTARQAGAKPIKMTAPBAALYGRFTIKSDVMSFGILITELTTKGRVPPGMVNRV 480
DB 421 EDNEYTARQAGAKPIKMTAPBAALYGRFTIKSDVMSFGILITELTTKGRVPPGMVNRV 480
QY 481 LDQVERGYRMPCCPECSLHDLMOQWCKEPEERPTFEYLQAFLEDYPTSTEPQYQGE 540
DB 481 LDQVERGYRMPCCPECSLHDLMOQWCKEPEERPTFEYLQAFLEDYPTSTEPQYQGE 540
QY 541 NL 542
DB 541 NL 542

RESULT 2
ADY84075
ADY84075 standard; protein; 542 AA.

XX AC ADY84075;
XX DB 02-JUN-2005 (first entry)
XX DE Human Src protein isoform 1 SEQ ID NO:1.
XX KW pharmaceutical; Alzheimer's disease; neuroprotective; nootropic;
XX KW Src tyrosine kinase.
XX OS Homo sapiens.
XX PN EPI413887-A1.
XX PD 28-APR-2004.
XX PF 22-OCT-2002; 2002EP-00292608.
XX PR 22-OCT-2002; 2002EP-00292608.
XX

PA (AVET) AVENTIS PHARMA SA.
XX Mercken L, Zambrano N, Russo T;
XX WPI; 2004-332834/31.
XX

PT Identifying therapeutic compound for treating Alzheimer's disease,
PT Involves providing Src protein and determining inhibitory effect of
PT compound on Src activity.
XX

PS Claim 4; SEQ ID NO 1; 45p; English.

XX The invention relates to a novel method for identifying (M1) a
XX therapeutic compound for the treatment of Alzheimer's disease, involving
XX providing a Src protein and determining the inhibitory effect of a
XX compound on the Src activity. The method optionally involves providing a
XX sequence which regulates Src expression and determining if a compound
XX inhibits the expression of Src protein. A compound of the invention has
XX neuroprotective and nootropic activity. The compound identified by the
XX method of the invention is useful for preparing a pharmaceutical for
XX treating Alzheimer's disease. The present sequence represents isoform 1
XX of human Src protein.

Query Match 100.0%; Score 2863; DB 8; Length 542;
Best Local Similarity 100.0%; Pred. No. 1.5e-245;
Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSNKKPKDASQRRRSLEPAENVHAGGAGFPASQTPSPASADGHRGSAAPAPAAE 60
DB 1 MGSNKKPKDASQRRRSLEPAENVHAGGAGFPASQTPSPASADGHRGSAAPAPAAE 60
QY 61 PKLFGFNSSDVTYSPQAGPLAGVTFVALYDSESTETDLSFKKGERLQIVNTRKY 120
DB 61 PKLFGFNSSDVTYSPQAGPLAGVTFVALYDSESTETDLSFKKGERLQIVNTRKY 120
QY 121 DVREGDMWLAHSLSTGQGYIPSNVYAPSDSIQAEEMFYFKITRRSERLLNAENPRGT 180
DB 121 DVREGDMWLAHSLSTGQGYIPSNVYAPSDSIQAEEMFYFKITRRSERLLNAENPRGT 180
QY 181 FLVRESSETTKGAYCLSVSPDNAGLVNKHKKIRKLDGSGFYITSTRQFNSLQOLVAAYS 240
DB 181 FLVRESSETTKGAYCLSVSPDNAGLVNKHKKIRKLDGSGFYITSTRQFNSLQOLVAAYS 240
QY 241 KHADGLCHRLTTCPTSKPTQGLADAMEIPRESLRLEVKLGQCGFGEVMMGTWGTTR 300
DB 241 KHADGLCHRLTTCPTSKPTQGLADAMEIPRESLRLEVKLGQCGFGEVMMGTWGTTR 300
QY 301 VAIKTLKPGTMSPEAFLOEAQVMKCLRHEKLVOLYAVVSEEPITYITEYMSKSLDPLFK 360
DB 301 VAIKTLKPGTMSPEAFLOEAQVMKCLRHEKLVOLYAVVSEEPITYITEYMSKSLDPLFK 360
QY 361 GETGKYLRLPOLVDMAAQIASGMAYVERMYVHRDLRAANILVGENLVCKVADFGLARLI 420
DB 361 GETGKYLRLPOLVDMAAQIASGMAYVERMYVHRDLRAANILVGENLVCKVADFGLARLI 420
QY 421 EDNEYTARQAGAKPIKMTAPBAALYGRFTIKSDVMSFGILITELTTKGRVPPGMVNRV 480
DB 421 EDNEYTARQAGAKPIKMTAPBAALYGRFTIKSDVMSFGILITELTTKGRVPPGMVNRV 480
QY 481 LDQVERGYRMPCCPECSLHDLMOQWCKEPEERPTFEYLQAFLEDYPTSTEPQYQGE 540
DB 481 LDQVERGYRMPCCPECSLHDLMOQWCKEPEERPTFEYLQAFLEDYPTSTEPQYQGE 540
QY 541 NL 542
DB 541 NL 542

RESULT 3
AAR39706
AAR39706 standard; protein; 536 AA.

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 5, 2006, 17:01:34 ; Search time 118,845 Seconds
(without alignments)
2085.165 Million cell updates/sec

Title: US-10-691-079-1

Perfect score: 2863
Sequence: 1 MSNKSQPKASQRRSLRP.....AFLEDYFTSTPEQYQENL 542

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: A_Geneseq.8:*
2: geneseqp1980s:*
3: geneseqp1990s:*
4: geneseqp2000s:*
5: geneseqp2001s:*
6: geneseqp2002s:*
7: geneseqp2003as:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

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SUMMARIES

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5	2821	98.5	536	5	AAU78678 Human SH2
6	2821	98.5	536	6	ABP57260 Human Src
7	2821	98.5	536	7	AD120072 Human C-S
8	2821	98.5	536	8	ADQ88400 Human MP2
9	2821	98.5	536	8	ADQ88400 Human w1
10	2821	98.5	536	8	ADQ97772 Human c1
11	2821	98.5	536	8	ADU04517 Protein t
12	2821	98.5	536	8	ADY84076 Human Src
13	2821	98.5	536	9	ADV94834 Human w1
14	2821	98.5	536	9	AEA35914 Human Src
15	2821	98.5	541	8	ADY84080 Human Src
16	2820.5	98.5	541	8	ABP57261 Mouse Src
17	2820.5	98.5	541	8	ADY84077 Murine Sr
18	2816	98.4	535	7	ADF45087 Human Kin
19	2816	98.4	535	9	AED21154 Human non
20	2788	97.4	530	8	ADQ88402 Human mut
21	2788	97.4	530	9	ADV94836 Human mut
22	2650.5	92.6	533	3	AAV44447 Wild-type
23	2650.5	92.6	533	4	AAAB84661 Amino aci

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25	2646.5	92.4	533	3	AAV44449 Mutant ch
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28	2469	86.2	523	9	AEBO7190 Rous bsrc
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32	2110.5	73.7	543	4	ABG10302 Novel hum
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34	2110.5	73.7	543	7	ADF45099 Human Kin
35	2110.5	73.7	543	8	ADL22913 Human MP2
36	2110.5	73.7	543	8	ADQ19329 Human PRO
37	2110.5	73.7	543	8	ADQ19331 Human PRO
38	2110.5	73.7	543	8	ADQ26047 v-yes-1 Y
39	2110.5	73.7	543	8	ADU06318 Novel bro
40	2110.5	73.7	543	9	ADW78761 Human Yam
41	2110.5	73.7	543	9	ADY19868 PRO polyP
42	2110.5	73.7	543	9	AEA23955 Human PRO
43	2110.5	73.7	543	9	AEA35915 Human Yes
44	2110.5	73.7	543	9	AEBO1122 Human c-Y
45	2104.5	73.5	541	5	AAU74614 Perinucle

ALIGNMENTS

RESULT 1
ABB97339 standard; protein; 542 AA.
ID ABB97339
AC ABB97339;
DT 27-JUN-2002 (first entry)
XX
DE Novel human protein SEQ ID NO: 607.
XX
KW Human; anti-neoplastic; anti-inflammatory; immunomodulator;
KW antileukemia; cerebroprotective; cytoskeletal; rheumatic; gene therapy;
KW neuroprotective; antiparkinsonian; protein therapy; EST;
KW expressed sequence tag.
XX
OS Homo sapiens.
XX
PN WO200222660-A2.
XX
PD 21-MAR-2002.
XX
PE 10-SEP-2001; 2001WO-US026015.
XX
PR 11-SEP-2000; 2000US-00659671.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Zhou P, Aseundi V, Zhang J, Zhao QA, Ren F;
PI Xue AD, Yang Y, Wehrman T, Drmanac RT;
PI WPI; 2002-292408/33.
DR N-PSDB; ABN32525.
XX
PT An isolated polynucleotide for treating diseases associated with its
PT encoded polypeptide such as cancer and multiple sclerosis.
XX
PS Example 2; SEQ ID NO 607; 509bp; English.
XX
CC The present invention provides the protein and coding sequences of 444
CC novel human proteins. These were isolated from expressed sequences tags
CC (ESTs). They can be used to treat aplastic anaemia, to help tissue regrowth
CC haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth
CC e.g. in burn treatment, to regulate the immune system e.g. to treat
CC multiple sclerosis, to regulate activin or inhibin e.g. to treat
CC infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke
CC and cancer, to screen for drugs, to treat inflammatory conditions e.g.

CC rheumatoid arthritis, and to treat nervous system disorders e.g.
 CC Parkinson's disease. The present sequence is a protein of the invention
 XX
 SQ Sequence 542 AA;

Query Match 100.0%; Score 2863; DB 5; Length 542;
 Best Local Similarity 100.0%; Pred. No. 1.5e-245;
 Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MGSNKSXPKQASQRRSLRLEPAENVHAGGAFPPASQTPSKPASADGHRGSAFAFAAAE 60
DB 1 MGSNKSXPKQASQRRSLRLEPAENVHAGGAFPPASQTPSKPASADGHRGSAFAFAAAE 60
QY 61 PKLPGFNSSDVTYSPQAGPLAGGVTTFVALYDYSERTDLSFKKGERLQIVNNTRKY 120
DB 61 PKLPGFNSSDVTYSPQAGPLAGGVTTFVALYDYSERTDLSFKKGERLQIVNNTRKY 120
QY 121 DVEBGDMWLHSLSTGQTGYIPSNYVAPSDSIQAEWYFGKITRRESERLLNAENPRGT 180
DB 121 DVEBGDMWLHSLSTGQTGYIPSNYVAPSDSIQAEWYFGKITRRESERLLNAENPRGT 180
QY 181 FLVRESETTKGAYCLSVDFDNAGKLVNKHKIRKLDGSGFYITSRTOFNSLQQLVAIYYS 240
DB 181 FLVRESETTKGAYCLSVDFDNAGKLVNKHKIRKLDGSGFYITSRTOFNSLQQLVAIYYS 240
QY 241 KHADGLCHRLITVCPYSPKQTOGLAKDAMEIPRESRLLEVKGCGCFGEVWMTNGTTR 300
DB 241 KHADGLCHRLITVCPYSPKQTOGLAKDAMEIPRESRLLEVKGCGCFGEVWMTNGTTR 300
QY 301 VALKTLKPGTMSPEAFLOEAQVMMKLRHEKLVQLYAVVSEBPIYITEYMSKSLDPLK 360
DB 301 VALKTLKPGTMSPEAFLOEAQVMMKLRHEKLVQLYAVVSEBPIYITEYMSKSLDPLK 360
QY 361 GETGKTLRLPOLYDMAAQIASGMAYVERMYVHRDLRAANILVGENLVCKVADFGIARLI 420
DB 361 GETGKTLRLPOLYDMAAQIASGMAYVERMYVHRDLRAANILVGENLVCKVADFGIARLI 420
QY 421 EDNEYTAROGAKFPIKWTAPBAALYGRFTIKSDVMSFGILLTETTKGRVPPGMVNRV 480
DB 421 EDNEYTAROGAKFPIKWTAPBAALYGRFTIKSDVMSFGILLTETTKGRVPPGMVNRV 480
QY 481 LDQVERGYRMPCEPCBESLHDLCCQMKRKEBERPTEFYLOAFLEDYFTSTBPQYQPG 540
DB 481 LDQVERGYRMPCEPCBESLHDLCCQMKRKEBERPTEFYLOAFLEDYFTSTBPQYQPG 540
QY 541 NL 542
DB 541 NL 542

RESULT 2
ADY84075 standard; protein; 542 AA.
ID ADY84075 standard; protein; 542 AA.
XX
AC ADY84075;
XX
XX 02-JUN-2005 (first entry)
XX
XX Human Src protein isoform 1 SEQ ID NO:1.
XX
XX pharmaceutical; Alzheimer's disease; neuroprotective; nootropic;
XX Src tyrosine kinase.
XX
XX Homo sapiens.
XX
XX EP1413887-A1.
XX
XX 28-APR-2004.
XX
XX 22-OCT-2002; 2002EP-00292608.
XX
XX 22-OCT-2002; 2002EP-00292608.
XX
XX

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PA (AVET) AVENTIS PHARMA SA.
 XX
 PI Mercken L, Zambrano N, Ruseo T;
 XX
 DR WPI; 2004-332834/31.
 XX
 PT Identifying therapeutic compound for treating Alzheimer's disease.
 PT Involves providing Src protein and determining inhibitory effect of
 PT compound on Src activity.

PS Claim 4; SEQ ID NO 1; 45pp; English.

XX
 CC The invention relates to a novel method for identifying (M) a
 CC therapeutic compound for the treatment of Alzheimer's disease, involving
 CC providing a Src protein and determining the inhibitory effect of a
 CC compound on the Src activity. The method optionally involves providing a
 CC sequence which regulates Src expression and determining if a compound
 CC inhibits the expression of Src protein. A compound of the invention has
 CC neuroprotective and nootropic activity. The compound identified by the
 CC method of the invention is useful for preparing a pharmaceutical for
 CC treating Alzheimer's disease. The present sequence represents isoform 1
 CC of human Src protein.

SQ Sequence 542 AA;

Query Match 100.0%; Score 2863; DB 8; Length 542;
 Best Local Similarity 100.0%; Pred. No. 1.5e-245;
 Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MGSNKSXPKQASQRRSLRLEPAENVHAGGAFPPASQTPSKPASADGHRGSAFAFAAAE 60
DB 1 MGSNKSXPKQASQRRSLRLEPAENVHAGGAFPPASQTPSKPASADGHRGSAFAFAAAE 60
QY 61 PKLPGFNSSDVTYSPQAGPLAGGVTTFVALYDYSERTDLSFKKGERLQIVNNTRKY 120
DB 61 PKLPGFNSSDVTYSPQAGPLAGGVTTFVALYDYSERTDLSFKKGERLQIVNNTRKY 120
QY 121 DVEBGDMWLHSLSTGQTGYIPSNYVAPSDSIQAEWYFGKITRRESERLLNAENPRGT 180
DB 121 DVEBGDMWLHSLSTGQTGYIPSNYVAPSDSIQAEWYFGKITRRESERLLNAENPRGT 180
QY 181 FLVRESETTKGAYCLSVDFDNAGKLVNKHKIRKLDGSGFYITSRTOFNSLQQLVAIYYS 240
DB 181 FLVRESETTKGAYCLSVDFDNAGKLVNKHKIRKLDGSGFYITSRTOFNSLQQLVAIYYS 240
QY 241 KHADGLCHRLITVCPYSPKQTOGLAKDAMEIPRESRLLEVKGCGCFGEVWMTNGTTR 300
DB 241 KHADGLCHRLITVCPYSPKQTOGLAKDAMEIPRESRLLEVKGCGCFGEVWMTNGTTR 300
QY 301 VALKTLKPGTMSPEAFLOEAQVMMKLRHEKLVQLYAVVSEBPIYITEYMSKSLDPLK 360
DB 301 VALKTLKPGTMSPEAFLOEAQVMMKLRHEKLVQLYAVVSEBPIYITEYMSKSLDPLK 360
QY 361 GETGKTLRLPOLYDMAAQIASGMAYVERMYVHRDLRAANILVGENLVCKVADFGIARLI 420
DB 361 GETGKTLRLPOLYDMAAQIASGMAYVERMYVHRDLRAANILVGENLVCKVADFGIARLI 420
QY 421 EDNEYTAROGAKFPIKWTAPBAALYGRFTIKSDVMSFGILLTETTKGRVPPGMVNRV 480
DB 421 EDNEYTAROGAKFPIKWTAPBAALYGRFTIKSDVMSFGILLTETTKGRVPPGMVNRV 480
QY 481 LDQVERGYRMPCEPCBESLHDLCCQMKRKEBERPTEFYLOAFLEDYFTSTBPQYQPG 540
DB 481 LDQVERGYRMPCEPCBESLHDLCCQMKRKEBERPTEFYLOAFLEDYFTSTBPQYQPG 540
QY 541 NL 542
DB 541 NL 542

RESULT 3
AAR39706 standard; protein; 536 AA.
ID AAR39706 standard; protein; 536 AA.

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XX AC AAR39706;
XX XX
XX DT 25-MAR-2003 (revised)
XX DT 23-DEC-1993 (first entry)
XX XX
XX DE Human pp60 c-src protein.
XX KM Endothelial; tyrosine kinase protein; pp60 c-src; ss.
XX XX
XX OS Homo sapiens.
XX XX
XX PN MO9314193-A1.
XX PD 22-JUL-1993.
XX XX
XX PF 05-JAN-1993; 93WO-US000445.
XX PR 06-JAN-1992; 92US-00820011.
XX PA (UYTA ) UNIV YALE.
XX PI Bell L, Madri JA, Warren SL, Luthringer DJ;
XX XX
XX DR WPI; 1993-243209/30.
XX DR P-PSDB; AAR39705.
XX PT Genetically engineered endothelial cells - which exhibit enhanced cell
XX PT migration, urokinase-type plasminogen activator activity, and reduced
XX PT mononuclear cell adhesion and fibronectin prodn.
XX PS Disclosure; Page 75-77; 91pp; English.
XX XX
XX CC The DNA encoding a portion or (more preferably) the entire pp60 c-src
XX CC polypeptide (Given in AAQ46688) is used to transform endothelial cells.
XX CC Transformed cells produce increased amounts of pp60 c-src and have
XX CC improved therapeutic properties. They migrate at faster rates than non-
XX CC transformed counterparts; have an enhanced ability to inhibit the
XX CC formation of thrombi and/or dissolve thrombi once they have formed and
XX CC exhibit reduced mononuclear cell adhesion. They can also be used to
XX CC improve the success of surgical procedures such as coronary angioplasty,
XX CC heart bypass surgery, vessel graft and stent implantation. (Updated on 25
XX CC -MAR-2003 to correct PN field.)
XX SQ Sequence 536 AA;

Query Match 98.5%; Score 2821; DB 2; Length 536;
Best Local Similarity 98.9%; Pred. No. 8.2e-242;
Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

QY 1 MGSNKSXPKDASQRRSLPEPAENVHAGAGFPAASQTPPSKPSADGHRGPSAAPAPAAE 60
DB 1 MGSNKSXPKDASQRRSLPEPAENVHAGAGFPAASQTPPSKPSADGHRGPSAAPAPAAE 60
QY 61 PKLPGFNSSSTVTTSFQAGPLAGCVTTFVALIYESTETEDLSFKKGERLQYNNTRKV 120
DB 61 PKLPGFNSSSTVTTSFQAGPLAGCVTTFVALIYESTETEDLSFKKGERLQYNNTRKV 120
DB 61 PKLPGFNSSSTVTTSFQAGPLAGCVTTFVALIYESTETEDLSFKKGERLQYNNTRKV 117
QY 121 DVREGBMWLHSLSTGQGTGYPSNYVAPSDSIQAEWYFGKITRRESERLLNENPQGT 180
DB 121 DVREGBMWLHSLSTGQGTGYPSNYVAPSDSIQAEWYFGKITRRESERLLNENPQGT 180
QY 118 ---EGDMWMLHSLSTGQGTGYPSNYVAPSDSIQAEWYFGKITRRESERLLNENPQGT 174
DB 118 ---EGDMWMLHSLSTGQGTGYPSNYVAPSDSIQAEWYFGKITRRESERLLNENPQGT 174
QY 181 FLVRESSTTKGAYCLSVSDPDNAKGLNVKHKIRKLDGSGFYITSRTQFNSLQQLVAYYS 240
DB 181 FLVRESSTTKGAYCLSVSDPDNAKGLNVKHKIRKLDGSGFYITSRTQFNSLQQLVAYYS 240
QY 175 FLVRESSTTKGAYCLSVSDPDNAKGLNVKHKIRKLDGSGFYITSRTQFNSLQQLVAYYS 234
DB 175 FLVRESSTTKGAYCLSVSDPDNAKGLNVKHKIRKLDGSGFYITSRTQFNSLQQLVAYYS 234
QY 241 KHAAGLCRLTLTTCPTSKPQTQGLAKDAMEIPRESLRLEVLDGGCFEGBVMWGTMGTR 300
DB 241 KHAAGLCRLTLTTCPTSKPQTQGLAKDAMEIPRESLRLEVLDGGCFEGBVMWGTMGTR 300
QY 235 KHAAGLCRLTLTTCPTSKPQTQGLAKDAMEIPRESLRLEVLDGGCFEGBVMWGTMGTR 294
DB 235 KHAAGLCRLTLTTCPTSKPQTQGLAKDAMEIPRESLRLEVLDGGCFEGBVMWGTMGTR 294
QY 301 VAIKTLKPGTMSPPAFLOEAQVMKKLRHEKLVOLYAVVSEPIYIVTEYMSKSLDPLK 360
DB 301 VAIKTLKPGTMSPPAFLOEAQVMKKLRHEKLVOLYAVVSEPIYIVTEYMSKSLDPLK 360
QY 295 VAIKTLKPGTMSPPAFLOEAQVMKKLRHEKLVOLYAVVSEPIYIVTEYMSKSLDPLK 354
DB 295 VAIKTLKPGTMSPPAFLOEAQVMKKLRHEKLVOLYAVVSEPIYIVTEYMSKSLDPLK 354
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QY 361 GENGKYLRLPOLVMAAQIASGMAVVERMNVYHRDLRANILVGENLVCKVADFGIARLI 420
DB 355 GETGYLRLPOLVMAAQIASGMAVVERMNVYHRDLRANILVGENLVCKVADFGIARLI 414
QY 421 EDNEYTARQGAKEPFIKMTAPALYGRFTTISDVMSFGILLTELTTKGRVYPCGVNREV 480
DB 415 EDNEYTARQGAKEPFIKMTAPALYGRFTTISDVMSFGILLTELTTKGRVYPCGVNREV 474
QY 481 LDQYRGYRMCPECEPSLHDLMCQCRKKEPERPFEYIQAFLDYFTSTEPQYQGE 540
DB 475 LDQYRGYRMCPECEPSLHDLMCQCRKKEPERPFEYIQAFLDYFTSTEPQYQGE 534
QY 541 NL 542
DB 535 NL 536

RESULT 4
ABG95123
ID ABG95123 standard; protein; 536 AA.
XX AC ABG95123;
XX XX
XX DT 04-DEC-2002 (first entry)
XX XX
XX DE Human v-src isoform.
XX XX
XX CC Chromosome aberration; oncogenic fusion protein; cancer; oncogene;
XX CC proliferative disease; cellular protein isoform; heat shock protein 90;
XX CC HSP-90; rheumatoid arthritis; cancer; hematopoietic disorder;
XX CC T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
XX CC acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
XX CC acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
XX CC papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
XX CC rhabdomyosarcoma; synovial sarcoma; viral infection.
XX OS Homo sapiens.
XX XX
XX PN WO200269900-A2.
XX XX
XX PD 12-SEP-2002.
XX XX
XX PF 01-MAR-2002; 2002WO-US006518.
XX PR 01-MAR-2001; 2001US-0272751P.
XX PA (CONF-) CONFORMA THERAPEUTICS CORP.
XX PI Fritz LC, Burrows PJ;
XX XX
XX DR WPI; 2002-698710/75.
XX DR N-PSDB; ABS73324.
XX PT Treating genetically-defined disease associated with chromosomal
XX PT aberrations yielding oncogenic fusion proteins; e.g. cell proliferative
XX PT diseases, involves administering an inhibitor of heat shock protein 90.
XX XX
XX PS Disclosure; Page 310-312; 389pp; English.
XX XX
XX CC The invention describes a method of treating genetically-defined disease
XX CC associated with chromosomal aberrations yielding oncogenic fusion
XX CC proteins (I), treating cancerous cells containing (I) in a heterogeneous
XX CC cell population, treating proliferative diseases associated with mutant
XX CC protein or cellular protein isoforms (II) dependent on heat shock protein
XX CC (HSP)-90, or selectively treating cells expressing (II) involving
XX CC administering HSP90-inhibitor. The method is useful for treating
XX CC genetically-defined disease with chromosomal aberration yielding
XX CC oncogenic fusion protein, treating cancerous cells containing fusion
XX CC protein in heterogeneous cell population, treating proliferative disease
XX CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
XX CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
XX CC p53), or selectively treating cells expressing mutant protein or cellular
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CC protein isoform in a patient heterozygous for (II). The method is useful
CC for treating a disease e.g. haematopoietic disorder such as T or B cell
CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CML,
CC or a disease characterised by a solid tumour such as papillary thyroid
CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
CC synovial sarcoma. The method is also useful for treating viral
CC infections. This is the amino acid sequence of a human oncogenic protein
XX

XX Sequence 536 AA;

Query Match 98.5%; Score 2821; DB 5; Length 536;

Best Local Similarity 98.9%; Pred. No. 8.2e-242;

Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

QY 1 MGSNKSXPXKASQRRSLRLEPAENVHAGGAGFAPSQTPSKPASADGHRGSAAPAAAE 60
DB 1 MGSNKSXPXKASQRRSLRLEPAENVHAGGAGFAPSQTPSKPASADGHRGSAAPAAAE 60

QY 61 PKLFGFNSSDTYTSPOKAGPLAGGVTTFVALYDYSRTEITDLSFKKGERLQIVNNTKV 120
DB 61 PKLFGFNSSDTYTSPOKAGPLAGGVTTFVALYDYSRTEITDLSFKKGERLQIVNNTKV 117

QY 121 DVBEGDWMLAHSLSTQGTGYIPSNYVAPSDSIQAEEMVFGKITRRESERLLNAENRGT 180
DB 118 ---EGDWMLAHSLSTQGTGYIPSNYVAPSDSIQAEEMVFGKITRRESERLLNAENRGT 174

QY 181 FLVRESETTGAGACLSVSDPDNAKGLNVKHYKIRKLDGSGFYTSRQFNSLQQLVAYYS 240
DB 175 FLVRESETTGAGACLSVSDPDNAKGLNVKHYKIRKLDGSGFYTSRQFNSLQQLVAYYS 234

QY 241 KHADGLCHRLTTCPTSKPOTQGLADAWIIPRESLRLEVLGQCGCFGEVWMTGNCTTR 300
DB 235 KHADGLCHRLTTCPTSKPOTQGLADAWIIPRESLRLEVLGQCGCFGEVWMTGNCTTR 294

QY 301 VAIKTLKPTGMSPEAFQEAQVMKRLHEKLVQLVAVSEPIYIVTEYMSKSLDPLK 360
DB 295 VAIKTLKPTGMSPEAFQEAQVMKRLHEKLVQLVAVSEPIYIVTEYMSKSLDPLK 354

QY 361 GEGKYLRLPOLVMAQIASGMAVYERMYVHNDLPAANILVGENIVCYVADGRLRL 420
DB 355 GEGKYLRLPOLVMAQIASGMAVYERMYVHNDLPAANILVGENIVCYVADGRLRL 414

QY 421 EDNEYTARQAGKFPKWTAPAEALYGRFTIKSDVMSFGILLTETLTGRVYPQMVAREV 480
DB 415 EDNEYTARQAGKFPKWTAPAEALYGRFTIKSDVMSFGILLTETLTGRVYPQMVAREV 474

QY 481 LDQVGRGYRMPCEPCESLHDLMCQCRKEPEERPTFEYLQAFLEDYFTSTEBQYQGE 540
DB 475 LDQVGRGYRMPCEPCESLHDLMCQCRKEPEERPTFEYLQAFLEDYFTSTEBQYQGE 534

QY 541 NL 542
DB 535 NL 536

RESULT 5

AAU78678

ID AAU78678 standard; protein; 536 AA.

XX

AC AAU78678;

XX

DT 18-JUN-2002 (first entry)

XX

DE Human SH2/SH3 domain containing protein, v-src.

XX

KM Protein profiling; c-src; SH2; SH3; antibody microarray;

KM protein microarray; DNA microarray; expression profiling; immunology;

XX

OS Homo sapiens.

XX

PN WO200214867-A2.

PD 21-FEB-2002.

PF 13-AUG-2001; 2001MO-US041709.

XX

XX 11-AUG-2000; 2000US-0224939P.

PR 12-APR-2001; 2001US-0283498P.

XX (AGIL-) AGILIX CORP.

PA

PI Chait BT, Latimer DR, Lizardi PM, Keshnar ER, Morrow JS;

PI Koch ME, Matcovich MJ, McConnell KJ;

XX WPI; 2002-304072/34.

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QY 301 VAITLKPGTMSPAFLQEAQVMKKLRHEKLVQLYAVVSEBPIYVTEYMSKSLDPLK 360
DB 295 VAITLKPGTMSPAFLQEAQVMKKLRHEKLVQLYAVVSEBPIYVTEYMSKSLDPLK 354
QY 361 GETGKYLRPLQVDMAAQIASGMAYVERMNVVHDLRAANILVGENLVCKVADFGIARLI 420
DB 355 GETGKYLRPLQVDMAAQIASGMAYVERMNVVHDLRAANILVGENLVCKVADFGIARLI 414
QY 421 EDNEYTRARQGAKEPIKWTAPPAALYGRFTIKSDVMSFGILLTELTTKGRVYPGVMNREV 480
DB 415 EDNEYTRARQGAKEPIKWTAPPAALYGRFTIKSDVMSFGILLTELTTKGRVYPGVMNREV 474
QY 481 LDQVERGYRMPCEPCEBSLHDLMCQCKRKEPERPFEYVQAFLEDFYFSTEPQYOPGE 540
DB 475 LDQVERGYRMPCEPCEBSLHDLMCQCKRKEPERPFEYVQAFLEDFYFSTEPQYOPGE 534
QY 541 NL 542
DB 535 NL 536
RESULT 6
ABP57260
ID ABP57260 standard; protein, 536 AA.
AC ABB57260;
XX 17-APR-2003 (first entry)
DT 17-APR-2003 (first entry)
XX
DE Human src-c protein SEQ ID NO:3.
XX
XX Human; src-c; tyrosine kinase; src-c inhibitor; cytostatic; osteopathic;
KM antiinflammatory; antibacterial; antisense therapy; vaccine; cancer;
KM antisense oligonucleotide; aberrant bone remodeling; breast cancer;
KM hyperproliferative disorder; pancreatic cancer; lung cancer; tumour;
KM ovarian cancer; oesophageal cancer; neuroblastoma; retinoblastoma;
KM Kaposi's sarcoma; infection; inflammation; tumour formation.
XX
OS Homo sapiens.
XX
PN WO200295053-A2.
XX
PD 28-NOV-2002.
XX
XX 16-MAY-2002; 2002MO-USO15684.
PF 16-MAY-2002; 2002MO-USO15684.
XX
PR 18-MAY-2001; 2001US-00860473.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett FC, Walt AT;
XX
PI WPI; 2003-120806/11.
DR N-PSDB; ABZ59382.
XX
XX
PT New antisense oligonucleotides targeted to nucleic acids encoding src-c,
PT useful for diagnosing, treating or preventing diseases associated with
PT the expression of src-c, e.g. cancer or inflammation, and in research
PT applications.
XX
PS Example 13; Page 97-100; 137pp; English.
XX
XX The present invention describes a compound (I) that is 8-50 nucleobases
CC in length targeted to a nucleic acid molecule encoding a 5'UTR, 3'UTR,
CC coding region, intron region, exon region, stop codon, intron:exon
CC junction, exon:exon junction, or 5' mRNA variant of src-c, and which
CC specifically hybridises with and inhibits the expression of src-c. (I)
CC have cytostatic, antiinflammatory, osteopathic and antibacterial
CC activities, and can be used in antisense therapy and in vaccines. The
CC antisense compounds (I) can be used for modulating the expression of src-
CC c and for treating diseases or conditions associated with expression of
CC src-c, e.g. aberrant bone remodeling or hyperproliferative disorders,
CC particularly cancer, such as breast cancer, pancreatic cancer, lung

CC cancer, ovarian cancer, oesophageal cancer, neuroblastoma, retinoblastoma
CC or Kaposi's sarcoma. (I) are also useful for diagnostic, therapeutics,
CC prophylaxis, e.g. to prevent or delay infection, inflammation or tumour
CC formation, as research reagents and kits, and in distinguishing between
CC functions of various members of a biological pathway. The present
CC sequence represents human src-c, which is used in an example from the
CC present invention
XX
SQ Sequence 536 AA;
Query Match 98.5%; Score 2821; DB 6; Length 536;
Best Local Similarity 98.9%; Pred. No. 8.2e-242;
Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;
QY 1 MGSNKSXPKQASQRRRLLEPAENVHAGGAGFPASQTPSPKASADGHRGSAAPPAAE 60
DB 1 MGSNKSXPKQASQRRRLLEPAENVHAGGAGFPASQTPSPKASADGHRGSAAPPAAE 60
QY 61 PKLFGFNSSDPTVTSPPQAGLAGVTFVALYDRESRTEDLSFKKGERLQIVNTRKV 120
DB 61 PKLFGFNSSDPTVTSPPQAGLAGVTFVALYDRESRTEDLSFKKGERLQIVNTRKV 117
QY 121 DVREGDWWLAHSLSTGQTGYIPSNYVAPSDSIQAEWYFGKITRRESERLLLNENPRGT 180
DB 118 ---EGDWWLAHSLSTGQTGYIPSNYVAPSDSIQAEWYFGKITRRESERLLLNENPRGT 174
QY 181 FLVRESSETTGAYCLSYSDPDNAKGLNVKHYKIRKLDGSGFYITSRQFNSLQOLVAYYS 240
DB 175 FLVRESSETTGAYCLSYSDPDNAKGLNVKHYKIRKLDGSGFYITSRQFNSLQOLVAYYS 234
QY 241 KHADGLCHRLTTVCPPTKSPQOGIAXDAWEIPRESLLEVLAGGCGREVMWGMGTNR 300
DB 235 KHADGLCHRLTTVCPPTKSPQOGIAXDAWEIPRESLLEVLAGGCGREVMWGMGTNR 294
QY 301 VAITLKPGTMSPAFLQEAQVMKKLRHEKLVQLYAVVSEBPIYVTEYMSKSLDPLK 360
DB 295 VAITLKPGTMSPAFLQEAQVMKKLRHEKLVQLYAVVSEBPIYVTEYMSKSLDPLK 354
QY 361 GETGKYLRPLQVDMAAQIASGMAYVERMNVVHDLRAANILVGENLVCKVADFGIARLI 420
DB 355 GETGKYLRPLQVDMAAQIASGMAYVERMNVVHDLRAANILVGENLVCKVADFGIARLI 414
QY 421 EDNEYTRARQGAKEPIKWTAPPAALYGRFTIKSDVMSFGILLTELTTKGRVYPGVMNREV 480
DB 415 EDNEYTRARQGAKEPIKWTAPPAALYGRFTIKSDVMSFGILLTELTTKGRVYPGVMNREV 474
QY 481 LDQVERGYRMPCEPCEBSLHDLMCQCKRKEPERPFEYVQAFLEDFYFSTEPQYOPGE 540
DB 475 LDQVERGYRMPCEPCEBSLHDLMCQCKRKEPERPFEYVQAFLEDFYFSTEPQYOPGE 534
QY 541 NL 542
DB 535 NL 536
RESULT 7
ADI20072
ID ADI20072 standard; protein, 536 AA.
XX
XX ADI20072;
XX
DT 22-APR-2004 (first entry)
XX
XX Human c-src.
XX
XX specific-binding agent; src; Cytostatic; Cardiant; Src-positive tumor;
KM heart disease.
XX
OS Homo sapiens.
XX
XX WO2003057238-A1.
XX
XX 17-JUL-2003.
PD

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XX 27-DEC-2002; 2002MO-US041564.
PF
XX
XX 28-DEC-2001; 2001US-0345888P.
XX
XX (UYOR-) UNIV OREGON HEALTH SCI.
XX
XX Schmitt JM, Stork PJS;
XX
XX WPI; 2003-587076/55.
XX
XX N-PSDB; ADI20071.
XX
XX
XX New specific-binding agent which specifically binds to Src when Src is
XX phosphorylated at serine-17 (Ser17) but does not detectably bind to Src
XX when Ser17 is not phosphorylated, useful for identifying abnormal cell
XX proliferation.
XX
XX Disclosure; SEQ ID NO 2; 40pp; English.
XX
XX
XX The present invention relates to a specific-binding agent which
XX specifically binds to Src when Src is phosphorylated at serine at
XX position 17 (Ser17) but does not detectably bind to Src when Ser17 is not
XX phosphorylated. The specific-binding agent is useful as a diagnostic
XX agent. The agent and the methods may also be used for treating Src-
XX positive tumors or heart disease. The present sequence represents human c-
XX Src.
XX
XX
XX Sequence 536 AA;
XX
XX
XX Query Match 98.5%; Score 2821; DB 7; Length 536;
XX Best Local Similarity 98.9%; Pred. No. 8.2e-242;
XX Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;
XX
XX 1 MGSNKSXPXKASQRRSLSPAENVHAGGAFPPASQTPSPKASADGHRGSAAPAPAAE 60
XX 1 MGSNKSXPXKASQRRSLSPAENVHAGGAFPPASQTPSPKASADGHRGSAAPAPAAE 60
XX
XX 61 PKLFGGNSDVTYSPQRAPIAGVTTFFVALYDYSRTETDLSFKKGERLQIVNTRKY 120
XX 61 PKLFGGNSDVTYSPQRAPIAGVTTFFVALYDYSRTETDLSFKKGERLQIVNTRKY 120
XX
XX 121 DVREGDWMHLAHSISTGQTGYIPSNYVAPSDSIQAEWYFGKTRRSEERLLNAENPRGT 180
XX 121 DVREGDWMHLAHSISTGQTGYIPSNYVAPSDSIQAEWYFGKTRRSEERLLNAENPRGT 180
XX
XX 118 ---EGDWMHLAHSISTGQTGYIPSNYVAPSDSIQAEWYFGKTRRSEERLLNAENPRGT 174
XX 118 ---EGDWMHLAHSISTGQTGYIPSNYVAPSDSIQAEWYFGKTRRSEERLLNAENPRGT 174
XX
XX 181 FLVRESEETTKGAYCLSVSDPDNAKGLNVKIKIRKLDGSGFYITTSRTQFNSLQQLVAYYS 240
XX 181 FLVRESEETTKGAYCLSVSDPDNAKGLNVKIKIRKLDGSGFYITTSRTQFNSLQQLVAYYS 240
XX
XX 175 FLVRESEETTKGAYCLSVSDPDNAKGLNVKIKIRKLDGSGFYITTSRTQFNSLQQLVAYYS 234
XX 175 FLVRESEETTKGAYCLSVSDPDNAKGLNVKIKIRKLDGSGFYITTSRTQFNSLQQLVAYYS 234
XX
XX 241 KHAHDGCHRLTTCYPSKPTQGLADKAMEIPRESLLEVKLQGGCGEYVMGWTNCTTR 300
XX 241 KHAHDGCHRLTTCYPSKPTQGLADKAMEIPRESLLEVKLQGGCGEYVMGWTNCTTR 300
XX
XX 235 KHAHDGCHRLTTCYPSKPTQGLADKAMEIPRESLLEVKLQGGCGEYVMGWTNCTTR 294
XX 235 KHAHDGCHRLTTCYPSKPTQGLADKAMEIPRESLLEVKLQGGCGEYVMGWTNCTTR 294
XX
XX 301 VAIKTLKPGTMSPEAFLOEAQVMKQLRHEKLVOLYAVVSEEPYIYVTEYMSKSLDPLK 360
XX 301 VAIKTLKPGTMSPEAFLOEAQVMKQLRHEKLVOLYAVVSEEPYIYVTEYMSKSLDPLK 360
XX
XX 295 VAIKTLKPGTMSPEAFLOEAQVMKQLRHEKLVOLYAVVSEEPYIYVTEYMSKSLDPLK 354
XX 295 VAIKTLKPGTMSPEAFLOEAQVMKQLRHEKLVOLYAVVSEEPYIYVTEYMSKSLDPLK 354
XX
XX 361 GETGKTLRLPQLVDMAAQIASGMAYYERNYVHRDLRANILVGENLVCKVADFGRLRLI 420
XX 361 GETGKTLRLPQLVDMAAQIASGMAYYERNYVHRDLRANILVGENLVCKVADFGRLRLI 420
XX
XX 355 GETGKTLRLPQLVDMAAQIASGMAYYERNYVHRDLRANILVGENLVCKVADFGRLRLI 414
XX 355 GETGKTLRLPQLVDMAAQIASGMAYYERNYVHRDLRANILVGENLVCKVADFGRLRLI 414
XX
XX 421 ENDEYARQAGAKPIKMTAPEALYGRFTIKSDVMSGILLTETTGKRPYVGMVNRV 480
XX 421 ENDEYARQAGAKPIKMTAPEALYGRFTIKSDVMSGILLTETTGKRPYVGMVNRV 480
XX
XX 415 ENDEYARQAGAKPIKMTAPEALYGRFTIKSDVMSGILLTETTGKRPYVGMVNRV 474
XX 415 ENDEYARQAGAKPIKMTAPEALYGRFTIKSDVMSGILLTETTGKRPYVGMVNRV 474
XX
XX 481 LDQVERGYRMPCEPCESESLHDLMLCCWKREPERPFESYLQAFLEDYFTSTEQVQGE 540
XX 481 LDQVERGYRMPCEPCESESLHDLMLCCWKREPERPFESYLQAFLEDYFTSTEQVQGE 540
XX
XX 475 LDQVERGYRMPCEPCESESLHDLMLCCWKREPERPFESYLQAFLEDYFTSTEQVQGE 534
XX 475 LDQVERGYRMPCEPCESESLHDLMLCCWKREPERPFESYLQAFLEDYFTSTEQVQGE 534
XX
XX 541 NL 542
XX 541 NL 542
XX
XX 535 NL 536
XX 535 NL 536

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RESULT 8
ADL22904
ID ADL22904 standard; protein, 536 AA.
XX
XX ADL22904;
XX
XX 20-MAY-2004 (first entry)
XX
XX Human MP2153 polypeptide sequence SEQ ID NO: 24.
XX
XX human; MP2153; p21; p53; cancer.
XX
XX Homo sapiens.
XX
XX WO2004015069-A2.
XX
XX 19-FEB-2004.
XX
XX 06-AUG-2003; 2003MO-US024505.
XX
XX 07-AUG-2002; 2002US-0401701P.
XX
XX 16-SEP-2002; 2002US-0411017P.
XX
XX 30-DEC-2002; 2002US-0437107P.
XX
XX (EXEL-) EXELIXIS INC.
XX
XX Francis-Liang H, Friedman L, Kidd T, Roche S, Belvin M;
XX Plozman GD, Lickteig K, Zhang H, Amundsen CD;
XX
XX WPI; 2004-180653/17.
XX
XX N-PSDB; ADL22887.
XX
XX
XX Identifying a candidate p21 or p53 pathway modulating agent using an
XX assay system having a modulator of p21 or p53 (MP2153) polypeptide or
XX p21 nucleic acid, useful for diagnosing or treating cancer, such as colon or
XX breast cancer.
XX
XX Example 3; Page 87-90; 110pp; English.
XX
XX
XX The present invention relates to a method of identifying a candidate p21
XX or p53 pathway modulating agent. This comprises providing an assay system
XX comprising a modulator of p21 or p53 (MP2153) polypeptide or nucleic
XX acid, contacting the assay system with a test agent, where in its
XX presence the system provides a reference activity, and detecting a test
XX agent-biased activity of the assay system, wherein a difference between
XX the test agent-biased activity and the reference activity identifies the
XX test agent as a candidate p21 or p53 pathway modulating agent. The
XX methods and compositions of the present invention are useful for the
XX diagnosis and/or treatment of diseases or conditions associated with
XX aberrant expression or activity of the p21 or p53 pathway, such as
XX cancer, preferably colon or head and neck cancer. The present sequence is
XX a human MP2153 protein sequence of the invention.
XX
XX
XX Sequence 536 AA;
XX
XX
XX Query Match 98.5%; Score 2821; DB 8; Length 536;
XX Best Local Similarity 98.9%; Pred. No. 8.2e-242;
XX Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;
XX
XX 1 MGSNKSXPXKASQRRSLSPAENVHAGGAFPPASQTPSPKASADGHRGSAAPAPAAE 60
XX 1 MGSNKSXPXKASQRRSLSPAENVHAGGAFPPASQTPSPKASADGHRGSAAPAPAAE 60
XX
XX 61 PKLFGGNSDVTYSPQRAPIAGVTTFFVALYDYSRTETDLSFKKGERLQIVNTRKY 120
XX 61 PKLFGGNSDVTYSPQRAPIAGVTTFFVALYDYSRTETDLSFKKGERLQIVNTRKY 120
XX
XX 121 DVREGDWMHLAHSISTGQTGYIPSNYVAPSDSIQAEWYFGKTRRSEERLLNAENPRGT 180
XX 121 DVREGDWMHLAHSISTGQTGYIPSNYVAPSDSIQAEWYFGKTRRSEERLLNAENPRGT 180
XX
XX 118 ---EGDWMHLAHSISTGQTGYIPSNYVAPSDSIQAEWYFGKTRRSEERLLNAENPRGT 174
XX 118 ---EGDWMHLAHSISTGQTGYIPSNYVAPSDSIQAEWYFGKTRRSEERLLNAENPRGT 174
XX
XX 181 FLVRESEETTKGAYCLSVSDPDNAKGLNVKIKIRKLDGSGFYITTSRTQFNSLQQLVAYYS 240
XX 181 FLVRESEETTKGAYCLSVSDPDNAKGLNVKIKIRKLDGSGFYITTSRTQFNSLQQLVAYYS 240

```

Db 175 FLVRESSTTGAYCLSVSDPDNAKGLNVKHKYIKRLDSGGFYITSRTOFNSLQOLVAYYS 234
|||
Qy 241 KHADGLCHRLTTCPTSKPOTQGLAKDAMEIPRESLRLEVKGCGCFGEVMMGTWNGTTR 300
235 KHADGLCHRLTTCPTSKPOTQGLAKDAMEIPRESLRLEVKGCGCFGEVMMGTWNGTTR 294
Qy 301 VAIKTLKPGTMSPEAPFLOEAOVMKKLRHEKLVQLYAVVSEBPITYITERNYSGSLDPLK 360
295 VAIKTLKPGTMSPEAPFLOEAOVMKKLRHEKLVQLYAVVSEBPITYITERNYSGSLDPLK 354
Qy 361 GETGKYLRPLQOLVMAAOIASGMAYVERMNVVHDDLAAANTLVGENIVCKVADGLARLI 420
355 GETGKYLRPLQOLVMAAOIASGMAYVERMNVVHDDLAAANTLVGENIVCKVADGLARLI 414
Db 421 EDNEYTAROGAKPFPIKWTAPBAALYGRFTIKSDVMSFGILLTTLTGRVVPQGVNREV 480
415 EDNEYTAROGAKPFPIKWTAPBAALYGRFTIKSDVMSFGILLTTLTGRVVPQGVNREV 474
Qy 481 LDQYRGYRMPCEPCEPSLHDLQCQCKRKEPERPFEYIQAFLBDFYFTSTEPQYORGE 540
475 LDQYRGYRMPCEPCEPSLHDLQCQCKRKEPERPFEYIQAFLBDFYFTSTEPQYORGE 534
Qy 541 NL 542
|||
Db 535 NL 536

RESULT 9

ADQ88400 standard; protein: 536 AA.

ID ADQ88400;

AC ADQ88400;

DT 07-OCT-2004 (first entry)

XX 07-OCT-2004 (first entry)

XX Human wild-type tyrosine kinase protein p60.

XX Cellular oncogene Src; c-Src; tyrosine kinase protein p60; cancer;

XX Infection; inflammation; tumour; gene therapy; human.

XX Homo sapiens.

XX US6764833-B1.

XX 20-JUL-2004.

XX 24-NOV-1999; 99US-00444711.

XX 24-NOV-1999; 99US-00444711.

XX (UYSF-) UNIV SOUTH FLORIDA.

XX Yeastman TJ, Irbay RB;

XX WPI; 2004-532511/51.

XX N-PSDB; ADQ88399.

XX New isolated c-Src tyrosine kinase polynucleotide, useful for treating

XX diseases associated or caused by mutant Src, cancer, or for preventing

XX infection, inflammation, or tumor formation.

XX Disclosure; SEQ ID NO 2; 29pp; English.

XX The invention relates to novel mutant cellular oncogene Src (c-Src) which

XX codes for mutant tyrosine kinase protein p60. c-Src sequences are useful

XX for treating diseases which are associated or caused by mutant Src. They

XX are useful for treating cancer, to delay or prevent infection,

XX inflammation or tumour formation. The invention is also useful in gene

XX therapy. The present sequence is human wild-type tyrosine kinase protein

XX p60.

XX Sequence 536 AA;

Query Match 98.5%; Score 2821; DB 8; Length 536;
Best Local Similarity 98.9%; Pred. No. 8.2e-242;
Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

Qy 1 MGSNKSXPDKASORRRSLRLEPENVHAGAGGAFPASQTPSPKASADGHRGSPAPAAAE 60
1 MGSNKSXPDKASORRRSLRLEPENVHAGAGGAFPASQTPSPKASADGHRGSPAPAAAE 60
Db 61 PKLFGFNSSDVTYTSPPORAPLAGVTFVALYDRESRTETDLSFKGGERLQIVNTRKV 120
61 PKLFGFNSSDVTYTSPPORAPLAGVTFVALYDRESRTETDLSFKGGERLQIVNTRKV 117
Qy 121 DVREGDWMLAHSJSTGQTGYTPSNYVAPSDSIQAEWYFGKITRRESRLLNANPRGT 180
118 ---EGDWMLAHSJSTGQTGYTPSNYVAPSDSIQAEWYFGKITRRESRLLNANPRGT 174
Db 181 FLVRESSTTGAYCLSVSDPDNAKGLNVKHKYIKRLDSGGFYITSRTOFNSLQOLVAYYS 240
175 FLVRESSTTGAYCLSVSDPDNAKGLNVKHKYIKRLDSGGFYITSRTOFNSLQOLVAYYS 234
Qy 241 KHADGLCHRLTTCPTSKPOTQGLAKDAMEIPRESLRLEVKGCGCFGEVMMGTWNGTTR 300
235 KHADGLCHRLTTCPTSKPOTQGLAKDAMEIPRESLRLEVKGCGCFGEVMMGTWNGTTR 294
Qy 301 VAIKTLKPGTMSPEAPFLOEAOVMKKLRHEKLVQLYAVVSEBPITYITERNYSGSLDPLK 360
295 VAIKTLKPGTMSPEAPFLOEAOVMKKLRHEKLVQLYAVVSEBPITYITERNYSGSLDPLK 354
Qy 361 GETGKYLRPLQOLVMAAOIASGMAYVERMNVVHDDLAAANTLVGENIVCKVADGLARLI 420
355 GETGKYLRPLQOLVMAAOIASGMAYVERMNVVHDDLAAANTLVGENIVCKVADGLARLI 414
Db 421 EDNEYTAROGAKPFPIKWTAPBAALYGRFTIKSDVMSFGILLTTLTGRVVPQGVNREV 480
415 EDNEYTAROGAKPFPIKWTAPBAALYGRFTIKSDVMSFGILLTTLTGRVVPQGVNREV 474
Qy 481 LDQYRGYRMPCEPCEPSLHDLQCQCKRKEPERPFEYIQAFLBDFYFTSTEPQYORGE 540
475 LDQYRGYRMPCEPCEPSLHDLQCQCKRKEPERPFEYIQAFLBDFYFTSTEPQYORGE 534
Qy 541 NL 542
|||
Db 535 NL 536

RESULT 10

ADQ97772 standard; protein: 536 AA.

ID ADQ97772;

AC ADQ97772;

DT 07-OCT-2004 (first entry)

XX 07-OCT-2004 (first entry)

XX Human cancer associated sequence HP10-043, SEQ ID 749.

XX Cytostatic; Gene Therapy; cancer; leukemia; lymphoma; Human.

XX Homo sapiens.

XX WO2004060304-A2.

XX 22-JUL-2004.

XX 22-DEC-2003; 2003WO-US041389.

XX 27-DEC-2002; 2002US-00330773.

XX (SAGR-) SAGRES DISCOVERY INC.

XX Morris DW, Malandro MS;

XX WPI; 2004-543781/52.

XX New isolated cancer associated nucleic acids comprising at least 10
PT contiguous nucleotides, useful for diagnosing, preventing and/or treating
PT cancers such as leukemia and lymphoma.
XX
XX Claim 1; SEQ ID NO 749; 199pp; English.
XX
XX The present invention relates to cancer associated sequences (ADQ97025-
CC ADQ98004). The sequences are useful for the diagnosis, prevention and/or
CC treatment of cancer, such as leukemia and lymphoma. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 536 AA.

Query Match 98.5%; Score 2821; DB 8; Length 536;
Best Local Similarity 98.9%; Pred. No. 8.2e-242;
Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

QY 1 MGSNKKPKDASQRRSLPEAENVHAGGAFPASQTPSKPASADGHRGSAAPAAAE 60
Db 1 MGSNKKPKDASQRRSLPEAENVHAGGAFPASQTPSKPASADGHRGSAAPAAAE 60
QY PKLFGGFNSSDVTSPQRAGPLAGVTFVALYDYESRTETDLSFKKGERLQIVNNTKV 120
Db 61 PKLFGGFNSSDVTSPQRAGPLAGVTFVALYDYESRTETDLSFKKGERLQIVNNTKV 117
QY 121 DVREGDMWMLAHSISTGQTGYIPSNVYAPSDSIQAEEMVFGKTRRESERLLNAENPRGT 180
Db 118 ---EGDMWMLAHSISTGQTGYIPSNVYAPSDSIQAEEMVFGKTRRESERLLNAENPRGT 174
QY 181 FLVRESETTKGAYCLSVSDFDNAKGLNVKIKRKLDGSGFYITSRTQFNSLQQLVAAYS 240
Db 175 FLVRESETTKGAYCLSVSDFDNAKGLNVKIKRKLDGSGFYITSRTQFNSLQQLVAAYS 234
QY 241 KHADGCLRLLTTCPTSKPQTQGLAKDAMEIPRESLLEVKLGQGCGEVWMTGTTTR 300
Db 235 KHADGCLRLLTTCPTSKPQTQGLAKDAMEIPRESLLEVKLGQGCGEVWMTGTTTR 294
QY 301 VAIKTLKPGTMSPEAFLOEAQVKKLRHEKLVOLYAVVSEEPYIVTEYMSKSLDPLK 360
Db 295 VAIKTLKPGTMSPEAFLOEAQVKKLRHEKLVOLYAVVSEEPYIVTEYMSKSLDPLK 354
QY 361 GEGTKRLRLPOLYDMAQAISGMAVYERMYVHRDLAANIIVGENLVCCVADFGRLRI 420
Db 355 GEGTKRLRLPOLYDMAQAISGMAVYERMYVHRDLAANIIVGENLVCCVADFGRLRI 414
QY 421 EDNEYTARQAGKFPKWTAPREALYGRFTIKSDVMSFGILLTETLTKGRVPYFGMVREV 480
Db 415 EDNEYTARQAGKFPKWTAPREALYGRFTIKSDVMSFGILLTETLTKGRVPYFGMVREV 474
QY 481 LDQVERGYRMPCEPECESLHDLMCQWRKEPERPTFEYLQAFLEDTFTSTPEOYQGE 540
Db 475 LDQVERGYRMPCEPECESLHDLMCQWRKEPERPTFEYLQAFLEDTFTSTPEOYQGE 534
QY 541 NL 542
Db 535 NL 536

RESULT 11
ADU04517
ID ADU04517 standard; peptide; 536 AA.
XX
XX ADU04517;
XX
XX 13-JUN-2005 (first entry)
XX
XX Protein tyrosine kinase Src.
XX
XX Protein tyrosine kinase; Src; proto-oncogene; phosphorylation;
XX protein structure; enzyme; EC_2.7.1.112.

XX Unidentified.
OS
XX Key Location/Qualifiers
FH Modified-site 216
FT Modified-site /note="Tyr phosphorylation site"
FT Modified-site 419
FT Modified-site /note="Tyr phosphorylation site"
FT Modified-site 530
FT Modified-site /note="Tyr phosphorylation site"
XX
XX WO2004092703-A2.
XX
XX 28-OCT-2004.
XX
XX 09-APR-2004; 2004MO-US010834.
XX
XX 11-APR-2003; 2003US-0462083P.
XX 11-APR-2003; 2003US-0462472P.
XX 25-JUL-2003; 2003US-0490057P.
XX 08-MAR-2004; 2004US-0551311P.
XX 19-MAR-2004; 2004US-0554701P.
XX 08-APR-2004; 2004US-00821231.
XX
XX (Purd) PURDUE RES FOUND.
XX
XX Zhang D, Amotz B, Xie Y, Davison VJ, Mrozek M, Ortiz C;
XX WPI; 2004-784629/77.
XX
XX Obtaining structural characteristic information for separation and
PT detection of e.g. proteins comprises irradiating a region formed by
PT evaporating specimen-containing solvent in a droplet on planar solvo-
PT phobic sample support.
XX
XX Example C; Page 25; 91pp; English.
XX
XX The present sequence is that of proto-oncogene protein tyrosine kinase
CC Src (p60-src, c-src). The invention relates to the combined use of solid
CC substrates, micro-deposition techniques, spectral imaging methods, and
CC data processing to facilitate the concentration and separate detection of
CC biological molecules including proteins, peptides, polysaccharides,
CC glycans and nucleotides, in a liquid mixture, using spectral analysis
CC such as normal Raman spectroscopy, infrared spectroscopy and matrix-
CC assisted laser desorption/ionization (MALDI) time-of-flight mass
CC spectrometry. The methods were demonstrated in examples from the high
CC resolution using peptide fragments of Src. These demonstrated the high
CC level of analyte discrimination that can be achieved and that the method
CC can be used to detect and quantify Tyr phosphorylation in tryptic digests
CC of physiologically important proteins.
XX
XX Sequence 536 AA;

Query Match 98.5%; Score 2821; DB 8; Length 536;
Best Local Similarity 98.9%; Pred. No. 8.2e-242;
Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

QY 1 MGSNKKPKDASQRRSLPEAENVHAGGAFPASQTPSKPASADGHRGSAAPAAAE 60
Db 1 MGSNKKPKDASQRRSLPEAENVHAGGAFPASQTPSKPASADGHRGSAAPAAAE 60
QY 61 PKLFGGFNSSDVTSPQRAGPLAGVTFVALYDYESRTETDLSFKKGERLQIVNNTKV 120
Db 61 PKLFGGFNSSDVTSPQRAGPLAGVTFVALYDYESRTETDLSFKKGERLQIVNNTKV 117
QY 121 DVREGDMWMLAHSISTGQTGYIPSNVYAPSDSIQAEEMVFGKTRRESERLLNAENPRGT 180
Db 118 ---EGDMWMLAHSISTGQTGYIPSNVYAPSDSIQAEEMVFGKTRRESERLLNAENPRGT 174
QY 181 FLVRESETTKGAYCLSVSDFDNAKGLNVKIKRKLDGSGFYITSRTQFNSLQQLVAAYS 240
Db 175 FLVRESETTKGAYCLSVSDFDNAKGLNVKIKRKLDGSGFYITSRTQFNSLQQLVAAYS 234

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QY 241 KHADGLCHRLTTVCPTSKPOTGLAKDAMEIPRESLRLEVLGGCCFGEVMMGTNGTTR 300
DB 235 KHADGLCHRLTTVCPTSKPOTGLAKDAMEIPRESLRLEVLGGCCFGEVMMGTNGTTR 294
QY 301 VAIKTLKPGTMSPEAFIOEAQVMKKLRHEKLVOLYAVVSEBPIYIVTEYMSKSLDPLK 360
DB 295 VAIKTLKPGTMSPEAFIOEAQVMKKLRHEKLVOLYAVVSEBPIYIVTEYMSKSLDPLK 354
QY 361 GETGKYLRPLPOLVMAAQAISGMAVVERMNVYHDLRAANILVGENLVCKVADFGIARLI 420
DB 355 GETGKYLRPLPOLVMAAQAISGMAVVERMNVYHDLRAANILVGENLVCKVADFGIARLI 414
QY 421 EDNEYTAROGAKFPKIKWTAPPAALYGRFTIKSDVWSFGILLTELTTKGRVYPPGVNREV 480
DB 415 EDNEYTAROGAKFPKIKWTAPPAALYGRFTIKSDVWSFGILLTELTTKGRVYPPGVNREV 474
QY 481 LDQVERGYRMPCEPCESLHDLMCQCCKRKEPERPTEFYLOAFLEDFYFSTEPQYORGE 540
DB 475 LDQVERGYRMPCEPCESLHDLMCQCCKRKEPERPTEFYLOAFLEDFYFSTEPQYORGE 534
QY 541 NL 542
DB 535 NL 536
```

RESULT 12
ADV84076 standard; protein; 536 AA.

```
XX AC ADV84076;
XX DT 02-JUN-2005 (first entry)
XX DE Human Src protein isoform 2 SEQ ID NO:2.
XX KW pharmaceutical; Alzheimer's disease; neuroprotective; nootropic;
XX OS Homo sapiens.
XX PN BP1413887-A1.
XX PD 28-APR-2004.
XX PF 22-OCT-2002; 2002EP-00292608.
XX PR 22-OCT-2002; 2002EP-00292608.
XX PA (AVENTIS PHARMA SA.
XX PI MerckKen L, Zambrano N, Russo T;
XX DR WPI; 2004-332834/31.
XX PT Identifying therapeutic compound for treating Alzheimer's disease,
XX PT involves providing Src protein and determining inhibitory effect of
XX PS compound on Src activity.
XX PS Claim 4; SEQ ID NO 2; 45pp; English.
```

```
XX CC The invention relates to a novel method for identifying (M1) a
XX CC therapeutic compound for the treatment of Alzheimer's disease, involving
XX CC providing a Src protein and determining the inhibitory effect of a
XX CC compound on the Src activity. The method optionally involves providing a
XX CC sequence which regulates Src expression and determining if a compound
XX CC inhibits the expression of Src protein. A compound of the invention has
XX CC neuroprotective and nootropic activity. The compound identified by the
XX CC method of the invention is useful for preparing a pharmaceutical for
XX CC treating Alzheimer's disease. The present sequence represents isoform 2
XX CC of human Src protein.
XX SQ Sequence 536 AA;
```

Query Match 98.5%; Score 2821; DB 8; Length 536;
Best Local Similarity 98.9%; Pred. No. 8.2e-242;
Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

```
QY 1 MGSNKSXPKQASQRRSLPEAENVHAGGAFPPASQTPSKPASADGHRGPSAAFPAPAAE 60
DB 1 MGSNKSXPKQASQRRSLPEAENVHAGGAFPPASQTPSKPASADGHRGPSAAFPAPAAE 60
QY 61 PKLFGGNSSPTVTSPPQAGPLAGGVTFVALIYTESSTENDLSFKKEERQIVNNTKV 120
DB 61 PKLFGGNSSPTVTSPPQAGPLAGGVTFVALIYTESSTENDLSFKKEERQIVNNTKV 117
QY 121 DVREGDWMLAHSLSGTGGYI PSNYVAPSDSIQAEEMVFGKITRRESRLLLNANPRGT 180
DB 118 --BGDWMLAHSLSGTGGYI PSNYVAPSDSIQAEEMVFGKITRRESRLLLNANPRGT 174
QY 181 FLVSEETTKGAYCLSVSDPDNAKGLNVKHKIKLDSGGFYITSRTQFNSLQQLVAYYS 240
DB 175 FLVSEETTKGAYCLSVSDPDNAKGLNVKHKIKLDSGGFYITSRTQFNSLQQLVAYYS 234
QY 241 KHADGLCHRLTTVCPTSKPOTGLAKDAMEIPRESLRLEVLGGCCFGEVMMGTNGTTR 300
DB 235 KHADGLCHRLTTVCPTSKPOTGLAKDAMEIPRESLRLEVLGGCCFGEVMMGTNGTTR 294
QY 301 VAIKTLKPGTMSPEAFIOEAQVMKKLRHEKLVOLYAVVSEBPIYIVTEYMSKSLDPLK 360
DB 295 VAIKTLKPGTMSPEAFIOEAQVMKKLRHEKLVOLYAVVSEBPIYIVTEYMSKSLDPLK 354
QY 361 GETGKYLRPLPOLVMAAQAISGMAVVERMNVYHDLRAANILVGENLVCKVADFGIARLI 420
DB 355 GETGKYLRPLPOLVMAAQAISGMAVVERMNVYHDLRAANILVGENLVCKVADFGIARLI 414
QY 421 EDNEYTAROGAKFPKIKWTAPPAALYGRFTIKSDVWSFGILLTELTTKGRVYPPGVNREV 480
DB 415 EDNEYTAROGAKFPKIKWTAPPAALYGRFTIKSDVWSFGILLTELTTKGRVYPPGVNREV 474
QY 481 LDQVERGYRMPCEPCESLHDLMCQCCKRKEPERPTEFYLOAFLEDFYFSTEPQYORGE 540
DB 475 LDQVERGYRMPCEPCESLHDLMCQCCKRKEPERPTEFYLOAFLEDFYFSTEPQYORGE 534
QY 541 NL 542
DB 535 NL 536
```

RESULT 13
ADV94834 standard; protein; 536 AA.

```
XX AC ADV94834;
XX DT 10-MAR-2005 (first entry)
XX DE Human wild type c-Src protein.
XX KW cytoskeletal; gene therapy; mutagenesis; tumor; sarcoma; neuroblastoma;
XX KW breast carcinoma; c-Src; tyrosine kinase inhibitor; enzyme.
XX OS Homo sapiens.
```

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XX PN US2004261142-A1.
XX PD 23-DEC-2004.
XX PF 09-JUN-2004; 2004US-00887588.
XX PR 24-NOV-1999; 99US-00444711.
XX PA (YEATMAN T J.
XX PA (IRBY/) IRBY R B.
XX PI Yeatman TJ, Irby RB;
```

DR WPI: 2005-038910/04.
 DR N-PSDB; ADV94833.
 XX New truncated c-Src polypeptide, useful for treating and/or preventing
 PT clinical conditions associated with or caused by Src mutation, e.g.
 PT tumors.
 XX
 XX Disclosure; SEQ ID NO 2; 28pp; English.
 XX
 CC The invention relates to a truncated c-Src polypeptide comprising a
 CC sequence of 530 amino acids given in the specification. The polypeptide,
 CC composition and method are useful for treating and/or preventing clinical
 CC conditions associated with or caused by Src mutation e.g. tumors
 CC (sarcoma, neuroblastoma, breast carcinoma). This sequence corresponds to
 CC the wild type c-Src protein.
 XX
 XX Sequence 536 AA:
 SQ
 Query Match 98.5%; Score 2821; DB 9; Length 536;
 Best Local Similarity 98.9%; Pred. No. 8.2e-242;
 Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;
 QY 1 MGSNKSXPDOASQRRSLPEAENVHAGGAGFAPASQTPSKPASADGHRGSAAPAPAAAE 60
 DB 1 MGSNKSXPDOASQRRSLPEAENVHAGGAGFAPASQTPSKPASADGHRGSAAPAPAAAE 60
 QY PKLFGFNSSDVTYTSQORAGPLAGGTTFTVALYDYSRTETDLSFKKGERLQIVNTRKY 120
 DB 61 PKLFGFNSSDVTYTSQORAGPLAGGTTFTVALYDYSRTETDLSFKKGERLQIVNTRKY 117
 QY 121 DVREGDMWLAHSISTQGTGYPNSNYVAPSDSIQAEEMYPFKITRRRESERLLNAENPRGT 180
 DB 118 ---EGDMWLAHSISTQGTGYPNSNYVAPSDSIQAEEMYPFKITRRRESERLLNAENPRGT 174
 QY 181 FLVRESEETTKGAYCLSVSDFDNAKGLNVKXIKRLKDSGGFYITTSRTQFNSLQOLVAYYS 240
 DB 175 FLVRESEETTKGAYCLSVSDFDNAKGLNVKXIKRLKDSGGFYITTSRTQFNSLQOLVAYYS 234
 QY 241 KHADGCHLUTTCPTSPKPTQGLANDAMEIPRESLRLEFKLQGGCGEYVMGTNGTTR 300
 DB 235 KHADGCHLUTTCPTSPKPTQGLANDAMEIPRESLRLEFKLQGGCGEYVMGTNGTTR 294
 QY 301 VAIKTLKPGTMSPEAFLOEAQVMKCLRHEKLVOLYAVVSEPIYIVTEYMSKSLDLFLK 360
 DB 295 VAIKTLKPGTMSPEAFLOEAQVMKCLRHEKLVOLYAVVSEPIYIVTEYMSKSLDLFLK 354
 QY 361 GETGKYLRLPOLVDMAAQIASGNAVYERNMYVARDLRANILVGENLVCKVADFGIARLI 420
 DB 355 GETGKYLRLPOLVDMAAQIASGNAVYERNMYVARDLRANILVGENLVCKVADFGIARLI 414
 QY 421 EDNEYTAROGAKRPKMTAPBALYGRFTKSDVWSFGILLTELTKGRVPYFGMNVREV 480
 DB 415 EDNEYTAROGAKRPKMTAPBALYGRFTKSDVWSFGILLTELTKGRVPYFGMNVREV 474
 QY 481 LDOVEGYNMPCCPECPESLHDMCCOMRKEPERPFEXLOAFLEDYFTSTPEYOXPGE 540
 DB 475 LDOVEGYNMPCCPECPESLHDMCCOMRKEPERPFEXLOAFLEDYFTSTPEYOXPGE 534
 QY 541 NL 542
 DB 535 NL 536
 RESULT 14
 AEA35914
 ID AEA35914 standard; protein; 536 AA.
 XX
 AC AEA35914;
 XX
 XX 25-AUG-2005 (first entry)
 DT
 XX Human Src kinase amino acid sequence SEQ ID NO:1.
 DE
 XX

KM Src family kinase; Src kinase.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT MISC-difference 238
 FT /note= "constant amino acid K in domain SH2"
 FT MISC-difference 341
 FT /note= "constant amino acid T in domain SH2"
 FT MISC-difference 530
 FT /note= "constant amino acid Y in domain SH1"
 PN EP1541694-A1.
 PD 15-JUN-2005.
 XX
 XX 12-DEC-2003; 2003EP-00028713.
 XX
 PR 12-DEC-2003; 2003EP-00028713.
 XX
 PA (SIRE-) SIRENADE PHARM AG.
 XX
 PI Obermeier A, Bieger B;
 XX
 DR WPI: 2005-428084/44.
 XX
 PT Identifying compound which modulates Src family kinase (SFK) activity, by
 PT contacting cells expressed with SFK or mutated SFK with test compound,
 PT where change in phenotype of cells indicates that test compound modulates
 PT SFK activity.
 XX
 XX Disclosure; SEQ ID NO 1; 114pp; English.
 PS
 XX
 XX The invention relates to a method (M1) for identifying, selecting and/or
 CC characterizing a compound which modulates Src family kinase (SFK)
 CC activity, by expressing nucleic acids encoding SFK or mutated SFK in
 CC cells, contacting cells with test compound and determining whether
 CC phenotype of cells is changed as compared with phenotype of cells not
 CC expressed with above nucleic acids, where difference in phenotype
 CC indicates that test compound modulate SFK activity. Also described: (1) a
 CC compound (I) identified, selected and/or characterized by (M1); and (2) a
 CC pharmaceutical composition (PCI) containing (I), and a carrier, adjuvant
 CC or vehicle. (I) is useful as a medicament, particularly for the treatment
 CC of diseases, which are at least in part caused by a Src family kinase.
 CC (I) and PCI are useful for producing a medicament for the treatment of
 CC diseases, which are at least in part caused by a Src family kinase,
 CC particularly by a dysfunction of a Src family kinase, in particular
 CC cancer, hypercalcemia, restenosis, osteoporosis, osteoarthritis,
 CC symptomatic treatment of bone metastasis, rheumatoid arthritis,
 CC inflammatory bowel disease, multiple sclerosis, psoriasis, lupus, graft
 CC versus host disease, T-cell mediated hypersensitivity disease,
 CC Hashimoto's thyroiditis, Guillain-Barre syndrome, chronic obstructive
 CC pulmonary disorder, contact dermatitis, Paget's disease, asthma, ischemic
 CC or reperfusion injury, allergic disease, atopic dermatitis, transplant
 CC rejection or allergic rhinitis. The present sequence represents human Src
 CC kinase, which is given in the exemplification of the present invention.
 XX
 XX Sequence 536 AA:
 SQ
 Query Match 98.5%; Score 2821; DB 9; Length 536;
 Best Local Similarity 98.9%; Pred. No. 8.2e-242;
 Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;
 QY 1 MGSNKSXPDOASQRRSLPEAENVHAGGAGFAPASQTPSKPASADGHRGSAAPAPAAAE 60
 DB 1 MGSNKSXPDOASQRRSLPEAENVHAGGAGFAPASQTPSKPASADGHRGSAAPAPAAAE 60
 QY PKLFGFNSSDVTYTSQORAGPLAGGTTFTVALYDYSRTETDLSFKKGERLQIVNTRKY 120
 DB 61 PKLFGFNSSDVTYTSQORAGPLAGGTTFTVALYDYSRTETDLSFKKGERLQIVNTRKY 117
 QY 121 DVREGDMWLAHSISTQGTGYPNSNYVAPSDSIQAEEMYPFKITRRRESERLLNAENPRGT 180
 DB 118 ---EGDMWLAHSISTQGTGYPNSNYVAPSDSIQAEEMYPFKITRRRESERLLNAENPRGT 174

Db 118 ---EGDWMLAHSLSTGQTGYIPSNYVAPSDSIQAEMVYFGKITRRESERLLNLENPRGT 174
 QY 181 FLVRESSTTGAYCLSYSDPDNAGLVNKHKIKRLDSGGYITSRTOFNSLQOLVAYYS 240
 Db 175 FLVRESSTTGAYCLSYSDPDNAGLVNKHKIKRLDSGGYITSRTOFNSLQOLVAYYS 234
 QY 241 KHAAGLCHRLTTVCPSTKPTQGLAKDAMEIPRESLRLEVLAGGCGFGEVMMGTWNGTTR 300
 Db 235 KHAAGLCHRLTTVCPSTKPTQGLAKDAMEIPRESLRLEVLAGGCGFGEVMMGTWNGTTR 294
 QY 301 VAITLKPGTMSPEAFLOEAQVMKKLRHEKLVQLYAVVSEBPIYIVTEYMSKSLDPLK 360
 Db 295 VAITLKPGTMSPEAFLOEAQVMKKLRHEKLVQLYAVVSEBPIYIVTEYMSKSLDPLK 354
 QY 361 GETGKYRLPOLVMAAQIASGMAYVERMNVHRDLAANILVGENLVCKVADFGLARLI 420
 Db 355 GETGKYRLPOLVMAAQIASGMAYVERMNVHRDLAANILVGENLVCKVADFGLARLI 414
 QY 421 EDNEYTAROGAKFPDKMTAPPAALYGRFTIKSDVMSFGILLTETTTGGRVYPGMVNRV 480
 Db 415 EDNEYTAROGAKFPDKMTAPPAALYGRFTIKSDVMSFGILLTETTTGGRVYPGMVNRV 474
 QY 481 LDQVERGYRMPCEPCESLHDLQCQCRKEPBERPTEFYLOAFLEDFYFTSTEPQYQGE 540
 Db 475 LDQVERGYRMPCEPCESLHDLQCQCRKEPBERPTEFYLOAFLEDFYFTSTEPQYQGE 534
 QY 541 NL 542
 Db 535 NL 536

RESULT 15

ADY84080 standard; protein; 549 AA.

ADY84080;

02-JUN-2005 (first entry)

Human Src cDNA encoded amino acid #1.

pharmaceutical; Alzheimer's disease; neuroprotective; nootropic;

Src tyrosine kinase.

Homo sapiens.

EPI413887-A1.

28-APR-2004.

22-OCT-2002; 2002EP-00292608.

22-OCT-2002; 2002EP-00292608.

(AVENTIS PHARMA SA.

Mercken L, Zambirano N, Russo T;

WPI; 2004-332834/31.

N-PSDB; ADY84078.

Identifying therapeutic compound for treating Alzheimer's disease,

involves providing Src protein and determining inhibitory effect of

compound on Src activity.

Disclosure; SEQ ID NO 4; 45bp; English.

The invention relates to a novel method for identifying (M1) a
 therapeutic compound for the treatment of Alzheimer's disease, involving
 providing a Src protein and determining the inhibitory effect of a
 compound on the Src activity. The method optionally involves providing a
 sequence which regulates Src expression and determining if a compound
 inhibits the expression of Src protein. A compound of the invention has

CC neuroprotective and nootropic activity. The compound identified by the
 CC method of the invention is useful for preparing a pharmaceutical for
 CC treating Alzheimer's disease. The present sequence is encoded by the
 CC human Src cDNA. The sequence is represented as part of SEQ ID NO:4 in the
 CC sequence listing of the specification.

SO Sequence 549 AA;

Query Match 98.5%; Score 2821; DB 8; Length 549;
 Best Local Similarity 98.9%; Pred. No. 8.6e-242;
 Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

QY 1 MGSNKSXPKASORRSLBPENYVHAGGAFPAQSOTPSKXPASADGHRGPAAPAAAE 60
 Db 14 MGSNKSXPKASORRSLBPENYVHAGGAFPAQSOTPSKXPASADGHRGPAAPAAAE 73
 QY 61 PKLFGFNSSDPTVTSPPRAGPLAGVTTFVALYDRESRTETDLSFKKGERLQIVNNT 120
 Db 74 PKLFGFNSSDPTVTSPPRAGPLAGVTTFVALYDRESRTETDLSFKKGERLQIVNNT 130
 QY 121 DVREGDWMLAHSLSTGQTGYIPSNYVAPSDSIQAEMVYFGKITRRESERLLNLENPRGT 180
 Db 131 ---EGDWMLAHSLSTGQTGYIPSNYVAPSDSIQAEMVYFGKITRRESERLLNLENPRGT 187
 QY 181 FLVRESSTTGAYCLSYSDPDNAGLVNKHKIKRLDSGGYITSRTOFNSLQOLVAYYS 240
 Db 188 FLVRESSTTGAYCLSYSDPDNAGLVNKHKIKRLDSGGYITSRTOFNSLQOLVAYYS 247
 QY 241 KHAAGLCHRLTTVCPSTKPTQGLAKDAMEIPRESLRLEVLAGGCGFGEVMMGTWNGTTR 300
 Db 248 KHAAGLCHRLTTVCPSTKPTQGLAKDAMEIPRESLRLEVLAGGCGFGEVMMGTWNGTTR 307
 QY 301 VAITLKPGTMSPEAFLOEAQVMKKLRHEKLVQLYAVVSEBPIYIVTEYMSKSLDPLK 360
 Db 308 VAITLKPGTMSPEAFLOEAQVMKKLRHEKLVQLYAVVSEBPIYIVTEYMSKSLDPLK 367
 QY 361 GETGKYRLPOLVMAAQIASGMAYVERMNVHRDLAANILVGENLVCKVADFGLARLI 420
 Db 368 GETGKYRLPOLVMAAQIASGMAYVERMNVHRDLAANILVGENLVCKVADFGLARLI 427
 QY 421 EDNEYTAROGAKFPDKMTAPPAALYGRFTIKSDVMSFGILLTETTTGGRVYPGMVNRV 480
 Db 428 EDNEYTAROGAKFPDKMTAPPAALYGRFTIKSDVMSFGILLTETTTGGRVYPGMVNRV 487
 QY 481 LDQVERGYRMPCEPCESLHDLQCQCRKEPBERPTEFYLOAFLEDFYFTSTEPQYQGE 540
 Db 488 LDQVERGYRMPCEPCESLHDLQCQCRKEPBERPTEFYLOAFLEDFYFTSTEPQYQGE 547
 QY 541 NL 542
 Db 548 NL 549

Search completed: June 5, 2006, 17:07:40
 Job time : 119.845 secs

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OM protein - protein search, using sw model

Run on: June 5, 2006, 17:08:03 ; Search time 21.7603 Seconds

(without alignments)

2396.538 Million cell updates/sec

Title: US-10-691-079-1

Sequence: 1 MGSNKSXPKNASQRRSLR.....AFLEDYFTSTPEYQPGENL 542

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2863	100.0	542	1	TVHUSC
2	2820.5	98.5	541	1	A43610
3	2648.5	92.5	533	1	TVCHS
4	2608.5	91.1	587	1	TVFVPR
5	2601.5	90.9	568	1	TVFVSI
6	2586.5	90.3	357	1	TVFVSI
7	2503.5	87.4	526	1	TVFV60
8	2484.5	86.8	526	2	S20808
9	2478.5	86.6	526	1	OKFVVR
10	2471.5	86.3	526	2	S15582
11	2468.5	86.2	526	1	TVFVR
12	2453.5	85.7	526	2	S26420
13	2450	85.6	532	1	B34104
14	2449	85.2	532	1	A34104
15	2440.5	85.2	545	2	S52313
16	2433.5	85.0	546	2	S52314
17	2405	84.0	523	1	TVFVMT
18	2121.5	74.1	537	1	A45501
19	2110.5	73.7	543	1	TVHUS
20	2108.5	73.6	541	1	TVCHVS
21	2105.5	73.5	541	2	S11645
22	2052.5	71.7	544	2	S15153
23	2039.5	71.2	528	1	TVFVSI
24	1965	68.6	534	1	A44991
25	1947.5	68.0	537	2	S15192
26	1943	67.9	534	1	S33568
27	1936	67.6	536	2	S33569
28	1919.5	67.0	537	1	TVHUSY
29	1916.5	66.9	542	2	A49114

30	1910	66.7	539	2	B49114	protein-tyrosine k
31	1908.5	66.7	537	1	A43806	protein-tyrosine k
32	1843	64.4	529	1	TVHUR	protein-tyrosine k
33	1832	64.0	517	2	A43807	protein-tyrosine k
34	1800	62.9	517	2	S24547	protein-tyrosine k
35	1594	55.7	663	1	TVMVR	protein-tyrosine k
36	1587.5	55.4	509	1	TVHAST	protein-tyrosine k
37	1573	54.9	392	2	S04205	protein-tyrosine k
38	1522.5	53.2	505	1	TVHUC	protein-tyrosine k
39	1517.5	53.0	503	1	JQ1321	protein-tyrosine k
40	1512.5	52.8	503	1	TVMSHC	protein-tyrosine k
41	1491	52.1	507	1	A39939	protein-tyrosine k
42	1461	51.0	509	1	OKHUK	protein-tyrosine k
43	1461	51.0	512	1	TVHUX	protein-tyrosine k
44	1453	50.8	512	1	I56160	protein-tyrosine k
45	1452	50.7	509	1	I48845	protein-tyrosine k

ALIGNMENTS

RESULT 1

TVHUSC protein-tyrosine kinase (EC 2.7.1.112) src, neuronal - human

C/Species: Homo sapiens (man)

C/Date: 30-Jun-1989 #sequence_revision 07-Oct-1994 #text change 05-Oct-2004

C/Accession: A26891; A61083; B61083; A23287; A28832; B34704

R/Tanaka, A.; Gibbs, C.P.; Arthur, R.R.; Anderson, S.K.; Kung, H.J.; Fujita, D.J.

Mol. Cell. Biol. 7, 1978-1983, 1987

A/Title: DNA sequence encoding the amino-terminal region of the human c-src protein: imp

A/Reference number: A26891; MUID:87257903; PMID:33293057

A/Accession: A26891

A/Molecule type: mRNA

A/Residues: 1-117;124-191 <TRAN>

A/Cross-references: UNIPROT:P12931; UNIPARC:UPI0000172578; UNIPARC:UPI0000172579; GB:M16.

J/Paper: J.M.; Bolen, J.B.

J. Neurosci. Res. 24, 89-96, 1989

A/Title: Neuron-specific splicing of C-SRC RNA in human brain.

A/Reference number: A61083; MUID:90040822; PMID:2681803

A/Accession: A61083

A/Molecule type: mRNA

A/Residues: 98-145 <PYP>

A/Cross-references: UNIPARC:UPI000017257A

A/Accession: B61083

A/Molecule type: mRNA

A/Residues: 98-117;124-145 <PY2>

A/Cross-references: UNIPARC:UPI000017257A

A/Accession: A23287

A/Molecule type: mRNA

A/Residues: 192-542 <AND>

A/Cross-references: UNIPARC:UPI000016063; GB:X02647; NID:G35588; P1DN:CAA26465.1; P1D:G

A/Accession: A23287

A/Molecule type: mRNA

A/Residues: 382-542 <PAR>

A/Cross-references: UNIPARC:UPI000017257D

A/Accession: A28832; MUID:85187981; PMID:2581127

A/Molecule type: mRNA

A/Residues: 382-542 <PAR>

A/Cross-references: UNIPARC:UPI000017257D

A/Accession: A28832; MUID:85187981; PMID:2581127

A/Molecule type: mRNA

A/Residues: 382-542 <PAR>

A/Cross-references: UNIPARC:UPI000017257D

A/Accession: A28832; MUID:85187981; PMID:2581127

A/Molecule type: mRNA

A/Residues: 382-542 <PAR>

A/Cross-references: UNIPARC:UPI000017257E

A/Accession: A28832; MUID:85187981; PMID:2581127

A/Molecule type: mRNA

A/Residues: 382-542 <PAR>

A/Cross-references: UNIPARC:UPI000017257E

A/Accession: A28832; MUID:85187981; PMID:2581127

A/Molecule type: mRNA

A:Cross-references: GDB:120750; OMIM:190090
A:Map position: 20q11.2-20q11.2
A:Introns: 84/1; 117/2; 123/2; 156/2; 191/1; 241/1; 293/1; 378/3; 430/1; 474/1
C:Function: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
C:Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C:Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; p16
F:1-542/Product: protein-tyrosine kinase src; neuronal #status predicted <MAT>
F:1-117,124-542/Product: protein-tyrosine kinase src; short form #status predicted <MA2>
F:91-146/Domains: SH3 homology <SH3>
F:157-254/Domains: SH2 homology <SH2>
F:214-532/Domains: protein kinase homology <KIN>
F:282-290/Region: protein kinase ATP-binding motif
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:304/Active site: Lys #status predicted
F:425,536/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 100.0%; Score 2863; DB 1; Length 542;
Best Local Similarity 100.0%; Pred. No. 9,7e-134;
Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGSNKSXPKASQRRSLRLEPAENVHAGGAFPASQTPSKRPASADGHRGSAAPAPAAE 60
DB 1 MGSNKSXPKASQRRSLRLEPAENVHAGGAFPASQTPSKRPASADGHRGSAAPAPAAE 60
QY 61 PKLFGFNSSDVTYSPQAPGLAGVTTFYALYDYSRRTETDLSFKKGERLQIVNTRKY 120
DB 61 PKLFGFNSSDVTYSPQAPGLAGVTTFYALYDYSRRTETDLSFKKGERLQIVNTRKY 120
QY 121 DVEBGDWMLAHSSTQGTGYIPSNYVAPSDSIQAEEMYGFKITRRESERLLNAENPRGT 180
DB 121 DVEBGDWMLAHSSTQGTGYIPSNYVAPSDSIQAEEMYGFKITRRESERLLNAENPRGT 180
QY 181 FLVRESEETTKGAYCLSVSDPDNAKGLNVKHYKIRKLDGSGFYITSRQFNSLQQLVAAYS 240
DB 181 FLVRESEETTKGAYCLSVSDPDNAKGLNVKHYKIRKLDGSGFYITSRQFNSLQQLVAAYS 240
QY 241 KHAADGCHRLTYTCPTSKPTQGLADAMEIPRESRLRYKLGCGCFGEYMWGTMNGTTR 300
DB 241 KHAADGCHRLTYTCPTSKPTQGLADAMEIPRESRLRYKLGCGCFGEYMWGTMNGTTR 300
QY 301 VAIKTLKPGTMSPEALQEAQVMKKLRHEKLVOLYAVVSEBPITYETEMSKSLDPLK 360
DB 301 VAIKTLKPGTMSPEALQEAQVMKKLRHEKLVOLYAVVSEBPITYETEMSKSLDPLK 360
QY 361 GETGKTLRLPOLVDMAQIASGMAVYERNVYHRDLRAANILVGENLVCKVADFGLARLI 420
DB 361 GETGKTLRLPOLVDMAQIASGMAVYERNVYHRDLRAANILVGENLVCKVADFGLARLI 420
QY 421 EDNEYTAROGAKFPFKWTAPBALYGRFTIKSDVMSFGILLTELTKGRVPYGMVNRREV 480
DB 421 EDNEYTAROGAKFPFKWTAPBALYGRFTIKSDVMSFGILLTELTKGRVPYGMVNRREV 480
QY 481 LDQVERGYRMPCEPCEBSLHDLMCQWRKEPERFTFYLAFLBEDYFTSTEPQYOPGE 540
DB 481 LDQVERGYRMPCEPCEBSLHDLMCQWRKEPERFTFYLAFLBEDYFTSTEPQYOPGE 540
QY 541 NL 542
DB 541 NL 542

RESULT 2

A43610
protein-tyrosine kinase (BC 2.7.1.112) src, neuronal [similarity] - mouse
N:Alternate names: Rouse sarcoma oncogene
C:Species: Mus musculus (house mouse)
C>Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 05-Oct-2004
C:Accession: A43610
R:Martinez, R.; Mathey-Prevot, B.; Bernards, A.; Baltimore, D.
Science 237, 411-415, 1987
A:Title: Neuronal p60(c-src) contains a six-amino acid insertion relative to its non-ne
A:Reference number: A43610; MUID:87263406; PMID:2440106

A:Accession: A43610
A:Molecule type: mRNA
A:Residues: 1-541 <NAR>
A:Cross-references: UNIPROT:P05480; UNIPARC:UP100000161D19; GB:M17031; NID:g201056; PIDN:
C:Comment: The neuronal c-src has an 6 residue insertion of RLNVNR within the amino-term
C:Gene: Src
A:Gene: Src
A:Cross-references: MGI:98397
A:Map position: 2.91.0
C:Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C:Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; p16
F:90-145/Domains: SH3 homology <SH3>
F:156-253/Domains: SH2 homology <SH2>
F:213-531/Domains: protein kinase homology <KIN>
F:281-289/Region: protein kinase ATP-binding motif
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:303/Active site: Lys #status predicted
F:424,535/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 98.5%; Score 2820.5; DB 1; Length 541;
Best Local Similarity 98.7%; Pred. No. 1.2e-131;
Matches 535; Conservative 3; Mismatches 3; Indels 1; Gaps 1;
QY 1 MGSNKSXPKASQRRSLRLEPAENVHAGGAFPASQTPSKRPASADGHRGSAAPAPAAE 60
DB 1 MGSNKSXPKASQRRSLRLEPAENVHAGGAFPASQTPSKRPASADGHRGSAAPAPAAE 59
QY 61 PKLFGFNSSDVTYSPQAPGLAGVTTFYALYDYSRRTETDLSFKKGERLQIVNTRKY 120
DB 61 PKLFGFNSSDVTYSPQAPGLAGVTTFYALYDYSRRTETDLSFKKGERLQIVNTRKY 119
QY 121 DVEBGDWMLAHSSTQGTGYIPSNYVAPSDSIQAEEMYGFKITRRESERLLNAENPRGT 180
DB 121 DVEBGDWMLAHSSTQGTGYIPSNYVAPSDSIQAEEMYGFKITRRESERLLNAENPRGT 179
QY 181 FLVRESEETTKGAYCLSVSDPDNAKGLNVKHYKIRKLDGSGFYITSRQFNSLQQLVAAYS 240
DB 181 FLVRESEETTKGAYCLSVSDPDNAKGLNVKHYKIRKLDGSGFYITSRQFNSLQQLVAAYS 239
QY 241 KHAADGCHRLTYTCPTSKPTQGLADAMEIPRESRLRYKLGCGCFGEYMWGTMNGTTR 300
DB 241 KHAADGCHRLTYTCPTSKPTQGLADAMEIPRESRLRYKLGCGCFGEYMWGTMNGTTR 299
QY 301 VAIKTLKPGTMSPEALQEAQVMKKLRHEKLVOLYAVVSEBPITYETEMSKSLDPLK 360
DB 301 VAIKTLKPGTMSPEALQEAQVMKKLRHEKLVOLYAVVSEBPITYETEMSKSLDPLK 359
QY 361 GETGKTLRLPOLVDMAQIASGMAVYERNVYHRDLRAANILVGENLVCKVADFGLARLI 420
DB 361 GETGKTLRLPOLVDMAQIASGMAVYERNVYHRDLRAANILVGENLVCKVADFGLARLI 419
QY 421 EDNEYTAROGAKFPFKWTAPBALYGRFTIKSDVMSFGILLTELTKGRVPYGMVNRREV 480
DB 421 EDNEYTAROGAKFPFKWTAPBALYGRFTIKSDVMSFGILLTELTKGRVPYGMVNRREV 479
QY 481 LDQVERGYRMPCEPCEBSLHDLMCQWRKEPERFTFYLAFLBEDYFTSTEPQYOPGE 540
DB 481 LDQVERGYRMPCEPCEBSLHDLMCQWRKEPERFTFYLAFLBEDYFTSTEPQYOPGE 539
QY 541 NL 542
DB 540 NL 541

RESULT 3

TVCHS
protein-tyrosine kinase (BC 2.7.1.112) src - chicken
N:Alternate names: kinase-related transforming protein src
C:Species: Gallus gallus (chicken)
C>Date: 19-Feb-1984 #sequence_revision 07-Oct-1994 #text_change 05-Oct-2004
C:Accession: A00630; 150217; A4156; C35650; A32432
R:Takeya, T.; Hanafusa, H.
Cell 32, 881-890, 1983

A>Title: Structure and sequence of the cellular gene homologous to the RSV sec gene and
A:Reference number: A00650; MUID:83155664; PMID:6293580
A:Accession: A00650
A:Molecule type: DNA
A:Residues: 1-500, 'R', 502-533 <TAK>
A:Cross-references: UNIPROT:P00523; UNIPROT:Q09093; UNIPARC:UP1000017257F; GB:J00844; NID:J00844; MUID:83155664; PMID:6293580
R:Takeya, T.; Hanafusa, H.
Cell 34, 319, 1983
A:Reference number: A90838
A:Contents: annotation; erratum, correct translation of residue 526
R:Takeya, T.; Hanafusa, H.
J. Virol. 44, 12-18, 1982
A>Title: DNA sequence of the viral and cellular src gene of chickens: II comparison of t
A:Reference number: I50217; MUID:83059861; PMID:6292480
A:Accession: I50217
A:Molecule type: DNA
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Residues: 1-7 <TRA2>
A:Cross-references: UNIPARC:UP10000118887; GB:J00908; NID:g211690; PIDN:AAA48732.1; PID:AAA48732.1; PID:AAA48732.1
A>Note: the authors translated the codons AAC and CAG for residues 301 and 526 as Thr and
R:Dorai, T.; Levy, J.B.; Kang, L.; Brugge, J.S.; Wang, L.H.
Mol. Cell. Biol. 11, 4165-4176, 1991
A>Title: Analysis of cDNAs of the proto-oncogene c-src: heterogeneity in 5' exons and po
A:Reference number: A41256; MUID:91304409; PMID:1712905
A:Accession: A41256
A:Molecule type: mRNA
A:Residues: 484-533 <DOR1>
A:Cross-references: UNIPARC:UP10000171468; GB:583579; NID:g1679664; PIDN:AAB19353.1; PID:AAA48732.1; PID:AAA48732.1
A>Note: the authors translated the codon CAG for residue 527 as Glu
R:Dorai, T.; Wang, L.H.
Mol. Cell. Biol. 10, 4068-4079, 1990
A>Title: An alternative non-cytosine protein kinase product of the c-src gene in chicken
A:Reference number: A35650; MUID:90318371; PMID:2115117
A:Accession: C35650
A:Molecule type: mRNA
A:Residues: 1-182, 'DPCIP,SGCLC', <DOR2>
A:Cross-references: UNIPARC:UP1000000F0344; GB:M57290; NID:g212703; PIDN:AAA49078.1; PID:AAA49078.1; PID:AAA49078.1
A>Note: alternatively spliced mRNA exclusively replaces the long form in skeletal muscle
R:Shenoy, S.; Choi, J.K.; Bagrodia, S.; Copeland, T.D.; Maller, J.L.; Shalloway, D.
Cell 57, 763-774, 1989
A>Title: Purified maturation promoting factor phosphorylates p60(c-src) at the sites ph
A:Reference number: A32432; MUID:85249341; PMID:2470512
A:Accession: A32432
A:Molecule type: protein
A:Residues: 2-88 <SHE>
A:Residues: 2-88 <SHE>
A:Cross-references: UNIPARC:UP10000172580
A>Note: 34-Thr, 46-Thr, and 72-Ser are phosphorylated during mitosis
C:Genetics:
A:Gene: src
C:Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homolog
C:Keywords: alternative splicing; ATP; autophosphorylation; blocked amino end; lipoprote
F:88-137/Domain: SH3 homology <SH3>
F:148-245/Domain: SH2 homology <SH2>
F:265-523/Domain: protein kinase homology <KIN>
F:273-281/Region: protein kinase ATP-binding motif
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:12,48/Binding site: myristylated (Ser) (covalent) (by protein kinase C) #status predicted
F:17/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted
F:73,46/Binding site: phosphate (Thr) (covalent) #status experimental
F:72/Binding site: phosphate (Ser) (covalent) #status experimental
F:295/Active site: Lys #status predicted
F:416,527/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Df

PtLPGFPTSDVTVTSBPQRAGALAGVITTFVALYDYSRTETDLSFKKGSRLOIINNNT--- 114

Qy 58 DVRGDDWMLAHSLSFGQGTGYIPSNVYAPSDSIQAEEMVFSGKITRBSERILLNANENPRT 180

Df 121 DVREDDWMLAHSLSFGQGTGYIPSNVYAPSDSIQAEEMVFSGKITRBSERILLNANENPRT 180

Qy 115 ---EEDDWMLAHSLSFGQGTGYIPSNVYAPSDSIQAEEMVFSGKITRBSERILLNANENPRT 171

Df 161 FLVRSSESTTKGAICYCLSVSPDNKAGLVNHXYKLRKLDSSGEFYITSRFQPSNLQOLVAAYS 240

Qy 172 FLVRSSESTTKGAICYCLSVSPDNKAGLVNHXYKLRKLDSSGEFYITSRFQPSNLQOLVAAYS 231

Df 241 KHAADGLCHRLTYVCPTSPKQTQGLADAMEIPRESLRLEKLGCGCEGVMMGTWGTTTR 300

Qy 232 KHAADGLCHRLTYVCPTSPKQTQGLADAMEIPRESLRLEKLGCGCEGVMMGTWGTTTR 291

Df 301 VAIKTILKPOTMSPEAFLEQAQVMKKLRHEKLVLQAVVSEPIITYTERMSKSSLDFLK 360

Qy 292 VAIKTILKPOTMSPEAFLEQAQVMKKLRHEKLVLQAVVSEPIITYTERMSKSSLDFLK 351

Df 361 GETGKYTLRPOLVDMAAQIASGMAYIERNNYYNRDLRAANIIVGENLVCKRYADEGLARLI 420

Qy 352 GEMGKYTLRPOLVDMAAQIASGMAYIERNNYYNRDLRAANIIVGENLVCKRYADEGLARLI 411

Df 421 EBNEXTAROGAKFPKIWTAPBEALYGRFTIKDSVWSFGILLTELTKGRVPYPGWVAREV 480

Qy 412 EBNEXTAROGAKFPKIWTAPBEALYGRFTIKDSVWSFGILLTELTKGRVPYPGWVAREV 471

Df 481 LDQVERGYRMPCPPPECESLHDMCCQWRKEPERPTFEYLQAFLEDYFTSTEPYOYQGE 540

Qy 472 LDQVERGYRMPCPPPECESLHDMCCQWRKEPERPTFEYLQAFLEDYFTSTEPYOYQGE 531

Df 541 NL 542

Qy 532 NL 533

RESULT 4

TVFVPR

protein-tyrosine kinase (EC 2.7.1.112) src - avian sarcoma virus PR2257

C|Species: avian sarcoma virus PR2257

C|Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 05-Oct-2004

C|Accession: A30174

R|Genyik, J.; Deseloe, P.; Barnier, J.V.; Svoboda, J.; Nehyba, J.; Karakoz, I.; Rynditch, J. Virol. 63, 461-492, 1989

A|Title: Transduction of the cellular src gene and 3' adjacent sequences in avian sarcom

A|Reference number: A30174; MUID:89094972; PMID:2463376

A|Accession: A30174

A|Molecule type: DNA

A|Residues: 1-587 <GER>

A|Cross-references: UNIPROT:P15054; UNIPARC:UPI0000135F23; GB:M21526; NID:G210264; PIDN::C|Genetics:

C|Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology C|Keywords: ATP, autophosphorylation; blocked amino end; lipoprotein; myristylation; onc F:148-137/Domain: SH3 homology <SH3> F:148-245/Domain: SH2 homology <SH2> F:265-523/Domain: protein kinase homology <KIN> F:273-281/Region: protein kinase ATP-binding motif F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted F:295/Active site: Lys #status predicted F:416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 91.1%; Score 2608.5; DB 1; Length 587;

Best Local Similarity 93.1%; Pred. No. 3.3e-121;

Matches 497; Conservative 10; Mismatches 18; Indels 9; Gaps 2;

Df 1 MGNSKSKPDASQRRSLDEPAENVHGAGGAPPASQTPSPASADGHRGSAAFAAPAAB 60

Qy 1 MGSSKSXPDPQORRRSLPPDSTH--HGFPASQTPNKTAAPDTARTSPRSRGYATE 57

Df 61 PTLPGFPTSDVTVTSBPQRAGALAGVITTFVALYDYSRTETDLSFKKGSRLOIINNNTKV 120

Qy 58 PTLPGFPTSDVTVTSBPQRAGALAGVITTFVALYDYSRTETDLSFKKGSRLOIINNNT--- 114

QY	121	IVREDMMIAHSLSIGQGYISPNVYAPSDSIOAEMWYFGKTRRSERLLNAENRG	180
Db	115	---EGDMIAHSLLTGQGYISPNVYAPSDSIOAEMWYFGKTRRSERLLNPNPRG	171
QY	181	FLVRESETTKGAYCLSVSDFDNAKGLNVHKKIKLDSGGFYITSRTOFNSLOOLVA	240
Db	172	FLVRESETTKGAYCLSVSDFDNAKGLNVGHYIKRKLDGSGFYITSRTOFNSLOOLVA	231
QY	241	KHAGDLCHRLTIVCTSKRQTOGLKDAWEIPRESLRLEVKLGCGCFGEYWMGTN	300
Db	232	KHAGDLCHRLTIVCTSKRQTOGLKDAWEIPRESLRLEVKLGCGCFGEYWMGTN	291
QY	301	VAIKTLKRGTSPEAFLOAQWMLRHKRLPOLVAVVSEEPYIYTEVMSKSLDPLK	360
Db	292	VAIKTLKRGTSPEAFLOAQWMLRHKRLPOLVAVVSEEPYIYTEVMSKSLDPLK	351
QY	361	GETGKYLRLPOLVDMAAOIASGMAVYERNNVYHRDLRAANIIVGENLVCKVAD	420
Db	352	GEMGKYLRLPOLVDMAAOIASGMAVYERNNVYHRDLRAANIIVGENLVCKVAD	411
QY	421	EDNETTAOGAKFPIKMTAPEALYGRFTIKSDWSPGILLTELTTKGRVPYGMNREV	480
Db	412	EDNETTAOGAKFPIKMTAPEALYGRFTIKSDWSPGILLTELTTKGRVPYGMNREV	471
QY	481	LDQVGRGMPCCPBCPSLHLMOCQMKKPEERTFLEYLOAFLDYFSTP	534
Db	472	LDQVGRGMPCCPBCPSLHLMOCQMKKPEERTFLEYLOAFLDYFSTP	525

RESULT 5

protein-tyrosine kinase (EC 2.7.1.112) src - avian sarcoma virus S1
C:Species: avian sarcoma virus S1
C:Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 05-Oct-2004
C:Accession: A25375
R:Ikawa, S.; Hagino-Yamagishi, K.; Kawai, S.; Yamamoto, T.; Toyoshima, K.
Mol. Cell. Biol. 6, 2420-2428, 1986
A>Title: Activation of the cellular src gene by transducing retrovirus.
A:Reference number: A25375; MUID:87064539; PMID:3097513
A:Accession: A25375
A:Molecule type: DNA
A:Residues: 1-568 <IKR>
A:Cross-references: UNIPROT:P14084; UNIPARC:UPI0000135F25
C:Genetic(s)
A:Gene: src
C:Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C:Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; phos
F:88-137/Domain: SH3 homology <SR3>
F:148-245/Domain: SH2 homology <SR2>
F:265-523/Domain: protein kinase homology <KIN>
F:273-281/Region: protein kinase ATP-binding motif
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:25/Active site: lys #status predicted
F:45/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match	90.9%	Score 2601.5	DB 1	Length 566
Best Local Similarity	92.7%	Pred. No. 7e-121		
Matches 495	Conservative 12	Mismatches 18	Indels 9	Gaps 2
QY	1	MGSNKSKKDAQSORRRSLLEPANNVGAAGGAFPASQTPSKPASADGHRGPPSAAPAAAE	60	
Db	1	MGSSKSKPKDPSQRRRLLEPPDSTH--HGFPASQTPNKTKAAPDTHTPSKSFGVATTE	57	
QY	61	PKLFGGFPNLSPTVYSPQAPAGLAVTTFFVALYDESRTEPDLSTKXGGERLOIVNNTKV	120	
Db	58	PKLFGGFPNLSPTVYSPQAGALAGVTTFFVALYDESRTEPDLSTKXGGERLOIVNNT--	114	
QY	121	DVREGDWWLALSLSGTQGYIPSNVVAPOSDIQAEEMVFGKTRRESERLLLNAAENPGT	180	
Db	115	---EGDWWLALSLSLTGTQGYIPSNVVAPOSDIQAEEMVFGKTRRESERLLLNENPGT	171	
QY	181	FLVRESSTTKAYCLSVSDPDNAKLANVKKYKIRKLSDGGFPYITSRTQFNSLQQLVAYYS	240	

Db	172	FLVBESETTKAAYCCLSVSDFDNARLANTYKHKIRLDSGGFTTBSRTQSSLIQOLVAYYS	231
Qy	241	KHADGLCHRLTTCPTSPKQTOGLAKDAMEIPRESLRLEBVKLGQCGFGEVMGTWGTTR	300
Db	232	KHADGLCHRLTNVCSTSPKQTOGLAKDAMEIPRESLRLEBVKLGQCGFGEVMGTWGTTR	291
Qy	301	VAITTIKRGTMSPKAFLOEAOVMKKLRHEKIVOLVAAYVSEEPYIYVTEBMSKSLDDPLK	360
Db	292	VAITTIKRGTMSPKAFLOEAOVMKKLRHEKIVOLVAAYVSEEPYIYVTEBMSKSLDDPLK	351
Qy	361	GETGKYTLRLPOLVDMAAQIASGMAYVERBNYVHRDLRAANIIVGENLVCKVADFGIARLI	420
Db	352	GEWGKYTLRLPOLVDMAAQIASGMAYVERBNYVHRDLRAANIIVGENLVCKVADFGIARLI	411
Qy	421	EDNEYTAAQAKFPFKMTAPAPALYGRITISDVWSFGILLTELTTRKGVPPFGMWNREV	480
Db	412	EDNEYTAAQAKFPFKMTAPAPALYGRITISDVWSFGILLTELTTRKGVPPFGMWNREV	471
Qy	481	LDQYERGRMCCPPECPSRLHDLMOQCRKEBPEBPRFEYLOAFLEDFYFTSTEP	534
Db	472	LDQYERGRMCCPPECPSRLHDLMOQCRKQBPBEPBPRFEYLOAFLEDFYFTSTEP	525

RESULT 6

C:protein-tyrosine kinase (EC 2.7.1.112) src - avian sarcoma virus S2
 C:Species: avian sarcoma virus S2
 C:Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 05-Oct-2004
 C:Accession: B25375
 R:Ikawa, S.; Hagino-Yamagishi, K.; Kawai, S.; Yamamoto, T.; Toyoshima, K.
 Mol. Cell. Biol. 6, 2420-2428, 1986
 A:Title: Activation of the cellular src gene by transducing retrovirus.
 A:Reference number: A25375; PMID:87064539; PMID:3097513
 A:Accession: B25375
 A:Molecule type: DNA
 A:Residues: 1-557 <IKA>
 A:Cross-references: UNIPROT:P14085; UNIPARC:UPI0000135F26
 C:GeneInfo:
 A:Gene: src
 C:Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology;
 C:Keywords: ATP; autophosphorylation; blocked amino end; lipidprotein; myristylation; onco
 F:88-137/Domain: SH3 homology <SH3>
 F:148-245/Domain: SH2 homology <SH2>
 F:265-523/Domain: protein kinase homology <KIN>
 F:273-281/Region: protein kinase ATP-binding motif
 F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F:25/Active site: Lys #status predicted
 F:41/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

	Query Match	90.3%	Score	256.5	DB 1	Length	557	
	Best Local Similarity	88.7%	Pred. No.	3.8e-120				
	Matches	496	Conservative	14	Mismatches	22	Indels	27
							Gaps	3
Qy	1	MGNSKSRPKDASQRRRLSLEPAENVHGAGGAFPAISQTPSPKASADGHRGSPAAAPAAAE	60					
Db	1	MGSSKSRPKDPSQRRRLSLEPDSYTH---HGFPFASQTPNKTAADYTHRTPSRSGYATE	57					
Qy	61	PKLFGGFSNDSTVYSPORAGPLAGGVTTFYALYYESRTETDLSFFKGERLQIYNNTRKY	120					
Db	58	PKLFGGNTSDSTVYSPORAGLAGGVTTFYALYYESRTETDLSFFKGERLQIYNNT---	114					
Qy	121	DVREGDWWLAHSLSTGQTGYIPSNYVAPSDSIQAEEMYPFGKITRRESRLILNAENPQGT	180					
Db	115	---EGDWWLAHSLTGGQTGYIPSNYVAPSDSIQAEEMYPFGKITRRESRLILNENPQGT	171					
Qy	181	FLVRESSTKGAYCLTSVDFDNAGLVNKKYIKRLDSGGFYITRSQTFNSLQOLVAYYS	240					
Db	172	FLVRESSTKGAYCLTSVDFDNAGLVNKKYIKRLDSGGFYITRSQTFNSLQOLVAYYS	231					
Qy	241	KHADGLCHRLTTCVPTSKPQTQGLAKDAWEIPRSLRLHYVLGGCGGCEVMWGMVGNQTR	300					
Db	232	KHADGLCHRLTTCVPTSKPQTQGLAKDAWEIPRSLRLHYVLGGCGGCEVMWGMVGNQTR	291					

QY 301 VAITLKPGTMSPEAFIQEAVMKLRHEKLVQYAVVSEPIYIVTEYMSKSGILDFLK 360
 DB 292 VAIKTLKPGTMSPEAFIQEAVMKLRHEKLVQYAVVSEPIYIVTEYMSKSGILDFLK 351
 QY 361 GETGKYRLPOLVYMAAQIASGMAVVERMYVHEDLRAANTLVGENLVCKVADGRLRLI 420
 DB 352 GEMKTYRLPOLVYMAAQIASGMAVVERMYVHEDLRAANTLVGENLVCKVADGRLRLI 411
 QY 421 EDNETYRQGAKEPFIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVYPCGVNREV 480
 DB 412 EDNETYRQGAKEPFIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVYPCGVNREV 471
 QY 481 LDQVERGYRMPCEPCESLHDLMCQCKRKEPERPFEYIQAFLDYF----- 529
 DB 472 LDQVERGYRMPCEPCESLHDLMCQCKRKEPERPFEYIQAFLDYIAGILANTPWEDK 511
 QY 530 -----TSTPEYQYQGEN 541
 DB 532 QEGRGSTASKQKQERGED 550

RESULT 7

TFV60

protein-tyrosine kinase (EC 2.7.1.112) src - Rous sarcoma virus

C:Species: Rous sarcoma virus

C:Date: 22-May-1981 #sequence_revision 17-Dec-1982 #text_change 05-Oct-2004

C:Accession: A38017; #sequence_revision 17-Dec-1982 #text_change 05-Oct-2004

R:Ceumilobsky, A.P.; Levinson, A.D.; Varmus, H.E.; Bishop, J.M.; Tischer, E.; Goodman,

Nature 301, 736-738, 1983

A:Title: Corrections to the nucleotide sequence of the src gene of Rous sarcoma virus.

A:Reference number: A38017; MUID:83141780; PMID:6298633

A:Accession: A38017

A:Molecule type: DNA

A:Residues: 1-526 <CZE>

A:Cross-references: UNIPROT:P00524; UNIPARC:UPI0000170DC3; GB:L29199; GB:J02018; GB:J020

R:Takeya, T.; Hanafusa, H.

Cell 32, 881-890, 1983

A:Title: Structure and sequence of the cellular gene homologous to the RSV sec gene and

A:Reference number: A00630; MUID:83155664; PMID:6299580

A:Accession: A00631

A:Molecule type: DNA

A:Residues: 1-62, 'D', 64-95, 'T', 97-123, 'V', 125-300, 'N', 302-526 <TK>

A:Cross-references: UNIPARC:UPI0000172582

R:Experimental source: strain Schmidt-Ruppin

R:Barnier, J.V.; Dezelee, P.; Marx, M.; Calochy, G.

Nucleic Acids Res. 17, 1252, 1989

A:Title: Nucleotide sequence of the src gene of the Schmidt-Ruppin strain of Rous Sarcom

A:Reference number: S02726; MUID:89160256; PMID:2531953

A:Accession: S02726

A:Molecule type: DNA

A:Residues: 1-9, 'G', 11-62, 'D', 64-123, 'V', 125-319, 'K', 321-495, 'S', 497-526 <BAR>

A:Cross-references: UNIPARC:UPI0000135F2C; EMBL:X13745; NID:961908; PIDN:CAA32012.1; PID

R:Takeya, T.; Feldman, R.A.; Hanafusa, H.

J. Virol. 44, 1-11, 1982

A:Title: DNA sequence of the viral and cellular src gene of chickens: I. Complete nucle

A:Reference number: A38018; MUID:83059858; PMID:6292477

A:Accession: A38018

A:Molecule type: DNA

A:Residues: 1-15, 'C', 17-94, 'RT', 97-116, 'D', 118-337, 'T', 339-526 <TA>

A:Cross-references: UNIPARC:UPI0000135F24; GB:K00928; NID:9210187; PIDN:AAA42565.1; PID:

R:Experimental source: strain RASV1441

R:Nell, J.C.; Ghyedael, J.; Vogt, P.K.; Smart, J.E.

Nature 291, 675-677, 1981

A:Title: Homologous tyrosine phosphorylation sites in transformation-specific gene prod

A:Reference number: A38019; MUID:81220979; PMID:6263320

C:Comments: annotation; phosphorylation site

C:Gene: src

C:Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology

C:Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; on

F:88-137/Domain: SH3 homology <SH3>
 F:148-245/Domain: SH2 homology <SH2>
 F:265-523/Domain: protein kinase homology <KIN>
 F:273-281/Region: protein kinase ATP-binding motif
 F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F:295/Active site: Lys #status predicted
 F:416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status experime

Query Match 87.4%; Score 2503.5; DB 1; Length 526;
 Best Local Similarity 91.2%; Pred. No. 4.2e-116;
 Matches 479; Conservative 13; Mismatches 24; Indels 9; Gaps 2;

QY 1 MGSKSKPCDASORRSLPEENVHAGGAFAPASQPSKAPASADGRGSAAPAAAE 60
 DB 1 MGSSKSKPCDPSQRRSLPEPDSTH--HGQFPASQTPNKTAAPDTHRTSRSGTYATE 57
 QY 61 PKLFGFNSSDPTVTSPPRAGLAGVTTFFVALYDRESTERETDLSFKKGERLQIVNTRKV 120
 DB 58 PKLFGFNSTDTVTSPPRAGLAGVTTFFVALYDRESTERETDLSFKKGERLQIVNNT--- 114
 QY 121 DVREGDWMLAHSLSGTGTYIPSNVYAPSDSIQAEENYFGKITRRESERLLANENRGT 180
 DB 115 ---EGNMWMLAHSLSGTGTYIPSNVYAPSDSIQAEENYFGKITRRESERLLANENRGT 171
 QY 181 FLVRESRTGAYCLSYSDPDNAKGLVVKYKTRKLDGSGFYTSRQFNSLQOLVAYYS 240
 DB 172 FLVRESRTGAYCLSYSDPDNAKGLVVKYKTRKLDGSGFYTSRQFNSLQOLVAYYS 231
 QY 241 KHADGLCHRLTTCPTSPKPTQGLAKDAWEIPRESLRLLEVLAGGCGEVMWGTWGTTR 300
 DB 232 KHADGLCHRLTTCPTSPKPTQGLAKDAWEIPRESLRLLEVLAGGCGEVMWGTWGTTR 291
 QY 301 VAIKTLKPGTMSPEAFIQEAVMKLRHEKLVQYAVVSEPIYIVTEYMSKSGILDFLK 360
 DB 292 VAIKTLKPGTMSPEAFIQEAVMKLRHEKLVQYAVVSEPIYIVTEYMSKSGILDFLK 351
 QY 361 GETGKYRLPOLVYMAAQIASGMAVVERMYVHEDLRAANTLVGENLVCKVADGRLRLI 420
 DB 352 GEMKTYRLPOLVYMAAQIASGMAVVERMYVHEDLRAANTLVGENLVCKVADGRLRLI 411
 QY 421 EDNETYRQGAKEPFIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVYPCGVNREV 480
 DB 412 EDNETYRQGAKEPFIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVYPCGVNREV 471
 QY 481 LDQVERGYRMPCEPCESLHDLMCQCKRKEPERPFEYIQAFL 525
 DB 472 LDQVERGYRMPCEPCESLHDLMCQCKRKEPERPFEYIQAFL 516

RESULT 8

protein-tyrosine kinase (EC 2.7.1.112) src - Rous sarcoma virus

C:Species: Rous sarcoma virus

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Oct-2004

C:Accession: S20808; S32774

R:Bobor, J.; Rozkot, F.; Svoboda, J.

submitted to the EMBL Data Library, May 1990

A:Description: Sequence organization of the adjacent chromosomal flanks the LTR.

A:Reference number: S20808

A:Accession: S20808

A:Molecule type: DNA

A:Residues: 1-526 <BD>

A:Cross-references: UNIPROT:Q60567; UNIPARC:UPI00001068B2; EMBL:X52822; NID:949656; PIDN

R:Experimental source: Mesocricetus auratus (golden hamster) provirus

C:Gene: src

C:Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology

C:Keywords: ATP; autophosphorylation; oncogene; phosphoprotein; phosphotransferase; tran

F:148-245/Domain: SH2 homology <SH2>

F:265-523/Domain: protein kinase homology <KIN>

F:273-281/Region: protein kinase ATP-binding motif

F:295/Active site: Lys #status predicted

F:116/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 86.8%; Score 2484.5; DB 2; Length 526;

Best Local Similarity 90.7%; Pred. No. 3,66-115;

Matches 476; Conservative 11; Mismatches 29; Indels 9; Gaps 2;

```

QY 1 MGSNKKPNDASORRRSLPEAENVHAGGAGFPAASQTPSKPASADGHRGSAAPAPAAE 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MGSNKKPNDASORRRSLPEPDSTH--HGFPASQTPDPTAAPDARNRPSRGVATE 57
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 PKLFGFNSSDVTSPQAGAPLAGVTTFVALYDYESRTETDLSFFKGERLQIVNTRKY 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 58 PKLFGFNSSDVTSPQAGALAGVTTFVALYDYESRTETDLSFFKGERLQIVNNT--- 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 DVREGMWLAHSITGQTGYIPSNVYAPSDSIOAEEMYPGKTRRSERLLNAENRGT 180
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 115 ---EGDWMWLAHSITGQTGYIPSNVYAPSDSIOAEEMYPGKTRRSERLLNAENRGT 171
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 181 FLVRESEETTKGAYCLSVDPDNAGLVNKHVKIRKLDGSGFYITSRTOFNSLQOLVAYYS 240
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 172 FLVRKSETAKGACLSVSDPDNAGKGVNKHVKICLYSGGFYITSRTOFNSLQOLVAYYS 231
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 241 KHAADGLCHRLTTCPTSPKPTQGLAKDAWEIPRESLRLEVKLGQCGFGEVWMTNGTTR 300
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 232 KHAADGLCHRLTTCPTSPKPTQGLAKDAWEIPRESLRLEVKLGQCGFGEVWMTNGTTR 291
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 301 VALKTLKPGTMSPEALQEAQVWKRLRHEKLVOLYAVVSEEPYIYIEYWSKSLDPLK 360
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 292 VALKTLKPGTMSPEALQEAQVWKRLRHEKLVOLYAVVSEEPYIYIEYWSKSLDPLK 351
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 361 GETGKTLRLPOLYDMAQAISGMAVYERMYVHRDLRAANIIVGENLVCKVADFGIARLI 420
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 352 GEMGKTLRLPOLYDMAQAISGMAVYERMYVHRDLRAANIIVGENLVCKVADFGIARLI 411
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 421 EDNEYTAROGAKPEIKMTAPEALYGRFTIKSDVMSFGILLTELTKGRVPGMVNREV 480
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 412 EDNEYTAROGAKPEIKMTAPEALYGRFTIKSDVMSFGILLTELTKGRVPGMVNREV 471
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 481 LDQVERGYRMPCCPECSLHDMCCMKRKEPERPFTFYLOAFL 525
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 472 LDQVERGYRMPCCPECSLHDMCCMKRKEPERPFTFYLOAFL 516
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

RESULT 9

OKREVR

protein-tyrosine kinase (EC 2.7.1.112) src - Rous sarcoma virus (strain H-19)

N:Alternate names: kinase-related transforming protein src

C:Species: Rous sarcoma virus

C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 05-Oct-2004

C:Accession: S09609

Nucleic Acids Res. 17, 8869, 1989

A:Title: Complete nucleotide sequence of LTR, v-src, LTR provirus H-19.

A:Reference number: S09609; PMID:2587228

A:Accession: S09609

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-526 <SOD>

A:Cross-references: UNIPROT:P25020; UNIPARC:UPI0000135F2A; EMBL:X15345; NID:561706; PIDN

C:Genetics:

C:Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology

C:Keywords: ATP; autophosphorylation; blocked amino end; lipidprotein; myristylation; onc

F:88-137/Domain: SH3 homology <SH3>

F:148-245/Domain: SH2 homology <SH2>

F:265-523/Domain: protein kinase homology <KIN>

F:273-281/Region: protein kinase ATP-binding motif

F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted

F:295/Active site: Lys #status predicted

F:116/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match

Best Local Similarity 90.5%; Pred. No. 7,1e-115;

Matches 475; Conservative 11; Mismatches 30; Indels 9; Gaps 2;

```

QY 1 MGSNKKPNDASORRRSLPEAENVHAGGAGFPAASQTPSKPASADGHRGSAAPAPAAE 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MGSNKKPNDASORRRSLPEPDSTH--HGFPASQTPDPTAAPDARNRPSRGVATE 57
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 PKLFGFNSSDVTSPQAGAPLAGVTTFVALYDYESRTETDLSFFKGERLQIVNTRKY 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 58 PKLFGFNSSDVTSPQAGALAGVTTFVALYDYESRTETDLSFFKGERLQIVNNT--- 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 DVREGMWLAHSITGQTGYIPSNVYAPSDSIOAEEMYPGKTRRSERLLNAENRGT 180
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 115 ---EGDWMWLAHSITGQTGYIPSNVYAPSDSIOAEEMYPGKTRRSERLLNAENRGT 171
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 181 FLVRESEETTKGAYCLSVDPDNAGLVNKHVKIRKLDGSGFYITSRTOFNSLQOLVAYYS 240
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 172 FLVRKSETAKGACLSVSDPDNAGKGVNKHVKICLYSGGFYITSRTOFNSLQOLVAYYS 231
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 241 KHAADGLCHRLTTCPTSPKPTQGLAKDAWEIPRESLRLEVKLGQCGFGEVWMTNGTTR 300
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 232 KHAADGLCHRLTTCPTSPKPTQGLAKDAWEIPRESLRLEVKLGQCGFGEVWMTNGTTR 291
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 301 VALKTLKPGTMSPEALQEAQVWKRLRHEKLVOLYAVVSEEPYIYIEYWSKSLDPLK 360
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 292 VALKTLKPGTMSPEALQEAQVWKRLRHEKLVOLYAVVSEEPYIYIEYWSKSLDPLK 351
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 361 GETGKTLRLPOLYDMAQAISGMAVYERMYVHRDLRAANIIVGENLVCKVADFGIARLI 420
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 352 GEMGKTLRLPOLYDMAQAISGMAVYERMYVHRDLRAANIIVGENLVCKVADFGIARLI 411
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 421 EDNEYTAROGAKPEIKMTAPEALYGRFTIKSDVMSFGILLTELTKGRVPGMVNREV 480
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 412 EDNEYTAROGAKPEIKMTAPEALYGRFTIKSDVMSFGILLTELTKGRVPGMVNREV 471
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 481 LDQVERGYRMPCCPECSLHDMCCMKRKEPERPFTFYLOAFL 525
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 472 LDQVERGYRMPCCPECSLHDMCCMKRKEPERPFTFYLOAFL 516
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

RESULT 10

S15582

protein-tyrosine kinase (EC 2.7.1.112) src - Rous sarcoma virus (strain Prague A)

C:Species: Rous sarcoma virus

C:Variety: strain Prague A

C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 05-Oct-2004

C:Accession: S15582; S09665

Nucleic Acids Res. 17, 3986, 1989

A:Title: Sequence variation of the Rous sarcoma virus PTA src gene.

A:Reference number: S15582; PMID:89282411; PMID:2543959

A:Accession: S15582

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-526 <LNU>

A:Cross-references: UNIPROT:Q64994; UNIPROT:Q92806; UNIPROT:Q60567; UNIPROT:Q07461; UNIP

A:Experimental source: strain Prague A

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1989

A>Note: only a list of differences from sequence S09665 is given; however, the list is in

R:Fincham, V.J.; Wyke, J.A.

J. Virol. 58, 694-699, 1986

A:Title: Localization of temperature-sensitive transformation mutations and back mutator

A:Reference number: S09665; PMID:86200422; PMID:3009882

A:Accession: S09665

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 231-241, 'TH', '244-287', 'G', '289-463', 'P', '465-501', 'N', '503-526 <FIN>

A:Cross-references: UNIPARC:UPI00001755F1

C:Genetics:

A:Gene: src

C:Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology;

C:Keywords: ATP; autophosphorylation; blocked amino end; lipidprotein; myristylation; onc

F:88-137/Domain: SH3 homology <SH3>

F:148-245/Domain: SH2 homology <SH2>

F:88-137/Domain: SH2 homology <SH2>
F:148-245/Domain: SH2 homology <SH2>
F:265-523/Domain: protein kinase homology <KIN>
F:273-281/Region: protein kinase ATP-binding motif
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:295/Active site: Lys #status predicted
F:416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 85.7%; Score 2453.5; DB 2; Length 526;
Best Local Similarity 89.5%; Pred. No. 1.2e-113;
Matches 470; Conservative 13; Mismatches 33; Indels 9; Gaps 2;

QY 1 MGSNKSXPDAQRRRLSPAEENVHAGGAPASQTPSPKASADGHRGSAAPAPAAE 60
DB 1 MGSNKSXPDAQRRRLSPAEENVHAGGAPASQTPSPKASADGHRGSAAPAPAAE 57
QY 61 PKLFGFNSSDVTSPQRAGPLAGVTFVALYDYSRTETDLSFKKGERLQIVNNTKV 120
DB 58 PKLFGFNSSDVTSPQRAGPLAGVTFVALYDYSRTETDLSFKKGERLQIVNNTKV 114
QY 121 DVREGDWMLAHSSTGQTYIPSNVYAPSDSIQAEWYFGKTRRESERLLMAENPRGT 180
DB 115 ---EGYWMIAHSJLTGQTYIPSNVYAPSDSIQAEWYFGKTRRESERLLMAENPRGT 171
QY 181 FLVRESEETTKGAYCLSVDPDNAGKLVNKHKIRKLDGSGFYITSRTOFNSLQOLVAAYS 240
DB 172 FLVRKSETAKGAYCLSVDPDNAGKLVNKHKIRKLDGSGFYITSRTOFNSLQOLVAAYS 231
QY 241 KHAADGCHRLTVTCPTSKPQTQGLADAMEIPRESIRLEVLKGCGCFGEVWMTGNQTR 300
DB 232 KHAADGCHRLTVTCPTSKPQTQGLADAMEIPRESIRLEVLKGCGCFGEVWMTGNQTR 291
QY 301 VAIKTKLPKGTMSPEALQEAQVWKKLRHEKLVQYAVVSEEPYIYIETMSKSLDPLK 360
DB 292 VAIKTKLPKGTMSPEALQEAQVWKKLRHEKLVQYAVVSEEPYIYIETMSKSLDPLK 351
QY 361 GETGKYLRLPOLVDMAQAISGMAVYERNNYVHRDLRAANILVGENLVCKVADFGIARLI 420
DB 352 GETGKYLRLPOLVDMAQAISGMAVYERNNYVHRDLRAANILVGENLVCKVADFGIARLI 411
QY 421 EDNEYTARQAGAKPPIKMTAPEALYGRFTIKSDVMSFGILLTELTKGRVYPGMVNRREV 480
DB 412 EDNEYTARQAGAKPPIKMTAPEALYGRFTIKSDVMSFGILLTELTKGRVYPGMVNRREV 471
QY 481 LDQVERGYRMPCCPEPSLHDMCQCKREPERPFEYLQAF 525
DB 472 LDQVERGYRMPCCPEPSLHDMCQCKREPERPFEYLQAF 516

RESULT 13
B34104
protein-tyrosine kinase (BC 2.7.1.112) src 2 [similarity] - African clawed frog
N/Alternate names: kinase-related transforming protein (src); kinase-related transforming
C/Species: Xenopus laevis (African clawed frog)
C/Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 05-Oct-2004
C/Accession: B34104; 151563
R/Steale, R.E.; Unger, T.F.; Mardis, M.J.; Fero, J.B.
J. Biol. Chem. 264, 10649-10653, 1989
A/Title: The two Xenopus laevis SRC genes are co-expressed and each produces functional
A/Reference number: A34104; PMID:89278134; PMID:2499582
A/Accession: B34104
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-532 <STE>
A/Cross-references: UNIPROT:P13116; UNIPARC:UPI000017159F; GB:M23422; GB:J04822; NID:g21
R/Steale, R.E.
Nucleic Acids Res. 13, 1747-1761, 1985
A/Title: Two divergent cellular src genes are expressed in Xenopus laevis.
A/Reference number: 151563; PMID:85215578; PMID:2387856
A/Accession: 151563
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 439-492 <ST2>

A/Cross-references: UNIPARC:UPI00001715A0; GB:M30858; NID:g214799; PIDN:AA51644.1; PID:5
C/Species: A.
A/Accession: 464/1
C/Species: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology;
C/Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; phos
F:147-136/Domain: SH2 homology <SH2>
F:147-244/Domain: SH2 homology <SH2>
F:264-522/Domain: protein kinase homology <KIN>
F:272-280/Region: protein kinase ATP-binding motif
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:294/Active site: Lys #status predicted
F:415/526/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predi

Query Match 85.6%; Score 2450; DB 1; Length 532;
Best Local Similarity 86.9%; Pred. No. 1.8e-113;
Matches 471; Conservative 24; Mismatches 37; Indels 10; Gaps 4;

QY 1 MGSNKSXPDAQRRRLSPAEENVHAGGAPASQTPSPKASADGHRGSAAPAPAAE 60
DB 1 MGSNKSXPDAQRRRLSPAEENVHAGGAPASQTPSPKASADGHRGSAAPAPAAE 56
QY 61 PKLFGFNSSDVTSPQRAGPLAGVTFVALYDYSRTETDLSFKKGERLQIVNNTKV 120
DB 57 PKLFGFNSSDVTSPQRAGPLAGVTFVALYDYSRTETDLSFKKGERLQIVNNTKV 113
QY 121 DVREGDWMLAHSSTGQTYIPSNVYAPSDSIQAEWYFGKTRRESERLLMAENPRGT 180
DB 114 ---EGYWMIAHSJLTGQTYIPSNVYAPSDSIQAEWYFGKTRRESERLLMAENPRGT 170
QY 181 FLVRESEETTKGAYCLSVDPDNAGKLVNKHKIRKLDGSGFYITSRTOFNSLQOLVAAYS 240
DB 171 FLVRKSETAKGAYCLSVDPDNAGKLVNKHKIRKLDGSGFYITSRTOFNSLQOLVAAYS 230
QY 241 KHAADGCHRLTVTCPTSKPQTQGLADAMEIPRESIRLEVLKGCGCFGEVWMTGNQTR 300
DB 231 KHAADGCHRLTVTCPTSKPQTQGLADAMEIPRESIRLEVLKGCGCFGEVWMTGNQTR 290
QY 301 VAIKTKLPKGTMSPEALQEAQVWKKLRHEKLVQYAVVSEEPYIYIETMSKSLDPLK 360
DB 291 VAIKTKLPKGTMSPEALQEAQVWKKLRHEKLVQYAVVSEEPYIYIETMSKSLDPLK 350
QY 361 GETGKYLRLPOLVDMAQAISGMAVYERNNYVHRDLRAANILVGENLVCKVADFGIARLI 420
DB 351 GETGKYLRLPOLVDMAQAISGMAVYERNNYVHRDLRAANILVGENLVCKVADFGIARLI 410
QY 421 EDNEYTARQAGAKPPIKMTAPEALYGRFTIKSDVMSFGILLTELTKGRVYPGMVNRREV 480
DB 411 EDNEYTARQAGAKPPIKMTAPEALYGRFTIKSDVMSFGILLTELTKGRVYPGMVNRREV 470
QY 481 LDQVERGYRMPCCPEPSLHDMCQCKREPERPFEYLQAF 540
DB 471 LDQVERGYRMPCCPEPSLHDMCQCKREPERPFEYLQAF 530
QY 541 NL 542
DB 531 NL 532

RESULT 14
A34104
protein-tyrosine kinase (BC 2.7.1.112) src 1 [similarity] - African clawed frog
N/Alternate names: kinase-related transforming protein (src); kinase-related transforming
C/Species: Xenopus laevis (African clawed frog)
C/Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 31-Dec-2004
C/Accession: A34104; 151564
R/Steale, R.E.; Unger, T.F.; Mardis, M.J.; Fero, J.B.
J. Biol. Chem. 264, 10649-10653, 1989
A/Title: The two Xenopus laevis SRC genes are co-expressed and each produces functional
A/Reference number: A34104; PMID:89278134; PMID:2499582
A/Accession: A34104
A/Status: not compared with conceptual translation
A/Molecule type: mRNA

A/Residues: 1-532 <STE>
A/Cross-references: UNIPROT:Q91851; UNIPARC:UPI0000172581; GB:M24704; GB:J04822; NID:g21
R/Seelie, R.E.; Choer, R.; Rai, B.B.A.; Winkur, S.T.; Unger, T.P.
Oncogene 7, 2345-2350, 1992
A/Title: Structural organization of a src gene from xenopus laevis.
A/Reference number: 151564; MUID:93064714; PMID:1437158
A/Accession: 151564
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-113 <ST2>
A/Cross-references: UNIPARC:UPI00000FD97A; GB:M33646; NID:g214808; PIDN:AAA49963.1; PID:
C/Genetics:
A/Introns: 80/1
C/Superfamily: protein kinase homology; SH2 homology; SH3 homology
C/Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
F/87-116/Domain: SH3 homology <SH3>
F/147-244/Domain: SH2 homology <SH2>
F/264-522/Domain: protein kinase homology <KIN>
F/272-280/Region: protein kinase ATP-binding motif
F/2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F/294/Active site: lys #status predicted
F/415.526/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 85.5%; Score 2449; DB 1; Length 532;
Best Local Similarity 86.5%; Pred. No. 2e-113;
Matches 469; Conservative 25; Mismatches 38; Indels 10; Gaps 4;

QY 1 MGSNKSFKPDASQRRSLRSLPAENVHAGAGGAFPAASQTPSKPASDGRGSPAPAPAAE 60
DB 1 MGATKSPKRPGRSRLDIVEGSH-QPFTSLASQTPNK--SLDSHRPPAPGCG-NCND 56
QY 61 PKLPGFNSSDVTYSPAPRPLAGGVTTPALVYSESTEDLSFKKGERLQIVNTRKY 120
DB 57 LTFPGGINFSDITTSPORTPLAGGVTTPALVYSESTEDLSFKKGERLQIVNNT--- 113
QY 121 DVREGDMLAHSLSTGQGYIPSNVYAPSPDSIQAEENYFGKITRRESERLLNAENRGT 180
DB 114 ---EGDMMILARSLSGGTGIIPSNVYAPSDSIQAEENYLGKITRREARLLSLDENRGT 170
QY 181 FLVRESSTTGAYCLSVSDPDNAKGLNVKHYKIRKLDGSGFYITSRTQFNSLQOLVAYYS 240
DB 171 FLVRESSTTGAYCLSVSDPDNARGLNVKHYKIRKLDGSGFYITSRTQFNSLQOLVAYYS 230
QY 241 KAADGLCHRLTTVCPTSKPOTQGLAKDAWEIPRESLRLVYKLGCGCGEYVMGWTNGTTR 300
DB 231 KAADGLCHRLTAVCTAPKPTQGLSRDAWEIPRDSLRLVYKLGCGCGEYVMGWTNGTTR 290
QY 301 VAIKTLKPGTMSPEAFIQEAVMKLRHEKLVQLYAVVSEPIYIVTEYMSKSLDLPLK 360
DB 291 VAIKTLKPGTMSPEAFIQEAVMKLRHEKLVQLYAVVSEPIYIVTEYMSKSLDLPLK 350
QY 361 GETGKYLRPLQVDMAAQIASGMAYVERMYVHRDLRAANILVGENIVCKVADGLARLI 420
DB 351 GEMGRYLRPLQVDMAAQIASGMAYVERMYVHRDLRAANILVGENIVCKVADGLARLI 410
QY 421 EDNEYTARQAKFPITKTAPBAALYGRFTIKSDVMSFGILLTELTTKGRVYPMVNRREV 480
DB 411 EDNEYTARQAKFPITKTAPBAALYGRFTIKSDVMSFGILLTELTTKGRVYPMVNRREV 470
QY 481 LDVERGYRMPCEPCESLHDLQCQWRKEPERPFEYIQAFLDYFSTEEQYQGE 540
DB 471 LDVERGYRMPCEPCESLHDLQCQWRKEPERPFEYIQAFLDYFSTEEQYQGE 530
QY 541 NL 542
DB 531 NL 532

RESULT 15
S52313
protein-tyrosine kinase (BC 2.7.1.112) src - Rous sarcoma virus
C/Species: Rous sarcoma virus
C/Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 05-Oct-2004

C/Accession: S52313
R/Tschoyan, A.; Yatsula, B.; Shutevan, M.; Molnova, E.; Kaverina, I.; Musackina, E.; Lee
submitted to the EMBL Data Library, January 1995
A/Description: Two new isoforms of v-src oncogene isolated from low and high metastatic i
A/Reference number: S52313
A/Accession: S52313
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-545 <TAT>
A/Cross-references: UNIPROT:Q86362; UNIPARC:UPI0000105D06; EMBL:X84074; NID:g663083; PID:
C/Superfamily: Tyrosine-protein kinase, proto-oncogene src type; protein kinase homology
C/Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
F/108-157/Domain: SH3 homology <SH3>
F/168-265/Domain: SH2 homology <SH2>
F/285-543/Domain: protein kinase homology <KIN>
F/293-301/Region: protein kinase ATP-binding motif
F/2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F/315/Active site: lys #status predicted
F/436/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 85.2%; Score 2440.5; DB 2; Length 545;
Best Local Similarity 87.0%; Pred. No. 5.4e-113;
Matches 474; Conservative 13; Mismatches 29; Indels 29; Gaps 4;

QY 1 MGSNKSFKPDASQRRSLRSLPAENVHAGAGGAFPAASQTPSK-----PAS--- 43
DB 1 MGSNKSFKPDASQRRSLRSLPEPDSTH---HGFPASQTPNKTAFLTAAPRSRRPASQHR 57
QY 44 ---ADGHRGSAAPAPAAEPKLFPGFNSSDVTYSPAPRPLAGGVTTPALVYSESTE 100
DB 58 AAPDTHRTSRSGVTANPKLFGDFTNSDVTYSPAPRPLAGGVTTPALVYSESTE 117
QY 101 TDSFKKGERLQIVNTRKXVDVREGDMLAHSLSTGQGYIPSNVYAPSDSIQAEENYFG 160
DB 118 TDSFKKGERLQIVNNT-----EGNMWMLAHSVTTGQGYIPSNVYAPSDSIQAEENYFG 171
QY 161 KITRRESERLLNAENRGTFLVRESSTTGAYCLSVSDPDNAKGLNVKHYKIRKLDGSG 220
DB 172 KITRRESERLLNAENRGTFLVRESSTTGAYCLSVSDPDNAKGLNVKHYKIRKLDGSG 231
QY 221 FYITSRTQFNSLQOLVAYYSKHAADGLCHRLTTVCPTSKPOTQGLAKDAWEIPRESLRLV 280
DB 232 FYITSRTQFNSLQOLVAYYSKHAADGLCHRLTTVCPTSKPOTQGLAKDAWEIPRESLRLV 291
QY 281 KLGGCGEYVMGWTNGTTRVAITKTLKPGTMSPEAFIQEAVMKLRHEKLVQLYAVVSE 340
DB 292 KLGGCGEYVMGWTNGTTRVAITKTLKPGTMSPEAFIQEAVMKLRHEKLVQLYAVVSE 351
QY 341 EPIYIVTEYMSKSLDLPLKGEQKYLRPLQVDMAAQIASGMAYVERMYVHRDLRAAN 400
DB 352 EPIYIVTEYMSKSLDLPLKGEQKYLRPLQVDMAAQIASGMAYVERMYVHRDLRAAN 411
QY 401 ILVGENIVCKVADGLARLIEDNEYTARQAKFPITKTAPBAALYGRFTIKSDVMSFGIL 460
DB 412 ILVGENIVCKVADGLARLIEDNEYTARQAKFPITKTAPBAALYGRFTIKSDVMSFGIL 471
QY 461 LTELTTKGRVYPMVNRREVLDVERGYRMPCEPCESLHDLQCQWRKEPERPFEY 520
DB 472 LTELTTKGRVYPMVNRREVLDVERGYRMPCEPCESLHDLQCQWRKEPERPFEY 531
QY 521 LQAF 525
DB 532 LQAF 536

Search completed: June 5, 2006, 17:16:40
Job time : 22.7603 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 5, 2006, 17:01:48 ; Search time 155.335 Seconds
(without alignments)
3227.587 Million cell updates/sec

Title: US-10-691-079-1

Perfect score: 2863
Sequence: 1 MGSNKSXPXASQRRSLRP.....AFLEDYFTSTPEYQPEBNL 542

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 7.2:*
1: uniprot_sprot:*
2: uniprot_tr embl:*

* Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2863	100.0	542	2	Q76P87 HUMAN
2	2828.5	98.8	541	2	Q2M414 MOUSE
3	2823	98.6	542	2	Q9J10 RAT
4	2816	98.4	535	1	SRC HUMAN
5	2815.5	98.3	540	1	SRC MOUSE
6	2786.5	97.3	535	2	Q80XU2 MOUSE
7	2759.5	96.7	535	2	Q3UKD6 MOUSE
8	2758	96.3	535	1	SRC RAT
9	2693	94.1	523	1	Q45QJ2 RAT
10	2648.5	92.5	532	1	SRC CHICK
11	2603.5	90.9	566	1	SRC AVIS2
12	2596.5	90.7	567	1	SRC AVIS
13	2595.5	90.7	587	1	Q64817 PRETR
14	2581.5	90.2	536	1	SRC AVIS1
15	2515.5	87.9	525	1	SRC AVISR
16	2515.5	87.9	525	1	SRC RSUSA
17	2484.5	86.8	526	2	Q60567 PRETR
18	2475.5	86.5	537	2	Q7ZX73 XENLA
19	2473.5	86.4	525	1	SRC RSVAH
20	2473	86.4	532	2	Q5MAS9 XENTR
21	2472.5	86.4	526	2	Q64994 PRETR
22	2470.5	86.3	526	2	Q93080 PRETR
23	2469	86.2	523	2	Q85477 PRETR
24	2469	86.2	535	2	Q92957 RSUSB
25	2468.5	86.2	526	2	Q92806 PRETR
26	2467.5	86.2	525	1	SRC RSUSR
27	2463.5	86.0	525	1	SRC RSVP
28	2457.5	85.8	526	2	Q64993 RSUSR
29	2453.5	85.7	526	2	Q07461 PRETR
30	2450	85.6	532	2	Q2TARI XENLA
31	2445	85.4	531	1	SRC2_XENLA

32	2441	85.3	531	1	SRC1 XENLA	P13115 xenopus lae
33	2440.5	85.2	545	2	Q86362 PRETR	Q86362 rous sarcom
34	2433.5	85.0	546	2	Q86363 PRETR	Q86363 rous sarcom
35	2400	83.8	522	1	SRC RSVP	P31693 rous sarcom
36	2305	80.5	534	2	Q6EWH0 BRARE	Q6EWH0 brachydanio
37	2180.5	76.2	527	2	Q91952 XIPXI	Q91952 xiphophorus
38	2124.5	74.2	537	2	Q64089 XENTR	Q64089 xenopus tro
39	2123.5	74.2	537	2	Q6PF70 XENLA	Q6PF70 xenopus lae
40	2116.5	73.9	537	2	Q498G3 XENLA	Q498G3 xenopus lae
41	2114.5	73.9	541	2	Q93PW1 RAT	Q93PW1 rattus norv
42	2112.5	73.8	536	1	YES XENLA	P10936 xenopus lae
43	2110.5	73.7	541	2	Q8C762 MOUSE	Q8C762 mus musculu
44	2109	73.7	542	1	YES HUMAN	P07947 homo sapien
45	2105.5	73.5	540	1	YES_MOUSE	Q04736 mus musculu

ALIGNMENTS

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RESULT 1
ID Q76P87 HUMAN PRELIMINARY; PRT; 542 AA.
AC Q76P87;
DT 05-JUN-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUN-2004, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE OTTHUMP0000030931.
GN Name=SRC; ORFNames=RP5-823N20.1-006;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Wallis J.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
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CC
EMBL: AL133293; CAC10573.1; -; Genomic DNA.
HSSP: P12931; 1A09.
SMR: Q76P87; 87-542.
Ensembl: ENSG00000197122; Homo sapiens.
GO: GO:0005524; F:ATP binding; IEA.
GO: GO:0004713; F:protein-tyrosine kinase activity; IEA.
GO: GO:0007242; P:intracellular signaling cascade; IEA.
GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
InterPro: IPR000719; Prot. kinase.
InterPro: IPR002290; Ser. Thr. kinase.
InterPro: IPR000980; SH2.
InterPro: IPR001452; SH3.
InterPro: IPR001245; Tyr. kinase.
InterPro: IPR008266; Tyr. kinase_AS.
Pfam: PF07714; Kinase_Tyr; 1.
Pfam: PF00017; SH2; 1.
Pfam: PF00018; SH3; 1.
PRINTS: PR00401; SH2DOMAIN.
PRINTS: PR00452; SH3DOMAIN.
PRINTS: PR00109; TYRKINASE.
ProDom: PD000001; Prot. kinase; 1.
ProDom: PD000093; SH2; 1.
ProDom: PD000066; SH3; 1.
SMART: SM00252; SH2; 1.
SMART: SM00326; SH3; 1.
SMART: SM00219; TyKc; 1.
PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE: PS50001; SH2; 1.
PROSITE: PS50002; SH3; 1.
SEQUENCE 542 AA; 60589 MW; C12D30FBBCDSFFEB CRC64;
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Query Match      100.0%; Score 2863; DB 2; Length 542;
Best Local Similarity 100.0%; Pred. No. 5,4e-181;
Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSNKKPKDASORRRSLRPAENVHAGGAFPASOTPSKPASADHGRGSAAPAPAAE 60
DB 1 MGSNKKPKDASORRRSLRPAENVHAGGAFPASOTPSKPASADHGRGSAAPAPAAE 60
QY 61 PKLFGFNSSDVTYSPOKAPPLAGVTTVALYDYSRTETDLSFKKGERLQIVNTRKV 120
DB 61 PKLFGFNSSDVTYSPOKAPPLAGVTTVALYDYSRTETDLSFKKGERLQIVNTRKV 120
QY 121 DVREGMWMALHSLSTGQTGYIPSNVYAPSDSIQAEEMYPGKLTTRRSERLLNAENPRT 180
DB 121 DVREGMWMALHSLSTGQTGYIPSNVYAPSDSIQAEEMYPGKLTTRRSERLLNAENPRT 180
QY 181 FLVRESEETTKGAYCLSVSPDNAGKLVNKHVKIRKLDGSGFYITSRTOFNSLQOLVAAYYS 240
DB 181 FLVRESEETTKGAYCLSVSPDNAGKLVNKHVKIRKLDGSGFYITSRTOFNSLQOLVAAYYS 240
QY 241 KHAADGLCHRLTTCPTSKPOTQGLADAMEIPRESLRLEVKLGQCGCFGEVMMGTWNGTTR 300
DB 241 KHAADGLCHRLTTCPTSKPOTQGLADAMEIPRESLRLEVKLGQCGCFGEVMMGTWNGTTR 300
QY 301 VALKTLKPGTMSPEALQEAQVWKLRHEKLVOLYAVVSEBPYIYTERMSKSLDPLK 360
DB 301 VALKTLKPGTMSPEALQEAQVWKLRHEKLVOLYAVVSEBPYIYTERMSKSLDPLK 360
QY 361 GETGKYLRLPOLVDMAQIASGMAVYERNVYVRDLRAANIIVGENLVCKVADFGIARLI 420
DB 361 GETGKYLRLPOLVDMAQIASGMAVYERNVYVRDLRAANIIVGENLVCKVADFGIARLI 420
QY 421 EDNEYTARQAKPPIKMTAPEALYGRFTIKSDVMSFGILLTELTKGRVPYGMVNRREV 480
DB 421 EDNEYTARQAKPPIKMTAPEALYGRFTIKSDVMSFGILLTELTKGRVPYGMVNRREV 480
QY 481 LDQVEGYRMPCCPBCPESLHDMCCMRKEPERPTFEYLOAFLDYFTSTEPQYOPGE 540
DB 481 LDQVEGYRMPCCPBCPESLHDMCCMRKEPERPTFEYLOAFLDYFTSTEPQYOPGE 540
QY 541 NL 542
DB 541 NL 542

RESULT 2
Q2M414 MOUSE PRELIMINARY; PRT; 541 AA.
AC Q2M414_
DT 21-FEB-2006, integrated into UniProtKB/TrEMBL.
DT 21-FEB-2006, sequence version 1.
DE 21-FEB-2006, entry version 1.
GN Name=Src;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
NCBI_TaxId=10090;
[1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CAS/BLU; TISSUE=Brain;
RA Farber C.R., Corva P.M., Medrano J.F.;
RT "Characterization of quantitative trait loci influencing growth and
RT adiposity using congenic mouse strains."
RT Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
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CC EMBL; AY902331; AAX90616.1; -; Genomic DNA.
DR SEQUENCE 541 AA; 60645 MW; 0534AF027783BCFC CRC64;
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Query Match      98.8%; Score 2828.5; DB 2; Length 541;
Best Local Similarity 98.9%; Pred. No. 1e-178;
Matches 536; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 1 MGSNKKPKDASORRRSLRPAENVHAGGAFPASOTPSKPASADHGRGSAAPAPAAE 60
DB 1 MGSNKKPKDASORRRSLRPAENVHAGGAFPASOTPSKPASADHGRGSAAPAPAAE 59
QY 61 PKLFGFNSSDVTYSPOKAPPLAGVTTVALYDYSRTETDLSFKKGERLQIVNTRKV 120
DB 61 PKLFGFNSSDVTYSPOKAPPLAGVTTVALYDYSRTETDLSFKKGERLQIVNTRKV 119
QY 121 DVREGMWMALHSLSTGQTGYIPSNVYAPSDSIQAEEMYPGKLTTRRSERLLNAENPRT 180
DB 121 DVREGMWMALHSLSTGQTGYIPSNVYAPSDSIQAEEMYPGKLTTRRSERLLNAENPRT 179
QY 181 FLVRESEETTKGAYCLSVSPDNAGKLVNKHVKIRKLDGSGFYITSRTOFNSLQOLVAAYYS 240
DB 181 FLVRESEETTKGAYCLSVSPDNAGKLVNKHVKIRKLDGSGFYITSRTOFNSLQOLVAAYYS 239
QY 241 KHAADGLCHRLTTCPTSKPOTQGLADAMEIPRESLRLEVKLGQCGCFGEVMMGTWNGTTR 300
DB 241 KHAADGLCHRLTTCPTSKPOTQGLADAMEIPRESLRLEVKLGQCGCFGEVMMGTWNGTTR 299
QY 301 VALKTLKPGTMSPEALQEAQVWKLRHEKLVOLYAVVSEBPYIYTERMSKSLDPLK 360
DB 301 VALKTLKPGTMSPEALQEAQVWKLRHEKLVOLYAVVSEBPYIYTERMSKSLDPLK 359
QY 361 GETGKYLRLPOLVDMAQIASGMAVYERNVYVRDLRAANIIVGENLVCKVADFGIARLI 420
DB 361 GETGKYLRLPOLVDMAQIASGMAVYERNVYVRDLRAANIIVGENLVCKVADFGIARLI 419
QY 421 EDNEYTARQAKPPIKMTAPEALYGRFTIKSDVMSFGILLTELTKGRVPYGMVNRREV 480
DB 421 EDNEYTARQAKPPIKMTAPEALYGRFTIKSDVMSFGILLTELTKGRVPYGMVNRREV 479
QY 481 LDQVEGYRMPCCPBCPESLHDMCCMRKEPERPTFEYLOAFLDYFTSTEPQYOPGE 540
DB 481 LDQVEGYRMPCCPBCPESLHDMCCMRKEPERPTFEYLOAFLDYFTSTEPQYOPGE 539
QY 541 NL 542
DB 540 NL 541

RESULT 3
Q9J10 RAT PRELIMINARY; PRT; 542 AA.
AC Q9J10_
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DE 07-FEB-2006, entry version 21.
DE Neuronal C-SRC tyrosine-specific protein kinase.
GN Name=Src;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
NCBI_TaxId=10116;
[1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=21148003; PubMed=11249956; DOI=10.1016/S0028-3908(00)00185-4;
RA Linden A., Storch M., Lakso M., Haapasalo A., Lee D., Wilkin J.M.,
RA Sei Y., Caestre E., Wong G.;
RT "Increased expression of neuronal Src and tyrosine phosphorylation of
RT NMDA receptors in rat brain after systemic treatment with MK-801."
RT Neuropharmacology 40:469-481(2001).
[2]
RP NUCLEOTIDE SEQUENCE.
RA Linden A.-M., Storch M., Lakso M., Wong G., Caestre E.;
RT Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC
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CC EMBL; AF157016; AAF80335.1; -; mRNA.
 CC HSSP; P12931; 1043.
 DR SMK; Q9J710; 87-542.
 DR Ensembl; ENSRNOG0000009495; Rattus norvegicus.
 DR RGD; 620795; Src.
 DR GO; GO:0016301; F-kinase activity; TAS.
 DR GO; GO:0004713; F-protein-tyrosine kinase activity; IDA.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR InterPro; IPR008266; Tyr_pkinase_AS.
 DR Pfam; PF07714; Pkinase_Tyr; 1.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00452; SH2DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot kinase; 1.
 DR ProDom; PD000093; SH2; 1.
 DR ProDom; PD000066; SH3; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00219; TYRK; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00107; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 DR Kinase.
 SO \$SEQUENCE 542 AA; 60727 MW; 6AC21D6DD6B0B39 CRC64;

Query Match 98.6%; Score 2823; DB 2; Length 542;
 Best Local Similarity 98.9%; Pred. No. 2,4e-178;
 Matches 537; Conservative 3; Mismatches 1; Indels 2; Gaps 2;

QY 1 MGSNKSAPKASQRRSLSEPNVHAGAGAFPSQTPSKPASADGHRGSAFAA-PAAA 59
 DB 1 MGSNKSAPKASQRRSLSEPNVHAGAGAFPSQTPSKPASADGHRGSAFAA-PAAA 59
 QY 60 EPLKFGFNSSDVTYSPQRAAGPLAGVYTFVALYDYSRTETDLSFKKGERLQIVNTRK 119
 DB 60 EPLKFGFNSSDVTYSPQRAAGPLAGVYTFVALYDYSRTETDLSFKKGERLQIVNTRK 119
 QY 120 VDVREGGWMVLAHSLSTGCTGTYIPSNYVAPSDSIQAEWYFGKTRRSEERLLLAENPRG 179
 DB 120 VDVREGGWMVLAHSLSTGCTGTYIPSNYVAPSDSIQAEWYFGKTRRSEERLLLAENPRG 179
 QY 180 TPLVRESETTKGAAYCLVSPDPDNAGLVNKHVYRKLDGSGFYTSRQFNSLQOLVAYY 239
 DB 180 TPLVRESETTKGAAYCLVSPDPDNAGLVNKHVYRKLDGSGFYTSRQFNSLQOLVAYY 239
 QY 240 SKHADGLCHRLITTVCPSTSKPQTQGLADAMEIPRESRLRLVKLGQSGFGGEVWMTWNGTT 299
 DB 240 SKHADGLCHRLITTVCPSTSKPQTQGLADAMEIPRESRLRLVKLGQSGFGGEVWMTWNGTT 299
 QY 300 RVALIKTLKPGTMSBEAFLQEAQVWKKLRHEKLVOLYAVVSEEPYIYITEYWNKSSLLDFL 359
 DB 300 RVALIKTLKPGTMSBEAFLQEAQVWKKLRHEKLVOLYAVVSEEPYIYITEYWNKSSLLDFL 359
 QY 360 KGETGKTLRLPOLVDMAAOIASGMAVYERMMYVHRDLRAANIILVGENLVCAVAFGLARL 419
 DB 360 KGETGKTLRLPOLVDMAAOIASGMAVYERMMYVHRDLRAANIILVGENLVCAVAFGLARL 419
 QY 420 IEDNEYTARQGAAPKPIKMTAPEALYGRFTIKSDVWFGILLTELTKGRVYPGQVWVRE 479
 DB 420 IEDNEYTARQGAAPKPIKMTAPEALYGRFTIKSDVWFGILLTELTKGRVYPGQVWVRE 479
 QY 480 VLDOVERGYRMPCCPBECPBSLHDLMCQCMKKEPEREPTFEYLQAFLEDYFTSTEPQYQPG 539

DB 480 VLDOVERGYRMPCCPBECPBSLHDLMCQCMKKEPEREPTFEYLQAFLEDYFTSTEPQYQPG 539
 QY 540 ENL 542
 DB 540 ENL 542

RESULT 4
 SRC_HUMAN STANDARD; PRT; 535 AA.
 ID P12531; O86V89; O9H5A8;
 AC 01-OCT-1989, integrated into UniProtKB/Swiss-Prot.
 DT 01-NOV-1995, sequence version 2.
 DT 07-MAR-2006, entry version 79.
 DE Proto-oncogene tyrosine-protein kinase Src (EC 2.7.1.112) (p60-Src)
 DE (c-Src) (pp60c-src).
 GN Name=SRC; Synonyms=SRC1;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414852a;
 RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavridis G., Almeida J.P., Babbage A.K., Bagguley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.B., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.B., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knight A., Laird G.K., Lawlor S.,
 RA Leivaesalho M.H., Leverhna M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConachie L.J., McIay K., McMurtry A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsey H.,
 RA Rice C.M., Rose M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
 RA Skuse C.D., Smyth M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin R., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20."
 RL Nature 414:865-871(2001).
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
 RC TISSUE=Lung, and Skin;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hatesh F.,
 RA Datschenko L., Marulisa K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stempleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshitsuyuki S., Carancini P., Prange C.,
 RA Baha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez Y., Bouffard G.G.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Kizywiniski M.I., Skalska U., Smallus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."; U.S.A. 99:16899-16903(2002).
 RN [3]
 RN NUCLEOTIDE SEQUENCE OF 1-184 (ISOFORM 1).
 RP MEDLINE=97257903; PubMed=3299057;
 RA Tanaka A., Gibbs C.P., Arthur R.R., Anderson S.K., Kung H.-J.,
 RA Fujita D.J.;
 RT "DNA sequence encoding the amino-terminal region of the human c-src
 RT protein: implications of sequence divergence among src-type kinase
 RT oncogenes."; Mol. Cell. Biol. 7:1978-1983(1987).
 RN [4]
 RN NUCLEOTIDE SEQUENCE OF 185-535 (ISOFORM 1).
 RP MEDLINE=95213483; PubMed=2582238;
 RA Anderson S.K., Gibbs C.P., Tanaka A., Kung H.-J., Fujita D.J.;
 RT "Human cellular src gene: nucleotide sequence and derived amino acid
 RT sequence of the region coding for the carboxy-terminal two-thirds of
 RT pp60c-src."; Mol. Cell. Biol. 5:1122-1129(1985).
 RN [5]
 RN NUCLEOTIDE SEQUENCE OF 97-138 (ISOFORM 2).
 RP MEDLINE=90040822; PubMed=2681803;
 RA Pyper J.M., Bolen J.B.;
 RT "Neuron-specific splicing of C-SRC RNA in human brain."; J. Neurosci. Res. 24:89-96(1989).
 RN [6]
 RN NUCLEOTIDE SEQUENCE OF 375-535 (ISOFORM 1).
 RP MEDLINE=95167981; PubMed=2581127;
 RA Parker R.C., Mardon G., Lebo R.V., Varnus H.E., Bishop J.M.;
 RT "Isolation of duplicated human c-src genes located on chromosomes 1
 RT and 20."; Mol. Cell. Biol. 5:831-838(1985).
 RN [7]
 RN ALTERNATIVE SPLICING.
 RP PubMed=1691439;
 RA Pyper J.M., Bolen J.B.;
 RT "Identification of a novel neuronal C-SRC exon expressed in human
 RT brain."; Mol. Cell. Biol. 10:2035-2040(1990).
 RN [8]
 RN X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 85-535.
 RP MEDLINE=97177105; PubMed=9024657; DOI=10.1038/385595a0;
 RA Xu W., Harrison S.C., Eck M.J.;
 RT "Three-dimensional structure of the tyrosine kinase c-Src."; Nature 385:595-602(1997).
 RN [9]
 RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 144-248.
 RP MEDLINE=97317069; PubMed=9174343; DOI=10.1021/bi970019n;
 RA Charifson P.S., Shewchuk L.M., Rocque W., Hummel C.W., Jordan S.R.,
 RA Mohr C., Pacofsky G.J., Feil M.R., Rodriguez M., Sternbach D.D.,
 RA Consler T.G.;
 RT "Peptide ligands of pp60(c-src) SH2 domains: a thermodynamic and
 RT structural study."; Biochemistry 36:6283-6293(1997).
 RN [10]
 RN STRUCTURE BY NMR OF 203-248.
 RP MEDLINE=95161382; PubMed=7532003;
 RA Xu R.X., Word J.M., Davis D.G., Rink M.J., Willard D.H. Jr.,
 RA Gampe R.T. Jr.;
 RT "Solution structure of the human pp60c-src SH2 domain complexed with a
 RT phosphorylated tyrosine pentapeptide."; Biochemistry 34:2107-2121(1995).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
 CC tyrosine phosphate.
 CC -1- INTERACTION:
 CC 06NVP1.cenD3 (xeno); NDBxp=3; InAct=EBI-621482, EBI-621463;
 CC 09Y6K9.KBKG; NDBxp=1; InAct=EBI-621482, EBI-81279;
 CC 060749.Chidbdl (xeno); NDBxp=1; InAct=EBI-621482, EBI-519077;
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;

CC IsoId=P12931-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P12931-2; Sequence=VSP_012134;
 CC -1- P-TM: Phosphorylated on Tyr-529 by c-Src kinase (CSK). The
 CC phosphorylated form is termed pp60c-src. The phosphorylated tail
 CC interacts with the SH2 domain thereby representing kinase activity.
 CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
 CC subfamily.
 CC -1- SIMILARITY: Contains 1 SH2 domain.
 CC -1- SIMILARITY: Contains 1 SH3 domain.
 CC -----
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 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL: AL133293; CAC34523.1; -; Genomic_DNA.
 DR EMBL: BC011566; AAH11566.1; -; mRNA.
 DR EMBL: BC051270; AAH51270.2; -; mRNA.
 DR EMBL: K03218; AAA60584.1; -; Genomic_DNA.
 DR EMBL: M16237; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL: M16243; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL: M16244; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL: M16245; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL: K03212; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL: K03213; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL: K03214; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL: K03215; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL: K03216; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL: K03217; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL: K02647; CAA26485.1; -; Genomic_DNA.
 DR EMBL: K03995; CAA26485.1; JOINED; Genomic_DNA.
 DR EMBL: K03996; CAA26485.1; JOINED; Genomic_DNA.
 DR EMBL: K03997; CAA26485.1; JOINED; Genomic_DNA.
 DR EMBL: K03998; CAA26485.1; JOINED; Genomic_DNA.
 DR EMBL: K03999; CAA26485.1; JOINED; Genomic_DNA.
 DR EMBL: X04000; CAA26485.1; JOINED; Genomic_DNA.
 DR PIR: A26891; TVHUSC.
 DR PDB: 1A07; X-ray; A/B=143-248.
 DR PDB: 1A08; X-ray; A/B=143-248.
 DR PDB: 1A09; X-ray; A/B=143-248.
 DR PDB: 1A1A; X-ray; A/B=143-248.
 DR PDB: 1A1B; X-ray; A/B=143-248.
 DR PDB: 1A1C; X-ray; A/B=143-248.
 DR PDB: 1A1E; X-ray; A/B=143-248.
 DR PDB: 1FMK; X-ray; @=85-535.
 DR PDB: 1HCS; NMR; B=143-248.
 DR PDB: 1HCT; NMR; B=143-248.
 DR PDB: 1KSW; X-ray; A=85-535.
 DR PDB: 1O41; X-ray; A=144-251.
 DR PDB: 1O42; X-ray; A=144-251.
 DR PDB: 1O43; X-ray; A=144-251.
 DR PDB: 1O44; X-ray; A=144-251.
 DR PDB: 1O45; X-ray; A=144-251.
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 DR PDB: 1O4B; X-ray; A=144-251.
 DR PDB: 1O4C; X-ray; A=144-251.
 DR PDB: 1O4D; X-ray; A=144-251.
 DR PDB: 1O4E; X-ray; A=144-251.
 DR PDB: 1O4F; X-ray; A=144-251.
 DR PDB: 1O4G; X-ray; A=144-251.
 DR PDB: 1O4H; X-ray; A=144-251.

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QY 122 VREGDWMLAHSLSGTQGYIPSNVYAPSDSIQAEWFGKTRRESRLLNANPRGTF 181
DB 117 --BGDWMLAHSLSGTQGYIPSNVYAPSDSIQAEWFGKTRRESRLLNANPRGTF 174
QY 182 LVRESSETTKAYCISVSPDNAGKLVNKHVKIRKLDGSGGYTTSRTQFNSIQQLVAYYSK 241
DB 175 LVRESSETTKAYCISVSPDNAGKLVNKHVKIRKLDGSGGYTTSRTQFNSIQQLVAYYSK 234
QY 242 HAQGLCHRLTVCTSPQOGLAKDAMEIPRESLRLEVLCGCCPPEVMMGTNCTRV 301
DB 235 HAQGLCHRLTVCTSPQOGLAKDAMEIPRESLRLEVLCGCCPPEVMMGTNCTRV 294
QY 302 AITKLGKGTMSPEAFLOEAQVMKLRHEKLVQLYAVVSEPIYIVTEYMSKSLDPLK 361
DB 295 AITKLGKGTMSPEAFLOEAQVMKLRHEKLVQLYAVVSEPIYIVTEYMSKSLDPLK 354
QY 362 ETGKYRLPOLVDMAQIASGMAYVERMNVYHDLRAANILVGENLVCKVADFGALRIE 421
DB 355 ETGKYRLPOLVDMAQIASGMAYVERMNVYHDLRAANILVGENLVCKVADFGALRIE 414
QY 422 DNEVTAQGAKEPIKWPAPPAALYGRFTIKSDVMSFGILLTELTKGRVPRGKVNREVL 481
DB 415 DNEVTAQGAKEPIKWPAPPAALYGRFTIKSDVMSFGILLTELTKGRVPRGKVNREVL 474
QY 482 DOVERGRMPCPECPESLHDLMOQCWRKEPERPTEYLOAFLEDFSTEPQYQGEN 541
DB 475 DOVERGRMPCPECPESLHDLMOQCWRKEPERPTEYLOAFLEDFSTEPQYQGEN 534
QY 542 L 542
DB 535 L 535

RESULT 5
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ID SRC_MOUSE
AC P05480;
DT 01-NOV-1988, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1995, sequence version 2.
DT 07-MAR-2006, entry version 65.
DE Neuronal proto-oncogene tyrosine-protein kinase Src (EC 2.7.1.112)
DE (p60-Src) (c-Src) (pp60c-src).
GN Name=Src;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC STRAIB=BAJB/c;
RX MEDLINE=87263406; PubMed=2440106;
RA Martinez R., Machey-Prevot B., Bernards A., Baltimore D.;
RT "Neuronal p60c-src contains a six-amino acid insertion relative to
its non-neuronal counterpart.";
RL Science 237:411-415(1987).
RN [2]
RP INTERACTION WITH DDEF1/ASAP1.
RX MEDLINE=99038209; PubMed=9819391;
RA Brown M.T., Andrade J., Radhakrishna H., Donaldson J.G., Cooper J.A.,
RA Randoz P.A.;
RT "ASAP1, a phospholipid-dependent arf GTPase-activating protein that
associates with and is phosphorylated by Src.";
RL Mol. Cell. Biol. 18:7038-7051(1998).
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
tyrosine phosphate.
CC -1- SUBUNIT: Interacts with DDEF1/ASAP1 via its SH3 domain.
CC -1- INTERACTION:
P07141:Cell; NbExp=2; IntAct=EBI-298680, EBI-777188;
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CC -1- PTM: Phosphorylated on Tyr-534 by c-Src kinase (CSK). The
CC phosphorylated form is termed pp60c-src. The phosphorylated tail
CC interacts with the SH2 domain thereby repressing kinase activity
CC (By similarity).
CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
CC subfamily.
CC -1- SIMILARITY: Contains 1 SH2 domain.
CC -1- SIMILARITY: Contains 1 SH3 domain.
CC -----
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CC Distributed under the Creative Commons Attribution-NonCommercial License
CC
EMBL: M17031; AAA40135.1; -; mRNA.
DR PIR: A43610; A43610.
DR HSP: P12931; 1A09.
DR SMK: P05480; 85-540.
DR Interact: P05480; -.
DR Ensembl: ENSMUSG0000027646; Mus musculus.
DR MGI: MGI:98397; Src.
DR GO: GO:0005515; F:Protein binding; IPI.
DR GO: GO:0004713; F:Protein-tyrosine kinase activity; IMP.
DR GO: GO:0006468; P:Protein amino acid phosphorylation; IDA.
DR InterPro: IPR000719; Prot kinase.
DR InterPro: IPR002290; Ser_Thr_kinase.
DR InterPro: IPR000980; SH2.
DR InterPro: IPR001452; SH3.
DR InterPro: IPR001245; Tyr_kinase.
DR Pfam: PF07714; Pkinase_Tyr; 1.
DR Pfam: PF00017; SH2; 1.
DR Pfam: PF00018; SH3; 1.
DR PRINTS: PR00401; SH2DOMAIN.
DR PRINTS: PR00452; SH3DOMAIN.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Prot kinase; 1.
DR ProDom: PD000093; SH2; 1.
DR ProDom: PD000065; SH3; 1.
DR SMART: SM00252; SH2; 1.
DR SMART: SM00326; SH3; 1.
DR SMART: SM00219; TYRK; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS00001; SH2; 1.
DR PROSITE: PS00002; SH3; 1.
DR ATP-binding; Kinase; Lipoprotein; Myristate; Nucleotide-binding;
KW Phosphorylation; Proto-oncogene; SH2 domain; SH3 domain; Transferase;
KW Tyrosine-protein kinase.
FT INT_MET 0
FT CHAIN 1 540
FT
FT DOMAIN 82 149
FT DOMAIN 155 252
FT DOMAIN 274 527
FT NP_BIND 280 288
FT ACT_SITE 393 393
FT BINDING 302 302
FT MOD_RES 423 423
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Query Match 98.3%; Score 2815.5; DB 1; Length 540;
Best Local Similarity 98.7%; Pred. No. 7.6e-178;
Matches 534; Conservative 3; Mismatches 3; Indels 1; Gaps 1;
QY 2 GSNKSKPKDASQRRSLPEAVNHGAGGAPPAASQTPSKPASADGHRGPSAAFAFPAAP 61
DB 1 GSNKSKPKDASQRRSLPEAVNHGAGGAPPAASQTPSKPASADGHRGPSAAFAFPAAP 59
QY 62 KLRGFGNSDVTYSPQABGLAGGVTTFVALLYDESESTETDLSFKGERLQIVNNTKVD 121
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Db 60 KLFGRNNSPTTYSPPQAGALAGVTTFFVALYDYESRTETDLSFKKGERLQIYNNTRKV
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Db 120 VREGDWMLAHSLSGTGCTGYTPSNVAPSDSIQAEWYFGKITRRESERLLLNANPRGT
Qy 182 LVRESSETTKAGYCLSVSDPFDNAKGLNVKHYKIRKLDSCGGFYITSRIOFNSLQOLVAAYSK
Db 180 LVRESSETTKAGYCLSVSDPFDNAKGLNVKHYKIRKLDSCGGFYITSRIOFNSLQOLVAAYSK
Qy 242 HADGLCHRLTTVTCPTSKPQTQGLAKDAWEIPRESLRLEVLKGGCCFGEVWNGTNGTTR
Db 240 HADGLCHRLTTVTCPTSKPQTQGLAKDAWEIPRESLRLEVLKGGCCFGEVWNGTNGTTR
Qy 302 AITKTLKPGTSPPAFLQEAQVMKKLRHEKLVQLYAVVSEEPYIYVTEYMGSLDLFLK
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Qy 362 ETGKYRLPQLVDMAAQIASGMAYVERMNVVHDLRAANLIVGENLVCKVADFGIARLIE
Db 360 ETGKYRLPQLVDMAAQIASGMAYVERMNVVHDLRAANLIVGENLVCKVADFGIARLIE
Qy 422 DNEYTARQGAKEPPIKWTAPPAALYGRFTIKSDYMSFGILLTELTGKRVPPGMVAREVL
Db 420 DNEYTARQGAKEPPIKWTAPPAALYGRFTIKSDYMSFGILLTELTGKRVPPGMVAREVL
Qy 482 DQVERGYRMPCEPCEBSLHDLMCQCKRKEPPEPPEYIQAFLDYFTSTEPQYQGEN
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Db 540 L 540

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RESULT 6
080XU2_MOUSE PRELIMINARY; PRT; 535 AA.
AC 080XU2;
DT 01-JUN-2003, Integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE Rous sarcoma oncogene, isoform 2.
GN Name=Src;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_Taxid=10990;
RN [1]
NUCSEQUENCE.
RC STRAIN=FVB/N; TISSUE=salivary gland;
RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schlier G.D.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
RA Diatchenko L., Martusola K., Farmer A.A., Rubin G.M., Hong L.,
RA Stempleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Tohbiyuki S., Carninci P., Prange C.,
RA Raha S.S., Locoellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.D., Hulyk S.W.,
RA Villalon D.K., Murthy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherf A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."

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RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=salivary gland;
RG NIH MGC Project;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL: BC039953; AAH39953.1; -; mRNA.
DR HSSP: P12931; 1043.
DR SMR: O80XU2; 86-535.
DR Ensembl: ENSMUSG00000027646; Mus musculus.
DR MGI: MGI:98397; Src.
DR GO: GO:000515; F:protein binding; IPI.
DR GO: GO:0004674; F:protein serine/threonine kinase activity; RCA.
DR GO: GO:0004713; F:protein-tyrosine kinase activity; IMP.
DR GO: GO:0006468; P:protein amino acid phosphorylation; IDA.
DR InterPro: IPR000719; Prot kinase.
DR InterPro: IPR002280; Ser_Thr_kinase.
DR InterPro: IPR000980; SH2.
DR InterPro: IPR001452; SH3.
DR InterPro: IPR001245; Tyr_kinase.
DR InterPro: IPR008266; Tyr_kinase_AS.
DR Pfam: PF07714; Pkinase_Tyr; 1.
DR Pfam: PF00017; SH2; 1.
DR Pfam: PF00018; SH3; 1.
DR PRINTS: PR00401; SH2DOMAIN.
DR PRINTS: PR00452; SH3DOMAIN.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Prot kinase; 1.
DR ProDom: PD000093; SH2; 1.
DR ProDom: PD000066; SH3; 1.
DR SMART: SM00252; SH2; 1.
DR SMART: SM00326; SH3; 1.
DR SMART: SM00219; TYRK; 1.
DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE: PS00011; PROTEIN KINASE DOM; 1.
DR PROSITE: PS00109; PROTEIN KINASE_TYR; 1.
DR PROSITE: PS50001; SH2; 1.
DR PROSITE: PS50002; SH3; 1.
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Best Local Similarity 97.8%; Pred. No. 6-2e-176;
Matches 530; Conservative 3; Mismatches 2; Indels 7; Gaps 2;

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Qy 121 DVREGDWMLAHSLSGTGCTGYTPSNVAPSDSIQAEWYFGKITRRESERLLLNANPRGT 180
Db 117 ---EGWMLAHSLSGTGCTGYTPSNVAPSDSIQAEWYFGKITRRESERLLLNANPRGT 173
Qy 181 FLVRESSETTKAGYCLSVSDPFDNAKGLNVKHYKIRKLDSCGGFYITSRIOFNSLQOLVAAYSK 240
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Qy 241 KHADGLCHRLTTVTCPTSKPQTQGLAKDAWEIPRESLRLEVLKGGCCFGEVWNGTNGTTR 300
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Qy 301 AITKTLKPGTSPPAFLQEAQVMKKLRHEKLVQLYAVVSEEPYIYVTEYMGSLDLFLK 360
Db 294 AITKTLKPGTSPPAFLQEAQVMKKLRHEKLVQLYAVVSEEPYIYVTEYMGSLDLFLK 353
Qy 361 GETGKYRLPQLVDMAAQIASGMAYVERMNVVHDLRAANLIVGENLVCKVADFGIARLIE 420

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DB 354 GEGTKILRFLQJLDMDSQJISGMAHYERMYTTRHDLRAAIIIVGENIVCVKADPGLARLI 413
 QY 421 EDNEYTARQGAKEPPIKWTAPBAALYGRFTIKSDVMSFGIILLTELTTGRVPYPCGMVREV 480
 DB 414 EDNEYTARQGAKEPPIKWTAPBAALYGRFTIKSDVMSFGIILLTELTTGRVPYPCGMVREV 473
 QY 481 LDQVGGYRMPCPPECPESLHDLMOCCWRKEPERPFYFLQALNLEBYFTSTEQYQPG 540
 DB 474 LDQVGGYRMPCPPECPESLHDLMOCCWRKEPERPFYFLQALNLEBYFTSTEQYQPG 533
 QY 541 NL 542
 DB 534 NL 535

RESULT 7
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 AC Q3UKD6;
 DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
 DT 07-FEB-2006, entry version 5.
 DE 12 days pregnant adult female placenta cDNA, RIKEN full-length
 DE enriched library, clone:1530027F01 product:Rous sarcoma oncogene, full
 DE insert sequence.
 GN Name=Src;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
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 RP NCLEBOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Placenta;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Methods Enzymol. 303:19-44(1999).
 RN [2]
 RP NCLEBOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Placenta;
 RX PubMed=16141072; DOI=10.1126/science.1112014;
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Fritch M.C., Maeda N.,
 RA Oyama R., Ravasi T., Lenhard B., Wells S., Kodzius R., Shimokawa K.,
 RA Davis M.J., Bremner S.E., Batalov S., Forrest A.R., Zavolan M.,
 RA Baisic M.J., Wilmshurst L.G., Aldous V., Allen J.E.,
 RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
 RA Banerji M., Baxter L., Belsel K.W., Bersano T., Bono H., Chalk A.M.,
 RA Chiu K.P., Choudhary V., Christofels A., Cluttenbuck D.R.,
 RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
 RA di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
 RA Fletcher C.F., Fukushima T., Furuno M., Furuki S., Gariboldi M.,
 RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
 RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
 RA Hill D., Hummelich L., Iacono M., Ikeo K., Ikawa A., Ishikawa T.,
 RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
 RA Kito H., Kollias G., Krishnan S.P., Kruger A., Kumerfeldt S.K.,
 RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
 RA Liuni S., McWilliam S., Medina Babu M., Madera M., Marchionni L.,
 RA Matsuda H., Matuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
 RA Moteugui-Tabar S., Mulder N., Nakano N., Nakachi H., Ng P.,
 RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
 RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavoni G., Pesole G.,
 RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
 RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
 RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Seesla L., Sheng Y.,
 RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
 RA Sperling S., Stupka E., Sugita K., Sultana R., Takenaka Y., Taki K.,
 RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
 RA Ueda H.R., van Nimwegen B., Verardo R., Wei C.L., Yagi K.,
 RA Yamashiki H., Zhabravsky E., Zhu S., Zimmer A., Hide W., Bult C.,
 RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,

RA Mahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
 RA Fukuda S., Kanemori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
 RA Ikida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
 RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Niimura N.,
 RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
 RA Tegan M., Waki K., Watanabe A., Okamura-Ohno Y., Suzuki H., Kawai J.,
 RA Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563(2005).
 RN [3]
 RP NCLEBOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Placenta;
 RX PubMed=16141073; DOI=10.1126/science.1112009;
 RA RIKEN Genome Exploration Research Group, and Genome Science Group
 RG (Genome Network Core Team) and the PANTOM Consortium;
 RT "Antisense transcription in the Mammalian Transcriptome.";
 RL Science 309:1564-1566(2005).
 RN [4]
 RP NCLEBOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Placenta;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Mikaido I., Osato N., Saito R., Suzuki H., Yamanaoka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schirini L.M., Kanapin A., Matsuda H., Batalov S., Belsel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chochia C., Corzani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.P., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson J.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Vervario R., Wagner L., Wahlestedt C., Wang Y., Wanabe Y., Wells C.,
 RA Wilmshurst L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kikukawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume M., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinaga Y.,
 RA Yamanishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [5]
 RP NCLEBOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Placenta;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aizawa K., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Pleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Mikaido I., Pesole G., Quackenbush J.,
 RA Schirini L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barin G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nodtore P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schonbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilmshurst L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai J., Kohetsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";

PL Nature 409:685-690(2001).
 RP [6].
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=CS7BL/6J; TISSUE=Placenta;
 RX MBLINLE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugihara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RL prepare full-length cDNA libraries for rapid discovery of new genes.";
 RN Genome Res. 10:1617-1630(2000).
 [7].
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=CS7BL/6J; TISSUE=Placenta;
 RC MBLINLE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RX Shibata K., Itoh M., Adzawa K., Nagaoaka S., Saeki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Kitsuana T., Tashiro T., Itoh M.,
 RA Sunit N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Ozawa Y., Izawa M., Ohara E., Watanabe M.,
 RA Yoneda Y., Ishikawa T., Toga K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RL sequencing pipeline with 384 multicapillary sequencer.";
 RN Genome Res. 10:1757-1771(2000).
 [8].

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Placenta;
RA Aikawa T., Carinci P., Fukuda S., Hashizume W., Hayashida K.,
RA Hoti F., Iida Y., Imamura K., Imocani K., Itoh M., Kanagawa S.,
RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Nishimura N.,
RA Nishiyori H., Nomura K., Ohno M., Sakagami N., Sano H., Sasaki D.,
RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA Muramatsu M., Hayashizaki Y.,
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL, AK146056; BA26865.1; -, mRNA.
DR MGI, MGI:98397, STC.
DR GO, GO:0005515; F:protein binding; ID1.
DR GO, GO:0004674; F:protein serine/threonine kinase activity; RCA.
DR GO, GO:0004713; F:protein-tyrosine kinase activity; IMP.
DR GO, GO:0006468; P:protein amino acid phosphorylation; IDA.
DR InterPro, IPR000719; Prot. kinase.
DR InterPro, IPR002290; Ser_Thr_kinase.
DR InterPro, IPR001452; SH3.
DR InterPro, IPR001245; Tyr_kinase.
DR InterPro, IPR008266; Tyr_kinase_AS.
DR Pfam, PF00714; Kinase_Tyr; 1.
DR Pfam, PF00017; Kinase_Tyr; 1.
DR Pfam, PF00018; SH3_1; 1.
DR PRINTS, PR00401; SH3DOMAIN.
DR PRINTS, PR00452; SH3DOMAIN.
DR PRINTS, PR00109; TYRKINASE.
DR ProDom, PD000001; Prot_kinase; 1.
DR ProDom, PD000093; SH2; 1.
DR ProDom, PD000066; SH3; 1.
DR SMART, SM00252; SH2; 1.
DR SMART, SM00326; SH3; 1.
DR SMART, SM00219; Tyrc; 1.
DR PROSITE, PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE, PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE, PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE, PS50001; SH2; 1.
DR PROSITE, PS50002; SH3; 1.
DR SEQUENCE, 535 AA; 59395 MW; 0B56EA36892D9715 CRC64;

Query Match	96.7%	Score 2769.5;	DB 2;	Length 535;
Best Local Similarity	97.2%;	Pred. No. 8.3e-175;		
Matches 527;	Conservative 3;	Mismatches 5;	Indels 7;	Gaps 2;

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Db	1	MSGNKSXPDAQSORBSLEPAMNCHAGGA	PPASQOTSPPASADCHGSPAAAPPAAE	59
OY	61	PKLPGFNSSDVTYSFORAGPLAGGTTTFVALYDSESTETDLSFKKSEBQIYVNTKRV		120
Db	60	PKLPGFNMDITYSFORAGPLAGGTTTFVALYDSESTETDLSFKKSEBQIYVNT---		119
OY	121	DYBEGDWLHLSLSTQGTGYIPSNVAPBDSIOAEEMYPGKITRRESERLLNANPRGT		180
Db	117	---EGDWLHLSLSTQGTGYIPSNVAPBDSIOAEEMYPGKITRRESERLLNANPRGT		179
OY	181	FVYBESBTTKGAACUSVSDPDNAKGLNMYHVKIRLDSGGFPYTSRQFNSLQOLVAYYS		240
Db	174	FVYBESBTTKGAACUSVSDPDNAKGLNMYHVKIRLDSGGFPYTSRQFNSLQOLVAYYS		239
OY	241	KHADGCHRLTTYCPTSKPQTQGLAKDAWEIPRESIRLEVKLGQCFGEVMWGTCNGTTR		300
Db	234	KHADGCHRLTTYCPTSKPQTQGLAKDAWEIPRESIRLEVKLGQCFGEVMWGTCNGTTR		299
OY	301	VAIKTLKPGTSPBEALQEAQVMKCLRHEKLVOLVAYVSEBPIYIVTEYMSKGSLLDFLK		360
Db	294	VAIKTLKPGTSPBEALQEAQVMKCLRHEKLVOLVAYVSEBPIYIVTEYMSKGSLLDFLK		359
OY	361	GEGTKLRLPOLYDMAAQIASCMAAYERNYVHRLRAANLVGENLYCKRADGGLARLI		420
Db	354	GEGTKLRLPOLYDMAAQIASCMAAYERNYVHRLRAANLVGENLYCKRADGGLARLI		419
OY	421	EDNEBTAPOGAKPFIKMTAPEALYGRFTIKSDVSPGILLTELTTKGRVYPGCMVAREV		480
Db	414	EDNEBTAPOGAKPFIKMTAPEALYGRFTIKSDVSPGILLTELTTKGRVYPGCMVAREV		479
OY	481	LDOVBEGYRMPCEBPCPSLHDLMOQCMRKEBEERPTFEYLQAFLEDYFTSTBQYOQGE		540
Db	474	LDOVBEGYRMPCEBPCPSLHDLMOQCMRKEBEERPTFEYLQAFLEDYFTSTBQYOQGE		539
OY	541	NL 542		
Db	534	NL 535		

RESULT #	SRC_RAT	STANDARD;	PRT;	535 AA.
ID	SRC_RAT			
AC	Q5WUD9;			
DT	30-MAY-2000,	integrated into UniProtKB/Swiss-Prot.		
DT	30-MAY-2000,	sequence version 2.		
DT	07-MAR-2006,	entry version 46.		
DE	Proto-oncogene tyrosine-protein kinase Src (BC 2.7.1.112) (p60-Src)			
DE	(c-Src) (pp60c-src).			
GN	Name=Src;			
OS	Rattus norvegicus (Rat).			
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi			
CC	Muridae; Murinae; Murinae; Rattus.			
OX	NCBI_TaxId=10116;			
RN	[1]_			
RP	NUCLEOTIDE SEQUENCE [MRNA].			
RC	SPRAIN-Sprague-Dawley; TISSUE=Testis;			
RA	Srockand J.D., Al-Khaili O., Spter B.J., Eaton D.C.;			
RT	"Rattus norvegicus proto-oncogene encoding tyrosine kinase			
RL	pp60-c-src."			
RL	Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.			
CC	-1- CATALYTIC ACTIVITY: ADP + a protein tyrosine			
CC	phosphate.			
CC	-1- PTM: Phosphorylated on Tyr-529 by c-Src kinase (GSK). The			
CC	phosphorylated form is termed pp60c-src. The phosphorylated tail			
CC	interacts with the SH2 domain thereby repressing kinase activity			
CC	(by similarity).			
CC	-1- SIMILARITY: Belongs to the Tyr protein kinase family. SRC			
CC	subfamily.			
CC	-1- SIMILARITY: Contains 1 SH2 domain.			
CC	-1- SIMILARITY: Contains 1 SH3 domain.			

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CC -----
DR EMBL: AF130457; AAD24180.1; -; mRNA.
DR HSSP: P12931, 1A09.
DR SMR: Q9MUD9; 86-535.
DR Ensembl: ENSRNOG0000009495; Rattus norvegicus.
DR RBD; 620795; Src.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR000980; SH3.
DR InterPro; IPR001452; SH2.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR008266; Tyr_pkinase_AS.
DR Pfam; PF07714; Pkinase_Tyr; 1.
DR Pfam; PF00018; SH3_1; 1.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRINTS; PR00452; SH3DOMAIN.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR ProDom; PD000093; SH2; 1.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS50001; SH2; 1.
DR PROSITE; PS50002; SH3; 1.
KW ATP-binding; Kinase; Lipoprotein; Myristate; Nucleotide-binding;
KW Phosphorylation; Proto-oncogene; SH2 domain; SH3 domain; Transferase;
KM Tyrosine-protein kinase.
FT INIT MET 0 0 By similarity.
FT CHAIN 1 535 Proto-oncogene tyrosine-protein kinase
FT SRC.
FT DOMAIN 83 144 /FTID=PRO_0000088143.
FT DOMAIN 150 247 SH3.
FT DOMAIN 269 522 SH2.
FT NP_BIND 275 283 Protein kinase.
FT ACT_SITE 386 388 ATP (By similarity).
FT BINDING 297 297 Proton acceptor (By similarity).
FT MOD_RES 419 419 Phosphothreonine (by autocatalysis) (By
FT similarity).
FT MOD_RES 529 529 Phosphotyrosine (by CSK) (By similarity).
FT LIPID 1 1 N-myristoyl glycine (By similarity).
SQ SEQUENCE 535 AA; 59947 MW; AD083DD237890EC CRC64;

Query Match 96.3%; Score 2758; DB 1; Length 535;
Best Local Similarity 97.2%; Pred. No. 4.8e-174;
Matches 527; Conservative 4; Mismatches 3; Indels 8; Gaps 3;

QY 2 GSNKSKPKDASQRRRSLEPAENVHAGCGAPASQTSKPSADGHRGPSAFA-PAAAE 60
DB 1 GSNKSKPKDASQRRRSLEPAENVHAGCGAPASQTSKPSADGHRGPSAFAFPAAAE 59
QY 61 PKLPGGNSSDVTYSPGRAGLAGVTTFVALVYRESRTEDLSFKKGERLQVNNRKV 120
DB 60 PKLPGGNSSDVTYSPGRAGLAGVTTFVALVYRESRTEDLSFKKGERLQVNNNT--- 116
QY 121 DVEBGDMLAHSLSTGQTGYIPSNVYAPSDSIQAEWYFGKITRRESERLLINAEPRGT 180
DB 117 ---EGDWMIAHSLSTGQTGYIPSNVYAPSDSIQAEWYFGKITRRESERLLINAEPRGT 173
QY 181 FLVRESSTTGAYCYLVSDFPNAGLVNKHVKIRKLDGSGFYITSRTQFNSLQQLVAYYS 240
DB 174 FLVRESSTTGAYCYLVSDFPNAGLVNKHVKIRKLDGSGFYITSRTQFNSLQQLVAYYS 233
QY 241 KHADELCHRLITTVCPSTKPTQGLAKDAMEIPRESLLEVLAGGCGFGEVWMTGNCTTR 300

DB 234 KHADELCHRLITTVCPSTKPTQGLAKDAMEIPRESLLEVLAGGCGFGEVWMTGNCTTR 293
QY 301 VAITLTKPGTMSPAFIOEAQWKKLRHEKLVQLYAVVSEPIYITVETMSKSLDPLK 360
DB 294 VAITLTKPGTMSPAFIOEAQWKKLRHEKLVQLYAVVSEPIYITVETMSKSLDPLK 353
QY 361 GETGTYRLPOLVMAAQIASGMAVVERMNVVHDDLPAANILVGENIVCKRADGLARLI 420
DB 354 GETGTYRLPOLVMAAQIASGMAVVERMNVVHDDLPAANILVGENIVCKRADGLARLI 413
QY 421 EDNEYTARQAKKPEIKNTAPEALYGRFTIKSDVMSFGILLTELTTKGRVYPPGMVREV 480
DB 414 EDNEYTARQAKKPEIKNTAPEALYGRFTIKSDVMSFGILLTELTTKGRVYPPGMVREV 473
QY 481 LDQVERGYRMPCEPCESLHDMCCQWRKSPERPFPEYLQAFLEDFYFSTEQYQGE 540
DB 474 LDQVERGYRMPCEPCESLHDMCCQWRKSPERPFPEYLQAFLEDFYFSTEQYQGE 533
QY 541 NL 542
DB 534 NL 535

RESULT 9
ID Q45QJ2_RAT PRELIMINARY; PRT; 523 AA.
AC Q45QJ2;
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Tyrosine protein kinase c-src (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SHR, and WKY;
RA Jackson B.K., Zhu C.;
RT "Genetic Similarity Between Spontaneously Hypertensive Rats and
RT Mistar-Kyoto Rats in the Coding Regions of Signal Transduction
RT Proteins";
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC tyrosine phosphate.
CC -1- SIMILARITY: Contains 1 SH3 domain.

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CC -----
DR EMBL: DQ120510; AA223849.1; -; mRNA.
DR EMBL: DQ120509; AA223848.1; -; mRNA.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0000166; F:nucleotide binding; IEA.
DR GO: GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0007242; P:intracellular signaling cascade; IEA.
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001452; SH3.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR008266; Tyr_pkinase_AS.
DR Pfam; PF07714; Pkinase_Tyr; 1.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH3_1; 1.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRINTS; PR00452; SH3DOMAIN.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR ProDom; PD000093; SH2; 1.

DR Prodom; PD000066; SH3; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00219; Tyrc; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00001; SH2; 1.
 DR PROSITE; PS00002; SH3; 1.
 DR ATP-binding; Kinase; Nucleotide-binding; SH3 domain; Transferase;
 KW Tyrosine-protein kinase.
 FT NON TER 1
 FT NON TER 523
 SQ SEQUENCE 523 AA; 58672 MW; 8D5D6C2644FD2FC CRC64;

Query Match 94.1%; Score 2693; DB 2; Length 523;
 Best Local Similarity 97.2%; Pred. No. 9,4e-170;
 Matches 515; Conservative 4; Mismatches 3; Indels 8; Gaps 3;

QY 7 KPXDASORRSLEPANNVHAGGAPASQTPSKPASADGHRGSAFA-PAAAPRLRG 65
 DB 1 KPXDASORRSLEPANNVHAGGAPASQTPSKPASADGHRGSAFA-PAAAPRLRG 59
 QY 66 GFNSDPTVTSPPRAGPLAGGVTFVALYDYSRTETDLSFKGGERLQIVNTRKVDVREG 125
 DB 60 GFNSDPTVTSPPRAGPLAGGVTFVALYDYSRTETDLSFKGGERLQIVNTRKVDVREG 113
 QY 126 DWMALHSLSTGQGTGYIPSNVAPDSIOAEEMTFGKTRRESRLILMAENPRGTELVRE 185
 DB 114 DWMALHSLSTGQGTGYIPSNVAPDSIOAEEMTFGKTRRESRLILMAENPRGTELVRE 173
 QY 186 SETTKAYCISVDPFNAGKLNKHYKIRLDSGFRTSRTOFNSIQOLVAYYSKADG 245
 DB 174 SETTKAYCISVDPFNAGKLNKHYKIRLDSGFRTSRTOFNSIQOLVAYYSKADG 233
 QY 246 LCHRLTTVCPSTKPTQGLAKDAMEIPRESLRLEVKLGOCFGEVMMGTNGTTRVALIKT 305
 DB 234 LCHRLTTVCPSTKPTQGLAKDAMEIPRESLRLEVKLGOCFGEVMMGTNGTTRVALIKT 293
 QY 306 LKPGTMSPEAFLOEAOVMKKLRHEKLVQLVAVVSEBPIVITYEYMSKSLDPLKGETGK 365
 DB 294 LKPGTMSPEAFLOEAOVMKKLRHEKLVQLVAVVSEBPIVITYEYMSKSLDPLKGETGK 353
 QY 366 YLRPLQVMAAOIAGMAVVERMYVHRDLRAANILVGNILVCKVADPGLALIDNEY 425
 DB 354 YLRPLQVMAAOIAGMAVVERMYVHRDLRAANILVGNILVCKVADPGLALIDNEY 413
 QY 426 TARQGAKPPIKMTAPAPALYGRFTIKSDVMSFGILLTELTKGRVPPGVNREVLDQVE 485
 DB 414 TARQGAKPPIKMTAPAPALYGRFTIKSDVMSFGILLTELTKGRVPPGVNREVLDQVE 473
 QY 486 RGYRMCPPECPESLHDLMOCKRKEPERPTEFYLOAFLEDYFTSTEPQ 535
 DB 474 RGYRMCPPECPESLHDLMOCKRKEPERPTEFYLOAFLEDYFTSTEPQ 523

RESULT 10
 SRC_CHICK STANDARD; PRT; 532 AA.
 AC P00523; Q90992; Q90993; Q91343; Q92013; Q98915;
 DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
 DT 15-JUL-1999, sequence version 3.
 DT 07-MAR-2006, entry version 78.
 DE Proto-oncogene tyrosine-protein kinase Src (EC 2.7.1.112) (p60-Src)
 DE (c-src) (pp60c-src).
 GN Name=SRC;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 NCBI_TaxID=9031;
 RN (1)
 RP NUCLEOTIDE SEQUENCE (ISOFORM 1).

RX MEDLINE=83155664; PubMed=6299580; DOI=10.1016/0092-8674(83)90073-9;
 RA Takeya T., Hanafusa H.;
 RT "Structure and sequence of the cellular gene homologous to the Rev arc
 gene and the mechanism for generating the transforming virus.";
 RL Cell 32:881-890(1983).
 RN (12)
 RP ERRATUM, AND SEQUENCE REVISION TO 525.
 RA Takeya T., Hanafusa H.;
 RL Cell 34:319-319(1983).
 RN (3)
 RP NUCLEOTIDE SEQUENCE (ISOFORM 2).
 RC TISSUE-Pectoralis muscle;
 RX MEDLINE=90318371; PubMed=21151117;
 RA Dorai T., Wang L.-H.;
 RT "An alternative non-tyrosine protein kinase product of the c-src gene
 in chicken skeletal muscle.";
 RL Mol. Cell. Biol. 10:4068-4079(1990).
 RN (4)
 RP NUCLEOTIDE SEQUENCE (ISOFORM 1), AND PHOSPHORYLATION SITES TYR-415 AND
 RP TYR-435.
 RX MEDLINE=97008971; PubMed=8856081;
 RA Weijand A., Neubauer G., Courtneidge S.A., Mann M., Wierenga R.K.,
 RA Superti-Furga G.;
 RT "The purification and characterization of the catalytic domain of Src
 expressed in Schizosaccharomyces pombe. Comparison of unphosphorylated
 and tyrosine phosphorylated species.";
 RL Eur. J. Biochem. 240:756-764(1996).
 RN (5)
 RP NUCLEOTIDE SEQUENCE OF 1-6.
 RX MEDLINE=83059861; PubMed=6292480;
 RA Takeya T., Hanafusa H.;
 RT "DNA sequence of the viral and cellular src gene of chickens. II.
 Comparison of the src genes of two strains of Avian sarcoma virus and
 of the cellular homolog.";
 RL J. Virol. 44:12-18(1982).
 RN (6)
 RP NUCLEOTIDE SEQUENCE OF 1-18 AND 484-533 (ISOFORM 1).
 RX MEDLINE=91304409; PubMed=1712905;
 RA Dorai T., Levy J.B., Kang L., Brugge J.S., Wang L.-H.;
 RT "Analysis of cDNAs of the proto-oncogene c-src: heterogeneity in 5'
 exon and possible mechanism for the genesis of the 3' end of v-src.";
 RL Mol. Cell. Biol. 11:4165-4176(1991).
 RN (7)
 RP ATP-BINDING SITE.
 RX MEDLINE=84270751; PubMed=6431300;
 RA Kampé M.P., Taylor S.S., Sefton B.M.;
 RT "Direct evidence that oncogenic tyrosine kinases and cyclic AMP-
 dependent protein kinase have homologous ATP-binding sites.";
 RL Nature 310:589-592(1984).
 RN (8)
 RP PHOSPHORYLATION.
 RX MEDLINE=86028181; PubMed=2996780; DOI=10.1016/0092-8674(85)90281-8;
 RA Gould K.L., Woodgett J.R., Cooper J.A., Buss J.E., Shalloway D.,
 RA Hunter T.;
 RT "Protein kinase C phosphorylates pp60src at a novel site.";
 RL Cell 42:849-857(1985).
 RN (9)
 RP PHOSPHORYLATION SITE TYR-415.
 RX MEDLINE=82082387; PubMed=6273838;
 RA Smart J.E., Oppermann H., Czernilofsky A.P., Purchio A.F.,
 RA Erikson R.L., Bishop J.M.;
 RT "Characterization of sites for tyrosine phosphorylation in the
 transforming protein of Rous sarcoma virus (pp60v-src) and its normal
 cellular homologue (pp60c-src).";
 RL Proc. Natl. Acad. Sci. U.S.A. 78:6013-6017(1981).
 RN (10)
 RP PHOSPHORYLATION SITE TYR-526.
 RX MEDLINE=86151652; PubMed=2420005;
 RA Cooper J.A., Gould K.L., Cartwright C.A., Hunter T.;
 RT "Ty527 is phosphorylated in pp60c-src: implications for regulation.";
 RL Science 231:1431-1434(1986).
 RN (11)
 RP PHOSPHORYLATION SITES THR-33; THR-45 AND SER-71.

RX MEDLINE:989243341; PubMed=2470512; DOI=10.1016/0092-8674(89)90791-5;
 RA Shenoy S., Choi J.K., Bagrodia S., Copeland T.D., Maller J.L.,
 RA Shailoway D.;
 RT "Purified maturation promoting factor phosphorylates pp60c-src at the
 RT sites phosphorylated during fibroblast mitosis.";
 RL Cell 57:763-774(1989).
 RN [12]
 RP X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 82-532.
 RX MEDLINE:98070614; PubMed=9405157; DOI=10.1006/jmbi.1997.1426;
 RA Williams J.C., Weiland A., Gonfalon S., Thompson A.,
 RA Courtneidge S.A., Superti-Furga G., Wieseng R.K.;
 RT "The 2.35 A crystal structure of the inactivated form of chicken Src:
 RT a dynamic molecule with multiple regulatory interactions.";
 RL J. Mol. Biol. 274:757-775(1997).
 RN [13]
 RP STRUCTURE BY NMR OF 80-139.
 RX MEDLINE:92279385; PubMed=8504863; DOI=10.1016/0014-5793(93)81538-B;
 RA Yu H., Rosen M.K., Schreiber S.L.;
 RT "d1h and 15N assignments and secondary structure of the Src SH3
 RT domain.";
 RL FEBS Lett. 324:87-92(1993).
 CC -1- FUNCTION: Unknown.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
 CC tyrosine phosphate.
 CC -1- ENZYME REGULATION: Becomes activated when its major tyrosine
 CC phosphorylation site is not phosphorylated. It can also be
 CC activated by point mutations as well as by truncations at the C-
 CC terminal end or by other mutations.
 CC -1- SUBUNIT: pp60c-src forms a complex with polyoma virus middle T
 CC antigen.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P00523-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P00523-2; Sequence=VSP_011844, VSP_011845;
 CC Note=Membrane-bound;
 CC -1- TISSUE SPECIFICITY: Expressed to high levels, and with a high
 CC degree of kinase activity, in certain fully differentiated cells
 CC such as neurons, platelets and macrophages. Isoform 1 is widely
 CC expressed. Isoform 2 is expressed only in the muscle.
 CC -1- PTM: Phosphorylated on Tyr-526 by c-Src kinase (CSK). The
 CC phosphorylated form is termed pp60c-src. The phosphorylated tail
 CC interacts with the SH2 domain thereby repressing kinase activity
 CC (By similarity).
 CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
 CC subfamily.
 CC -1- SIMILARITY: Contains 1 SH2 domain.
 CC -1- SIMILARITY: Contains 1 SH3 domain.
 CC -----
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 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL: V00402; CAA23596.1; -, Genomic DNA.
 DR EMBL: J00908; -, NOT ANNOTATED CDS; Genomic DNA.
 DR EMBL: M57290; AAA49078.1; -, mRNA.
 DR EMBL: S43604; AAD13831.1; -, mRNA.
 DR EMBL: S43616; AAD13835.1; -, mRNA.
 DR EMBL: S43587; AAD13830.1; -, mRNA.
 DR EMBL: S43609; AAD13832.1; -, mRNA.
 DR EMBL: S43614; AAD13834.1; -, mRNA.
 DR EMBL: S43579; AAB19353.2; -, mRNA.
 DR PIR: A00630; TVCHS.
 DR PDB: 1PTW; X-ray; A=144-246.
 DR PDB: 1FZF; X-ray; A=144-246.
 DR PDB: 1NLO; NMR; C=80-139.
 DR PDB: 1PLP; NMR; C=80-139.
 DR PDB: 1PL3; X-ray; A/B=144-245.
 DR PDB: 1PRL; NMR; C=76-139.
 DR PDB: 1PRM; NMR; C=76-139.
 DR PDB: 1RLP; NMR; C=76-139.
 DR PDB: 1RLQ; NMR; C=76-139.
 DR PDB: 1SRL; NMR; @=76-139.

DR	PDB: 1SRM; NMR: @=76-139.
DR	pdb; 2PTK; X-ray; @=-
DR	Ensembl; ENSGALG0000003855; Gallus gallus.
DR	LinkHub; P00523; -
DR	InterPro; IPR000719; Prot_kinase.
DR	InterPro; IPR002290; Ser_thr_kinase.
DR	InterPro; IPR000980; SH2
DR	InterPro; IPR001452; SH3
DR	InterPro; IPR001245; Tyr_kinase.
DR	InterPro; IPR008266; Tyr_kinase_AS.
DR	Pfam; PF07714; Pkinase_Tyr; 1.
DR	Pfam; PF00017; SH2; 1.
DR	Pfam; PF00019; SH3_1; 1.
DR	PRINTS; PR00401; SH2DOMAIN.
DR	PRINTS; PR00452; SH3DOMAIN.
DR	PRINTS; PR00109; TYRKINASE.
DR	Prodom; PD000001; Prot_kinase; 1.
DR	Prodom; PD000093; SH2; 1.
DR	Prodom; PD000066; SH3; 1.
DR	SMART; SM00252; SH2; 1.
DR	SMART; SM00326; SH3; 1.
DR	SMART; SM00219; Tykrc; 1.
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR	PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR	PROSITE; PS50001; SH2; 1.
DR	PROSITE; PS50002; SH3; 1.
KW	3D-structure; Alternative splicing; ATP-binding; Kinase; Lipoprotein;
KW	Myristate; Nucleotide-binding; Phosphorylation; Proto-oncogene;
KW	SH2 domain; SH3 domain; Transferase; Tyrosine-protein kinase.
FT	INIT_MET 0 0
FT	CHAIN 1 532
FT	/FTId=PRO_0000088144.
FT	SIC.
FT	DOMAIN 80 141
FT	DOMAIN 147 244
FT	DOMAIN 266 519
FT	NP_BIND 272 280
FT	ACT_SITE 385 385
Query Match:	92.5%; Score 2648.5; DB 1; Length 532;
Best Local Similarity	93.2%; Pred. No. 8.5e-167; Mismatches 18; Indels 9; Gaps 2
Matches 504; Conservative 10; Mismatches 18; Indels 9; Gaps 2	
OY	2 GSNSKSPDAQQRRLSLPAENVHAGCGAFASQTPSPASADGHRGSAAPAAAP 61
DB	1 GSSSKSPDPQRRSLSPEDSTH--HGFPASQTNNITAAPDTHRTTSRSRGVATEP 57
OY	62 KLPGGFNSSDTVTSPQRAAGPLAGGVTTVAIYDYESSRETDSLSPKKGERLQIVNTRKD 121
DB	58 KLPFGFNTSDTIVTSPQAGALAGGVTFVALVDYESSRETDSLSPKKGERLQIVNNT---- 113
OY	122 VREGGWMLAHLSLSTOCTGYIPBNVYAPDSIOAEEMYPEKTIIRBESERLLLNENRGTF 180
DB	114 --EGGWMLAHSLTIGQGTGYIPSNVYAPSDSIQAEEMYFEKTIIRBESERLLLNENRGTF 170
OY	182 LVRSSETTKGAYCLSVSDFDNAKGLNVKHXYIKRLKLDSGFYITSRPQFNLSLOLVAYYSK 241
DB	172 LVRSSETTKGAYCLSVSDFDNKGILNVKHXYIKRLKLDSGFYITSRKQFSLOLVAYYSK 231
OY	242 HADGICHRLTYVCPTSPKQTOGLADAMEIPRESLRLEVKLGOGCGEVMWGTMNGTTRV 301
DB	232 HADGICHRLTYNCPTSPKQTOGLADAMEIPRESLRLEVKLGOCGEVMWGTMNGTTRV 291
OY	302 AIKTLAKRGTMSPRALQEAQVWKTLRHETLVOLYAVVSEEPYLYITEVWSKSLDLFLKG 361
DB	292 AIKTLAKRGTMSPREALQEAQVWKTLRHETLVOLYAVVSEEPYLYITEVWSKSLDLFLKG 351
OY	362 ETGKYLRIIPOLYDMAAQIASGMAYVERMYVARDIRAANIIVGENIVCYADFGLARLIE 421
DB	352 EMGKYLRIIPOLYDMAAQIASGMAYVERMYVARDIRAANIIVGENIVCYADFGLARLIE 411
OY	422 DNEVYARQGAKEPIKMTAPEALVGRFTIKSDVMSFGILLTELITKGRVPVPMGNREV 481

Db 412 DNEYTAROGAKFPILKWTAPAEALYGRFTISDVWSFCILLTELTKGRVYPGVMVREVL 471
Qy 482 DQYRGYRMPCEPCESLHDLMOCCWRKPEERPFTEYLQAFLEDFYFSTEPYOGEN 541
Db 472 DQYRGYRMPCEPCESLHDLMOCCWRKPEERPFTEYLQAFLEDFYFSTEPYOGEN 531
Qy 542 L 542
Db 532 L 532

RESULT 11
SRC AVIS2 STANDARD; PRT; 586 AA.
AC P15054;
DT 01-APR-1990, integrated into UniProtKB/Swiss-Prot.
DT 30-AUG-2005, sequence version 2.
DT 07-MAR-2006, entry version 64.
DE Tyrosine-protein kinase transforming protein Src (BC 2.7.1.112) (p60-Src) (v-Src) (pp60v-src).
GN Name-v-SRC;
OS Avian sarcoma virus (strain PR257).
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Alpharetrovirus; unclassified Alpharetrovirus.
OX NCBI_TaxId=11879;
RN [1]
RP NUCLEOTIDE SEQUENCE (GENOMIC RNA).
RX MEDLINE=89094972; PubMed=2463376;
RA Geryk J., Dezele P., Barriere J.V., Svoboda J., Nehyba J., Karakoz I., Rynditch A.V., Yatsula B.A., Calochy G.;
RT "Transduction of the cellular src gene and 3' adjacent sequences in avian sarcoma virus PR257.";
RT J. Virol. 63:481-492 (1989).
RL [2]
RN NUCLEOTIDE SEQUENCE (GENOMIC RNA).
RA Yatsula B.A., Geryk J., Svoboda J., Rynditch A.V., Calochy G., Dezele P.;
RL Submitted (APR-1992) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: This phosphoprotein, required for both the initiation and the maintenance of neoplastic transformation, is a protein kinase that catalyzes the phosphorylation of tyrosine residues in vitro.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein tyrosine phosphate.
CC -1- PTM: The phosphorylated form is termed pp60v-src.
CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. SRC subfamily.
CC -1- SIMILARITY: Contains 1 SH2 domain.
CC -1- SIMILARITY: Contains 1 SH3 domain.
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CC Distributed under the Creative Commons Attribution-NonCommercial License

EMBL; M21526; AAA42583.1; -; Genomic RNA.
EMBL; X51863; CA36156.1; -; Genomic RNA.
DR PIR: A30174; TVFVPR.
DR HSSP: P00523; 2PTK.
DR SMR: P15054; 83-524.
DR InterPro: IPR000719; Prot Kinase.
DR InterPro: IPR002290; Ser Thr Kinase.
DR InterPro: IPR000980; SH2.
DR InterPro: IPR001452; SH3.
DR InterPro: IPR001245; Tyr Kinase.
DR InterPro: IPR008266; Tyr Kinase_AS.
DR Pfam: PF07714; Pkinase_Tyr; 1.
DR Pfam: PF00017; SH2_1; 1.
DR Pfam: PF00018; SH3_1; 1.
DR PRINTS: PR00401; SH2DOMAIN.
DR PRINTS: PR00452; SH3DOMAIN.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Prot Kinase; 1.
DR ProDom: PD000093; SH2_1.

DR ProDom: PD000066; SH3; 1.
DR SMART: SM00252; SH2; 1.
DR SMART: SM00326; SH3; 1.
DR SMART: SM00219; TyrcK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS50001; SH2; 1.
DR PROSITE; PS50002; SH3; 1.
KM ATP-binding; Kinase; Lipoprotein; Myristate; Nucleotide-binding;
KM Oncogene; Phosphorylation; SH2 domain; SH3 domain; Transferase;
KM Tyrosine-protein kinase.
FT INIT MET 0
FT CHAIN 1 586
FT By similarity.
FT Tyrosine-protein kinase transforming protein Src.
FT /Pfam=PRO_0000088148.
FT
FT DOMAIN 80 141
FT 147 244
FT DOMAIN 266 519
FT NP_BIND 272 280
FT ACT_SITE 385 385
FT BINDING 294 294
FT MOD_RES 415 415
FT
FT LIPID 1 1
FT N-myristoyl glycine (by host) (By similarity).
SQ SEQUENCE 586 AA; 65670 MW; 76520EF485B5CD02 CRC64;
Query Match 90.9%; Score 2603.5; DB 1; Length 586;
Best Local Similarity 93.1%; Pred. No. 9.3e-164;
Matches 496; Conservative 10; Mismatches 18; Indels 9; Gaps 2;
Qy 2 GSNKSRPKDASGRRLSRLEPENVHGAGAPASQTPSPASADGHRGSPAPAAAP 61
Db 1 GSSKSRPKDPSQRRRLSRLEPDSSTH--HGSPASQTPNKTAAPDTRTPRSRGTVATEP 57
Qy 62 KLFEGFNSSDPTVSPAPAGLAGVTFVALYDESERTETDLSFKKGERLQIVNNTKVD 121
Db 58 KLFEGNNTSTVTPSPAGLAGVTFVALYDESERTETDLSFKKGERLQIVNNT---- 113
Qy 122 VREGDWLHSLSTGQGYIPSNVYVAPSDSIQAEEMVFGKITRSESRLLINENPRGTF 181
Db 114 --EGDWLHSLSTGQGYIPSNVYVAPSDSIQAEEMVFGKITRSESRLLINENPRGTF 171
Qy 182 LVRESEETGAYCLSDPDNAGKLVNKKYKLRKDSGGFYLSRQFNSLOOLVAVYSK 241
Db 172 LVRESEETGAYCLSDPDNAGKLVNKKYKLRKDSGGFYLSRQFNSLOOLVAVYSK 231
Qy 242 HADGLCHRLTTCPTSKPOTQGLAKDAWEIPRESRLREVLGSGCGEVMGTWNGTTRV 301
Db 232 HADGLCHRLTTCPTSKPOTQGLAKDAWEIPRESRLREVLGSGCGEVMGTWNGTTRV 291
Qy 302 AITLTKPGTMSPEAFLOEAQVMKLRHEKLVLYAVVSEBPYIVTEYNSKSLDPLKG 361
Db 292 AITLTKPGTMSPEAFLOEAQVMKLRHEKLVLYAVVSEBPYIVTEYNSKSLDPLKG 351
Qy 362 EFGKYRLRLQVLYMAQIASGMAYVERNNYVRHDLAAINLVGENIVCVADGLARLIE 421
Db 352 EFGKYRLRLQVLYMAQIASGMAYVERNNYVRHDLAAINLVGENIVCVADGLARLIE 411
Qy 422 DNEYTAROGAKFPILKWTAPAEALYGRFTISDVWSFCILLTELTKGRVYPGVMVREVL 481
Db 412 DNEYTAROGAKFPILKWTAPAEALYGRFTISDVWSFCILLTELTKGRVYPGVMVREVL 471
Qy 482 DQYRGYRMPCEPCESLHDLMOCCWRKPEERPFTEYLQAFLEDFYFSTEP 534
Db 472 DQYRGYRMPCEPCESLHDLMOCCWRKPEERPFTEYLQAFLEDFYFSTEP 524

RESULT 12
SRC AVIS2 STANDARD; PRT; 567 AA.
AC P14084;

DT 01-JAN-1990, integrated into UniProtKB/Swiss-Prot.
 DT 30-ANG-2005, sequence version 2.
 DT 07-MAR-2006, entry version 60.
 DE Tyrosine-protein kinase transforming protein Src (EC 2.7.1.112) (p60-Src) (v-Src) (pp60v-src).
 GN Name=v-Src;
 OS Avian sarcoma virus (strain 51).
 OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
 OC Alpharetrovirus; unclassified Alpharetrovirus.
 OX NCBI_TaxID=11881;
 RN NUCLEOTIDE SEQUENCE.
 RP MEDLINE=87064539; PubMed=3097513;
 RA Ikawa S., Hagiino-Yamagishi K., Kawai S., Yamamoto T., Toyoshima K.;
 RT Activation of the cellular src gene by transducing retrovirus. "
 RL Mol. Cell. Biol. 6:2420-2428(1986).
 CC -1- FUNCTION: This phosphoprotein, required for both the initiation and the maintenance of neoplastic transformation, is a protein kinase that catalyzes the phosphorylation of tyrosine residues in vitro.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein tyrosine phosphate.
 CC -1- PTM: The phosphorylated form is termed pp60v-src.
 CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. SRC subfamily.
 CC -1- SIMILARITY: Contains 1 SH2 domain.
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 CC -----
 CC PIR; A25375; TVFVSI.
 DR HSSP; P00523; 2PTK.
 DR SMR; P14084; 83-524.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_Ehr_pkinase.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR InterPro; IPR008266; Tyr_pkinase_AS.
 DR Pfam; PF07714; Pkinase_Tyr; 1.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR ProDom; PD000093; SH2; 1.
 DR ProDom; PD000066; SH3; 1.
 DR SMART; SM00052; SH2; 1.
 DR SMART; SM00052; SH3; 1.
 DR SMART; SM00219; TYRKC; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 KM ATP-binding; Kinase; Lipoprotein; Myristate; Nucleotide-binding; Oncogene; Phosphorylation; SH2 domain; SH3 domain; Transferase;
 KM Tyrosine-protein kinase.
 FT INIT_MET 0
 FT CHAIN 1 567
 FT
 FT DOMAIN 80 141
 FT DOMAIN 147 244
 FT DOMAIN 266 519
 FT NP_BIND 272 280
 FT ACT_SITE 385 385
 FT BINDING 294 294
 FT MOD_RES 415 415
 FT LIPID 1 1
 N-myristoyl glycine (by hoact).

SEQ SEQUENCE 567 AA; 63501 MW; EA4FCC3B195A098D CRC64;
 Query Match 90.7%; Score 2596.5; DB 1; Length 567;
 Best Local Similarity 92.7%; Pred. No. 2,66-163;
 Matches 494; Conservative 12; Mismatches 18; Indels 9; Gaps 2;
 QY 2 GSNKSKPKDASORRRSLRPAENVHAGGAGFPASQTSKPSASACGHPSPAAPAAAP 61
 DB 1 GSSKSKPKDPSQRRSLRPPDSTH--HGFPASQTPKTKAAPDTHTPSSFGVATAP 57
 QY 62 KLFQGFNSDVTYSPQAGPLAGGVTFVALYDESRTEITDLSFKGSRLOIVNTRKVD 121
 DB 58 KLRGFNTSDTYTSPQAGALAGGVTFVALYDESRTEITDLSFKGSRLOIVNNT----- 113
 QY 122 VREGDWLAHSLSTGQTGYIPSNVAPSDSIQAEEMVFGKITRRESERLLINAEPRGT 181
 DB 114 --EGDWLAHSLTGTQGYIPSNVAPSDSIQAEEMVFGKITRRESERLLINAEPRGT 171
 QY 182 LVRESSTTKAYCLSVSDPNAKGLNKGKIRKLDGSGGFYTSRTQFNSIQQLVAYYSK 241
 DB 172 LVRESSTTKAYCLSVSDPNAKGLNKGKIRKLDGSGGFYTSRTQFNSIQQLVAYYSK 231
 QY 242 HADGLCHRLTTVCPTSPKOTQGLAKDAWEIPRESLRLEVKLGQCFGSVMNGTTRV 301
 DB 232 HADGLCHRLTNVCPTSPKOTQGLAKDAWEIPRESLRLEVKLGQCFGSVMNGTTRV 291
 QY 302 AIKTLKPGTMSPEAFLEQAVMKLRHEKLVQLYAVVSEBPIYVTEYMSKSLDPLKG 361
 DB 292 AIKTLKPGTMSPEAFLEQAVMKLRHEKLVQLYAVVSEBPIYVTEYMSKSLDPLKG 351
 QY 362 ETGKYLALPOLVMAAQAIAAGMAVERMNVYHPLRAANTLVGENLVCKVADFGALRI 421
 DB 352 EMGKYLRLPOLVMAAQAIAAGMAVERMNVYHPLRAANTLVGENLVCKVADFGALRI 411
 QY 422 DNEYTARQAKFPFKMTAPAPALYGRFTIKSDVVSFGILLTELTKGRVPPGAVNBEVL 481
 DB 412 DNEYTARQAKFPFKMTAPAPALYGRFTIKSDVVSFGILLTELTKGRVPPGAVNBEVL 471
 QY 482 DVERGYRMCPEPCPESLHDLMCQWRKSEERPTFEYIQAFLEDYFTSTEP 534
 DB 472 DVERGYRMCPEPCPESLHDLMCQWRKSEERPTFEYIQAFLEDYFTSTEP 524
 RESULT 13
 ID Q64817_9RETR PRELIMINARY; PRT; 587 AA.
 AC Q64817;
 DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
 DT 07-FEB-2006, entry version 28.
 DE Protein-tyrosine kinase.
 GN Name=src;
 OS Avian sarcoma virus.
 OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
 OC Alpharetrovirus; unclassified Alpharetrovirus.
 OX NCBI_TaxID=11876;
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=PR2257/16;
 RX MEDLINE=95016532; PubMed=7931166;
 RA Yatsuda B.A., Geryk J., Svoboda J., Rynditch A.V., Calochy G.,
 RT "Evolution and origin of virus PR2257, a recent c-src transducing virus."
 RT J. Gen. Virol. 75:2777-2781(1994).
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
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 CC -----
 CC EMBL; L21974; AAC37877.1; -; Genomic_DNA.
 DR HSSP; P00523; 2PTK.
 DR SMR; Q64817; 84-525.
 DR GO; GO:0005524; P:ATP binding; IEA.


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FT TURN 103 104
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Query Match 87.9%; Score 2515.5; DB 1; Length 525;
Best Local Similarity 91.8%; Pred. No. 5,4e-158;
Matches 481; Conservative 12; Mismatches 22; Indels 9; Gaps 2;
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QY 62 KLFGGFRSSPTVTSPQAGLAGVTFVALYDYESTETDLSFKGERLQIVNTRKVD 121
Db 58 KLFGGFNTSDVTSPQAGLAGVTFVALYDYESTETDLSFKGERLQIVNNT----- 113
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Db 114 --EGDWMLANSLTTGOTGYIPSNYVAPSDSIQAEEMVFGKITRRESERLLNENPRGTF 171
QY 182 LVRESETTKAYCLSVSDFPNAGLNVKHKIRKLDGSGFYITSRTQFNSLQQLVAYYSK 241
Db 172 LVRESETTKAYCLSVSDFPNAGLNVKHKIRKLDGSGFYITSRTQFNSLQQLVAYYSK 231
QY 242 HADGLCHRLTTVQPTSKPOTQGLAKDAWEIPRESLRLEVLDGQCFGEVWMTNGTTRV 301
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Db 292 AITLTKPGTSPPAFLQEAQVMKKLRHEKLVQLYAVVSEEPYIVTEYMSKSLDPLKG 351
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Db 412 DNEYTARQGAKEPIKWTAPAAALYGRFTIKSDVWSFGILLTELTKGRVPIPGWNGEVL 471
QY 482 DQVERGYRMCPEPCPESLHDLNMQCWRKEPEEPTEFYLOAF 525
Db 472 DQVERGYRMCPEPCPESLHDLNMQCWRKEPEEPTEFYLOAF 515
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Search completed: June 5, 2006, 17:15:30
Job time : 156.335 sec

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 5, 2006, 17:15:49 ; Search time 31.134 Seconds
(without alignments)
1523.786 Million cell updates/sec

Title: US-10-691-079-1

Perfect score: 2863
Sequence: 1 MGSNKSXPXASQRRSLP.....AFLEDYFTSTPEYQPGENL 542

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5 COMB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6 COMB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7 COMB.pep:*
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- 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/bactfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2821	98.5	536	1 US-07-820-011A-4	Sequence 4, Appli
2	2821	98.5	536	2 US-08-426-509A-13	Sequence 13, Appli
3	2821	98.5	536	2 US-08-232-545-13	Sequence 13, Appli
4	2821	98.5	536	2 US-09-444-711A-2	Sequence 2, Appli
5	2821	98.5	536	2 US-09-929-266-10	Sequence 10, Appli
6	2821	98.5	536	2 US-09-977-261-13	Sequence 13, Appli
7	2821	98.5	536	5 PCT-US93-00445-4	Sequence 4, Appli
8	2821	98.5	536	5 PCT-US95-05008-13	Sequence 13, Appli
9	2821	98.5	537	2 US-09-949-016-10282	Sequence 10282, A
10	2788	97.4	530	2 US-09-444-711A-4	Sequence 4, Appli
11	2650.5	92.6	533	2 US-09-470-881-3	Sequence 3, Appli
12	2647.5	92.5	533	1 US-07-820-011A-2	Sequence 2, Appli
13	2647.5	92.5	533	5 PCT-US93-00445-2	Sequence 2, Appli
14	2110.5	73.7	543	2 US-08-426-509A-14	Sequence 14, Appli
15	2110.5	73.7	543	2 US-08-232-545-14	Sequence 14, Appli
16	2110.5	73.7	543	2 US-09-470-881-8	Sequence 8, Appli
17	2110.5	73.7	543	2 US-09-538-092-870	Sequence 870, App
18	2110.5	73.7	543	2 US-09-977-261-14	Sequence 14, Appli
19	2110.5	73.7	543	5 PCT-US95-05008-14	Sequence 14, Appli
20	2108.5	73.6	541	2 US-09-864-281-20	Sequence 20, Appli
21	1936	67.6	536	2 US-08-426-509A-12	Sequence 12, Appli
22	1936	67.6	536	2 US-08-232-545-12	Sequence 12, Appli
23	1936	67.6	536	2 US-09-977-261-12	Sequence 12, Appli
24	1931	67.4	532	5 PCT-US95-05008-12	Sequence 12, Appli
25	1931	67.4	532	1 US-08-594-447-1	Sequence 1, Appli
26	1931	67.4	532	1 US-08-665-647-1	Sequence 1, Appli

27	1919.5	67.0	537	2 US-08-426-509A-11	Sequence 11, Appli
28	1919.5	67.0	537	2 US-08-232-545-11	Sequence 11, Appli
29	1919.5	67.0	537	2 US-09-977-261-11	Sequence 11, Appli
30	1919.5	67.0	537	5 PCT-US95-05008-11	Sequence 859, App
31	1919.5	67.0	536	2 US-09-538-092-859	Sequence 213, App
32	1911.5	66.8	537	2 US-09-771-161A-212	Sequence 213, App
33	1911.5	66.8	537	2 US-09-771-161A-213	Sequence 15, Appli
34	1843	64.4	529	2 US-08-426-509A-15	Sequence 15, Appli
35	1843	64.4	529	2 US-08-232-545-15	Sequence 15, Appli
36	1843	64.4	529	2 US-09-538-092-885	Sequence 885, App
37	1843	64.4	529	2 US-09-977-261-15	Sequence 15, Appli
38	1843	64.4	529	5 PCT-US95-05008-15	Sequence 15, Appli
39	1735.5	60.6	485	2 US-10-094-749-2726	Sequence 10415, A
40	1529	53.4	573	2 US-09-949-016-10415	Sequence 17, Appli
41	1525.5	53.3	505	2 US-08-426-509A-17	Sequence 17, Appli
42	1525.5	53.3	505	2 US-08-232-545-17	Sequence 17, Appli
43	1525.5	53.3	505	2 US-09-977-261-17	Sequence 17, Appli
44	1525.5	53.3	505	5 PCT-US95-05008-17	Sequence 17, Appli
45	1461	51.0	508	2 US-09-862-154-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-07-820-011A-4
; Sequence 4, Application US/07820011A
; Patent No. 5336615
; GENERAL INFORMATION:
; APPLICANT: Bell, Leonard
; APPLICANT: Madri, Joseph A.
; APPLICANT: Warren, Stephen L.
; APPLICANT: Luthinger, Daniel J.
; TITLE OF INVENTION: Genetically Engineered
; TITLE OF INVENTION: Endothelial Cells Exhibiting Enhanced
; TITLE OF INVENTION: Migration
; TITLE OF INVENTION: and Plasminogen Activator Activity
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESS: Maurice M. Klee
; STREET: 1951 Burr Street
; CITY: Fairfield
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06430
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 KB storage
; COMPUTER: IBM PC XT
; OPERATING SYSTEM: PC-DOS/MS-DOS 2.10
; SOFTWARE: Displaywrite 3
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/820, 011A
; FILING DATE: 19920106
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Klee, Maurice M.
; REGISTRATION NUMBER: 30,399
; REFERENCE/DOCKET NUMBER: LB-101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203) 255 1400
; TELEFAX: (203) 254 1101
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 536 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: Linear
; MOLECULE TYPE: Protein
; HYPOTHEICAL: No
; FRAGMENT TYPE: Complete Sequence
; ORIGINAL SOURCE:
; ORGANISM: Homo sapien
; PUBLICATION INFORMATION:
; AUTHORS: Anderson, Stephen K.

AUTHORS: Gidbs, Carol P.
AUTHORS: Tanaka, Akio
AUTHORS: Kung, Hsing-Jien
AUTHORS: Fujita, Donald J.
TITLE: Human Cellular src Gene:
TITLE: Nucleotide Sequence and Derived Amino
TITLE: Acid Sequence of the Region Coding for
TITLE: the Carboxy-Terminal Two-Thirds of
TITLE: pp60c-src
JOURNAL: Molecular and Cellular Biology
VOLUME: 5
ISSUE: 5
PAGES: 1122-1129
DATE: May, 1985
PUBLICATION INFORMATION:
AUTHORS: Tanaka, Akio
AUTHORS: Gidbs, Carol P.
AUTHORS: Arthur, Richard R.
AUTHORS: Anderson, Stephen K.
AUTHORS: Kung, Hsing-Jien
AUTHORS: Fujita, Donald J.
TITLE: DNA Sequence Encoding the
TITLE: Amino-Terminal Region of the Human c-src
TITLE: Protein: Implications of Sequence
TITLE: Divergence among src-Type Kinase
TITLE: Oncogenes
JOURNAL: Molecular and Cellular Biology
VOLUME: 7
ISSUE: 5
PAGES: 1978-1983
DATE: May, 1987
US-07-820-011A-4

Query Match 98.5%; Score 2821; DB 1; Length 536;
Best Local Similarity 98.9%; Pred. No. 6,4e-214;
Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

1 MGSNKKPKDASGRRLSLPDAENVHAGGAGAPPASQTPSKPASADGHRGSAAPAPAAAE 60
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118 ---EGDWMWLHSLSTQGTGYIPSNVYAPSDSIQAEWYFGKTRRSEERLLNAENPRGT 174
181 FLVRESEETTKGAYCLSVSPDNAGKLVNKHVYKIRKLDGSGFYITSTRTOFNSLQOLVAYYS 240
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421 EDNEYTARQAKPEPKMTABEALYGRFTIKSDVMSFGILLTELTKGRVYPGMYNREV 480
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Qy 541 NL 542
Db 535 NL 536

RESULT 2
US-08-426-509A-13
Sequence 13, Application US/08426509A
Patent No. 6326469
GENERAL INFORMATION:
APPLICANT: Ullrich, Axel
APPLICANT: Gishizky, Mikhail
APPLICANT: Sures, Irman G.
TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN
TITLE OF INVENTION: TYROSINE KINASES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York,
STATE: NY
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/426,509A
FILING DATE: 21-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/232,545
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-0074-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 536 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: No. 6326469e
US-08-426-509A-13

Query Match 98.5%; Score 2821; DB 2; Length 536;
Best Local Similarity 98.9%; Pred. No. 6,4e-214;
Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

1 MGSNKKPKDASGRRLSLPDAENVHAGGAGAPPASQTPSKPASADGHRGSAAPAPAAAE 60
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118 ---EGDWMWLHSLSTQGTGYIPSNVYAPSDSIQAEWYFGKTRRSEERLLNAENPRGT 174
181 FLVRESEETTKGAYCLSVSPDNAGKLVNKHVYKIRKLDGSGFYITSTRTOFNSLQOLVAYYS 240
175 FLVRESEETTKGAYCLSVSPDNAGKLVNKHVYKIRKLDGSGFYITSTRTOFNSLQOLVAYYS 234
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Db 235 KHADELCHRLTTVCPTSKPQTGLAKDAMEI PRESLELVKGGCGEVMGTMNGTTR 294
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Qy 421 EDNEYTAROGAKPFIKMTAPEALYGRFTIKSDVMSFGILLTBLTTKGRVYPGMVNRV 480
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Db 535 NL 536

RESULT 3
US-08-232-545-13
; Sequence 13, Application US/08232545
; Patent No. 6506578
; GENERAL INFORMATION:
; APPLICANT: Ullrich, Axel
; APPLICANT: Giehlitzky, Mikhail
; APPLICANT: Surea, Iman G.
; TITLE OF INVENTION: No. 6506578e1 Megakaryocytic Protein Tyrosine
; TITLE OF INVENTION: Kinases
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,545
; FILING DATE: 22-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)790-9090
; TELEFAX: (212)869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SRO ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 536 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-232-545-13

Query Match 98.5%; Score 2821; DB 2; Length 536;
Best Local Similarity 98.9%; Pred. No. 6,4e-214;
Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;
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Db 1 MGSNKSFKPKASQRRRLSEPAENVHAGGAGFPASQTPSKRPASADGHRGSAAPAPAAE 60
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Db 61 PKLPGFNSSDYTVTSPPRAGPLAGGVTTPVALYDSERTETDLSFKKGERLQIVNTRKV 117
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Db 175 FLVRESSTGAYCLASDSDPNAGLVKHKYIKRLDSGGFYTSRTOFNSLQOLVAYYS 234
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Db 235 KHADELCHRLTTVCPTSKPQTGLAKDAMEI PRESLELVKGGCGEVMGTMNGTTR 294
Qy 301 VAITKLPGTMSPEAFIQEAQVMKKLRHEKLVQLYAVVSEBPIYITEYMSKSLDPLK 360
Db 295 VAITKLPGTMSPEAFIQEAQVMKKLRHEKLVQLYAVVSEBPIYITEYMSKSLDPLK 354
Qy 361 GETGKYRLPOLVMAAQIASGMAYVERMNYVHRDLAAANILVGENLVCKVADGRLRI 420
Db 355 GETGKYRLPOLVMAAQIASGMAYVERMNYVHRDLAAANILVGENLVCKVADGRLRI 414
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Db 475 LDQVERGYRMPCEPCESLHDLMCQCRKEPERPFTEYLQAFLEDFYFSTEPQYQGE 534
Qy 541 NL 542
Db 535 NL 536

RESULT 4
US-09-444-711A-2
; Sequence 2, Application US/09444711A
; Patent No. 6764833
; GENERAL INFORMATION:
; APPLICANT: Yeatman, Timothy J.
; APPLICANT: Iddy, Rosalyn B.
; TITLE OF INVENTION: Mutated SRC Oncogene Composition and Methods
; FILE REFERENCE: USF-7136
; CURRENT APPLICATION NUMBER: US/09/444,711A
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent in version 3.1
; SRO ID NO 2
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(536)
; OTHER INFORMATION: amino acid sequence of non-receptor tyrosine kinase encoded
; OTHER INFORMATION: by the normal c-Src coding region
; US-09-444-711A-2

Query Match 98.5%; Score 2821; DB 2; Length 536;
Best Local Similarity 98.9%; Pred. No. 6,4e-214;
Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;
Qy 1 MGSNKSFKPKASQRRRLSEPAENVHAGGAGFPASQTPSKRPASADGHRGSAAPAPAAE 60
Db 1 MGSNKSFKPKASQRRRLSEPAENVHAGGAGFPASQTPSKRPASADGHRGSAAPAPAAE 60
Qy 61 PKLPGFNSSDYTVTSPPRAGPLAGGVTTPVALYDSERTETDLSFKKGERLQIVNTRKV 120

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Db 61 PKLFGFNSSDVTYTSQORAGPLAGGVTTFVALYDYSRTETDLSFKKGERLQIVNNT --- 117
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Qy 181 FLVRESEETTKGAYCLSVSPFDNAKGLNVGHYKIRKLDGSGFYITSTRTOFNSLQOLVAYYS 240
Db 175 FLVRESEETTKGAYCLSVSPFDNAKGLNVGHYKIRKLDGSGFYITSTRTOFNSLQOLVAYYS 234
Qy 241 KHADGCHRLTYTCPTSPKQTOGLADAMEIPRESRLRLEVKGCGCFGEVWMTGNCTTR 300
Db 235 KHADGCHRLTYTCPTSPKQTOGLADAMEIPRESRLRLEVKGCGCFGEVWMTGNCTTR 294
Qy 301 VAIKTLKPGTMSPEAFLOEAQVWKLRHEKLVOLYAVVSEBPIYIYTEWMSKSLDPLK 360
Db 295 VAIKTLKPGTMSPEAFLOEAQVWKLRHEKLVOLYAVVSEBPIYIYTEWMSKSLDPLK 354
Qy 361 GETGKTLRLPOLYDMAAOIASGMAVYERMMVYHRDLRAANILVGENLVCKVADPGLARLI 420
Db 355 GETGKTLRLPOLYDMAAOIASGMAVYERMMVYHRDLRAANILVGENLVCKVADPGLARLI 414
Qy 421 EDNEYTAROGAKPEPIKMTAPEALYGRFTIKSDVMSFGILLTELTKGRVYPGMVNRREV 480
Db 415 EDNEYTAROGAKPEPIKMTAPEALYGRFTIKSDVMSFGILLTELTKGRVYPGMVNRREV 474
Qy 481 LDQVERGYMPCPECPESLHDLMCQWKEPBERPTFEYLOAFLEDYFTSTEPYOYQGE 540
Db 475 LDQVERGYMPCPECPESLHDLMCQWKEPBERPTFEYLOAFLEDYFTSTEPYOYQGE 534
Qy 541 NL 542
Db 535 NL 536
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```
RESULT 5
US-09-929-266-10
; Sequence 10, Application US/09929266
; Patent No. 6824981
; GENERAL INFORMATION:
; APPLICANT: Brian T. Chait
; APPLICANT: Darin R. Lattimer
; APPLICANT: Paul M. Lizardi
; APPLICANT: Eric R. Kershner
; APPLICANT: Jon S. Morrow
; APPLICANT: Matthew E. Roth
; APPLICANT: Martin J. McConnell
; APPLICANT: Kevin J. McConnell
; TITLE OF INVENTION: ULTRA-SENSITIVE DETECTION SYSTEMS
; FILE REFERENCE: 01173.000302
; CURRENT APPLICATION NUMBER: US/09/929,266
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/224,939
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/283,498
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FaalSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-929-266-10
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Query Match 98.5%; Score 2821; DB 2; Length 536;
Best Local Similarity 98.9%; Pred. No. 6,4e-214;
Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;
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Qy 1 MGSNKKPYDASQRRSLSPAENVHAGGAGAPASQTPSKPASADGHRGSAAPAPAAAE 60
Db 1 MGSNKKPYDASQRRSLSPAENVHAGGAGAPASQTPSKPASADGHRGSAAPAPAAAE 60

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Qy 61 PKLFGFNSSDVTYTSQORAGPLAGGVTTFVALYDYSRTETDLSFKKGERLQIVNNT 120
Db 61 PKLFGFNSSDVTYTSQORAGPLAGGVTTFVALYDYSRTETDLSFKKGERLQIVNNT 117
Qy 121 DVREGDWMHLAHSISTGQTGYIPSNVYAPSDSIQAEEMYPGKITRRSERLLNAENPRGT 180
Db 118 ---EGDWMHLAHSISTGQTGYIPSNVYAPSDSIQAEEMYPGKITRRSERLLNAENPRGT 174
Qy 181 FLVRESEETTKGAYCLSVSPFDNAKGLNVGHYKIRKLDGSGFYITSTRTOFNSLQOLVAYYS 240
Db 175 FLVRESEETTKGAYCLSVSPFDNAKGLNVGHYKIRKLDGSGFYITSTRTOFNSLQOLVAYYS 234
Qy 241 KHADGCHRLTYTCPTSPKQTOGLADAMEIPRESRLRLEVKGCGCFGEVWMTGNCTTR 300
Db 235 KHADGCHRLTYTCPTSPKQTOGLADAMEIPRESRLRLEVKGCGCFGEVWMTGNCTTR 294
Qy 301 VAIKTLKPGTMSPEAFLOEAQVWKLRHEKLVOLYAVVSEBPIYIYTEWMSKSLDPLK 360
Db 295 VAIKTLKPGTMSPEAFLOEAQVWKLRHEKLVOLYAVVSEBPIYIYTEWMSKSLDPLK 354
Qy 361 GETGKTLRLPOLYDMAAOIASGMAVYERMMVYHRDLRAANILVGENLVCKVADPGLARLI 420
Db 355 GETGKTLRLPOLYDMAAOIASGMAVYERMMVYHRDLRAANILVGENLVCKVADPGLARLI 414
Qy 421 EDNEYTAROGAKPEPIKMTAPEALYGRFTIKSDVMSFGILLTELTKGRVYPGMVNRREV 480
Db 415 EDNEYTAROGAKPEPIKMTAPEALYGRFTIKSDVMSFGILLTELTKGRVYPGMVNRREV 474
Qy 481 LDQVERGYMPCPECPESLHDLMCQWKEPBERPTFEYLOAFLEDYFTSTEPYOYQGE 540
Db 475 LDQVERGYMPCPECPESLHDLMCQWKEPBERPTFEYLOAFLEDYFTSTEPYOYQGE 534
Qy 541 NL 542
Db 535 NL 536
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RESULT 6
US-09-977-261-13
; Sequence 13, Application US/09977261
; Patent No. 6908984
; GENERAL INFORMATION:
; APPLICANT: ULRICH, AXEL
; APPLICANT: GISHIZKY, MIKHAIL
; APPLICANT: SURES, IRMINGARD
; TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES
; FILE REFERENCE: 038602/1259
; CURRENT APPLICATION NUMBER: US/09/977,261
; PRIOR FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 08/232,545
; PRIOR FILING DATE: 1994-04-22
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-977-261-13
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Query Match 98.5%; Score 2821; DB 2; Length 536;
Best Local Similarity 98.9%; Pred. No. 6,4e-214;
Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;
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Qy 1 MGSNKKPYDASQRRSLSPAENVHAGGAGAPASQTPSKPASADGHRGSAAPAPAAAE 60
Db 1 MGSNKKPYDASQRRSLSPAENVHAGGAGAPASQTPSKPASADGHRGSAAPAPAAAE 60

Qy 61 PKLFGFNSSDVTYTSQORAGPLAGGVTTFVALYDYSRTETDLSFKKGERLQIVNNT 120
Db 61 PKLFGFNSSDVTYTSQORAGPLAGGVTTFVALYDYSRTETDLSFKKGERLQIVNNT 117

Qy 121 DVREGDWMHLAHSISTGQTGYIPSNVYAPSDSIQAEEMYPGKITRRSERLLNAENPRGT 180
Db 121 DVREGDWMHLAHSISTGQTGYIPSNVYAPSDSIQAEEMYPGKITRRSERLLNAENPRGT 180

Db 118 ---EGDMMWLAHSLSTGOTGYIPSNVAPSDSIQAEWYFGKITRRESRLILNENPRT 174
QY 181 FLVRESETTKAYCLISVDFPNAGLNVKHKIRKLDGSGFYTSRTQFNSIQOLVAYYS 240
Db 175 FLVRESETTKAYCLISVDFPNAGLNVKHKIRKLDGSGFYTSRTQFNSIQOLVAYYS 234
QY 241 KHAAGLCHRLTTVCPPTSKEPOTQGLAKDAMEIPRESLRLEVLDGCGCFGEVWMTNGTTR 300
Db 235 KHAAGLCHRLTTVCPPTSKEPOTQGLAKDAMEIPRESLRLEVLDGCGCFGEVWMTNGTTR 294
QY 301 VAITLKPGTMSPEAFLOEAOVMKKLRHEKLVOLYAVVSEBPIYIVTEYMSKSLDPLK 360
Db 295 VAITLKPGTMSPEAFLOEAOVMKKLRHEKLVOLYAVVSEBPIYIVTEYMSKSLDPLK 354
QY 361 GETGKYRLPLQVDMAAQIASGMAVERMNVYHRDLRAANILVGENLVCKVADGLARLI 420
Db 355 GETGKYRLPLQVDMAAQIASGMAVERMNVYHRDLRAANILVGENLVCKVADGLARLI 414
QY 421 EDNEYTARQGAKKFPIKMTAPBALYGRFTIKSDVMSFGILLTELTTKGRVYPGMVNREV 480
Db 415 EDNEYTARQGAKKFPIKMTAPBALYGRFTIKSDVMSFGILLTELTTKGRVYPGMVNREV 474
QY 481 LDQVERGYRMPCEPCEPSLHDLMCQCRKEPSEBPIYVQAFLEDYFTSTEPQYDGE 540
Db 475 LDQVERGYRMPCEPCEPSLHDLMCQCRKEPSEBPIYVQAFLEDYFTSTEPQYDGE 534
QY 541 NL 542
Db 535 NL 536

RESULT 7
PCT-US93-00445-4
; Sequence 4, Application PC/TUS9300445
; GENERAL INFORMATION:
; APPLICANT: Bell, Leonard
; APPLICANT: Madril, Joseph A.
; APPLICANT: Warren, Stephen L.
; APPLICANT: Luthringer, Daniel J.
; TITLE OF INVENTION: Genetically Engineered
; TITLE OF INVENTION: Endothelial Cells
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESS: Maurice M. Klee
; STREET: 1951 Burr Street
; CITY: Fairfield
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06430
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 760 Kb storage
; COMPUTER: DELL 486/50
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: Displaywrite 3
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/00445
; FILING DATE: 19930105
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/820,011
; FILING DATE: 06-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Klee, Maurice M.
; REGISTRATION NUMBER: 30,399
; REFERENCE/DOCKET NUMBER: ALX-101PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203) 255 1400
; TELEFAX: (203) 254 1101
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 536 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: Linear

MOLECULE TYPE: Protein
; HYPOTHETICAL: No
; FRAGMENT TYPE: Complete Sequence
; ORIGINAL SOURCE:
; ORGANISM: Homo sapien
; PUBLICATION INFORMATION:
; AUTHORS: Anderson, Stephen K.
; AUTHORS: Gibbs, Carol P.
; AUTHORS: Tanaka, Akio
; AUTHORS: Kung, Hsing-Jien
; AUTHORS: Fujita, Donald J.
; TITLE: Human Cellular src Gene:
; TITLE: Nucleotide Sequence and Derived Amino
; TITLE: Acid Sequence of the Region Coding for
; TITLE: the Carboxy-Terminal Two-Thirds of
; TITLE: p60c-src
; JOURNAL: Molecular and Cellular Biology
; VOLUME: 5
; ISSUE: 5
; PAGES: 1122-1129
; DATE: May, 1985
; PUBLICATION INFORMATION:
; AUTHORS: Tanaka, Akio P.
; AUTHORS: Gibbs, Carol P.
; AUTHORS: Arthur, Richard R.
; AUTHORS: Anderson, Stephen K.
; AUTHORS: Kung, Hsing-Jien
; AUTHORS: Fujita, Donald J.
; TITLE: DNA Sequence Encoding the
; TITLE: Amino-Terminal Region of the Human c-src
; TITLE: Protein: Implications of Sequence
; TITLE: Divergence among src-Type Kinase
; TITLE: Oncogenes
; JOURNAL: Molecular and Cellular Biology
; VOLUME: 7
; ISSUE: 5
; PAGES: 1978-1983
; DATE: May, 1987
; PCT-US93-00445-4
Query Match 98.5%; Score 2821; DB 5; Length 536;
Best Local Similarity 98.9%; Pred. No. 6.4e-214;
Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;
QY 1 MGSNKSXPKDASQRRRSLEPAENVHAGGAFPPASQTESKPSADGHRGSPAAPAAAE 60
Db 1 MGSNKSXPKDASQRRRSLEPAENVHAGGAFPPASQTESKPSADGHRGSPAAPAAAE 60
QY 61 PKLFGGRSSPTVTSPQAGPLAGVYTFVALYDSESTETDLSFKKGBRLQIVNNTKV 120
Db 61 PKLFGGRSSPTVTSPQAGPLAGVYTFVALYDSESTETDLSFKKGBRLQIVNNTKV 117
QY 121 DVREGDMMWLAHSLSTGOTGYIPSNVAPSDSIQAEWYFGKITRRESRLILNENPRT 180
Db 118 ---EGDMMWLAHSLSTGOTGYIPSNVAPSDSIQAEWYFGKITRRESRLILNENPRT 174
QY 181 FLVRESETTKAYCLISVDFPNAGLNVKHKIRKLDGSGFYTSRTQFNSIQOLVAYYS 240
Db 175 FLVRESETTKAYCLISVDFPNAGLNVKHKIRKLDGSGFYTSRTQFNSIQOLVAYYS 234
QY 241 KHAAGLCHRLTTVCPPTSKEPOTQGLAKDAMEIPRESLRLEVLDGCGCFGEVWMTNGTTR 300
Db 235 KHAAGLCHRLTTVCPPTSKEPOTQGLAKDAMEIPRESLRLEVLDGCGCFGEVWMTNGTTR 294
QY 301 VAITLKPGTMSPEAFLOEAOVMKKLRHEKLVOLYAVVSEBPIYIVTEYMSKSLDPLK 360
Db 295 VAITLKPGTMSPEAFLOEAOVMKKLRHEKLVOLYAVVSEBPIYIVTEYMSKSLDPLK 354
QY 361 GETGKYRLPLQVDMAAQIASGMAVERMNVYHRDLRAANILVGENLVCKVADGLARLI 420
Db 355 GETGKYRLPLQVDMAAQIASGMAVERMNVYHRDLRAANILVGENLVCKVADGLARLI 414
QY 421 EDNEYTARQGAKKFPIKMTAPBALYGRFTIKSDVMSFGILLTELTTKGRVYPGMVNREV 480

Db 415 EDNEYTARQAKPFIKMTAPEALYGRFTIKSDVMSGILLTELTTKGRVPGMVNREV 474
Qy 481 LDQVGRGYMPCPEPCESLHDLCCQWKREPERPTEFYLOAFLEDTSTEPQYQPG 540
Db 475 LDQVGRGYMPCPEPCESLHDLCCQWKREPERPTEFYLOAFLEDTSTEPQYQPG 534
Qy 541 NL 542
Db 535 NL 536

RESULT 8
PCT-US95-05008-13
Sequence 13: Application PC/TUS9505008
GENERAL INFORMATION:
APPLICANT: Sugen, Inc.
APPLICANT: 515 Galveston Drive
APPLICANT: Redwood City, California 94063-4720
APPLICANT: United States of America
APPLICANT: Wissenschaften E.V.
APPLICANT: Hofgarten Str. 2
APPLICANT: Munchen 80539
APPLICANT: Germany
TITLE OF INVENTION: Novel Megakaryocytic Protein Tyrosine
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05008
FILING DATE: 24-APR-1995
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/232,545
FILING DATE: 22-APR-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-074
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
TELEFAX: (212)869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 536 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
PCT-US95-05008-13

Query Match 98.5%; Score 2821; DB 5; Length 536;
Best Local Similarity 98.9%; Pred. No. 6,4e-214;
Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

Qy 1 MGSNKSXPDAQORRRSLPEAENVHAGAGGAFPASQTPSKPASAADGHRGSAFAFAAAE 60
Db 1 MGSNKSXPDAQORRRSLPEAENVHAGAGGAFPASQTPSKPASAADGHRGSAFAFAAAE 60
Qy 61 PKLFGGFNSSDVTSPQAGPLAGVTTFFVALYDYESRTEITDLSFKKGERLQIVNNTKRV 120

Db 61 PKLFGGFNSSDVTSPQAGPLAGVTTFFVALYDYESRTEITDLSFKKGERLQIVNNT--- 117
Qy 121 DVAREGMWLAHSISTQGTGYIPSNYVAPSDSIOAEMVYGKTRRSERLLNAENPRGT 180
Db 118 ---EGDMMWLAHSISTQGTGYIPSNYVAPSDSIOAEMVYGKTRRSERLLNAENPRGT 174
Qy 181 FLVRESEETTKGAYCLVSPDFDNAGKLVNKHVKLRKLDGSGGFYITSTRTOFNSLQQLVAAYS 240
Db 175 FLVRESEETTKGAYCLVSPDFDNAGKLVNKHVKLRKLDGSGGFYITSTRTOFNSLQQLVAAYS 224
Qy 241 KHAADGLCHRLTYCPTSKPOTQGLADAMEIPRESLRLEVKLGQCGFGEVMMGTWNGTTR 300
Db 235 KHAADGLCHRLTYCPTSKPOTQGLADAMEIPRESLRLEVKLGQCGFGEVMMGTWNGTTR 294
Qy 301 VAIKTLKPGTMSPEALQEAQVWKLRHEKLYOLVAVVEBPYIYTEYMSKSLDPLK 360
Db 295 VAIKTLKPGTMSPEALQEAQVWKLRHEKLYOLVAVVEBPYIYTEYMSKSLDPLK 354
Qy 361 GETGKTLRLPOLVDMAGIASGMAVYERMYVHRDLRAANILVGENLVCKVADFGLARLI 420
Db 355 GETGKTLRLPOLVDMAGIASGMAVYERMYVHRDLRAANILVGENLVCKVADFGLARLI 414
Qy 421 EDNEYTARQAKPFIKMTAPEALYGRFTIKSDVMSGILLTELTTKGRVPGMVNREV 480
Db 415 EDNEYTARQAKPFIKMTAPEALYGRFTIKSDVMSGILLTELTTKGRVPGMVNREV 474
Qy 481 LDQVGRGYMPCPEPCESLHDLCCQWKREPERPTEFYLOAFLEDTSTEPQYQPG 540
Db 475 LDQVGRGYMPCPEPCESLHDLCCQWKREPERPTEFYLOAFLEDTSTEPQYQPG 534
Qy 541 NL 542
Db 535 NL 536

RESULT 9
US-09-949-016-10282
Sequence 10282: Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL0010307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10282
LENGTH: 537
TYPE: PRT
ORGANISM: Human
US-09-949-016-10282

Query Match 98.5%; Score 2821; DB 2; Length 537;
Best Local Similarity 98.9%; Pred. No. 6,4e-214;
Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

Qy 1 MGSNKSXPDAQORRRSLPEAENVHAGAGGAFPASQTPSKPASAADGHRGSAFAFAAAE 60
Db 2 MGSNKSXPDAQORRRSLPEAENVHAGAGGAFPASQTPSKPASAADGHRGSAFAFAAAE 61
Qy 61 PKLFGGFNSSDVTSPQAGPLAGVTTFFVALYDYESRTEITDLSFKKGERLQIVNNTKRV 120
Db 62 PKLFGGFNSSDVTSPQAGPLAGVTTFFVALYDYESRTEITDLSFKKGERLQIVNNT--- 118


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MEDIUM TYPE: 3.5 inch, 760 Kb storage
COMPUTER: DELL 486/50
OPERATING SYSTEM: DOS 5.0
SOFTWARE: Displaywrite 3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00445
FILING DATE: 19930105
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/820,011
FILING DATE: 06-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399
REFERENCE/DOCKET NUMBER: ALX-101PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255 1400
TELEFAX: (203) 254 1101
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 533 amino acids
TYPE: AMINO ACID
TOPOLOGY: Linear
MOLECULE TYPE: Protein
HYPOTHETICAL: No
FRAGMENT TYPE: Complete Sequence
ORIGINAL SOURCE:
ORGANISM: Gallus, gallus
PUBLICATION INFORMATION:
AUTHORS: Takeya, Tatsuo
AUTHORS: Hanafusa, Hideaburo
TITLE: Structure and Sequence of the
TITLE: Cellular Gene Homologous to the RSV src
TITLE: Gene and the Mechanism for Generating the
TITLE: Transforming Virus
JOURNAL: Cell
VOLUME: 32
PAGES: 881-890
DATE: March, 1983
PCT-US93-00445-2

Query Match 92.5%; Score 2647.5; DB 5; Length 533;
Best Local Similarity 92.8%; Pred. No. 3e-200;
Matches 503; Conservative 12; Mismatches 18; Indels 9; Gaps 2;

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1 MGSNKRPKDASQRRSLPEAENVHAGAGAFASQTPSKPASADGHRGSAAPAAAE 60
 1 MGSNKRPKDASQRRSLPEAENVHAGAGAFASQTPSKPASADGHRGSAAPAAAE 57
 61 PKLFGFNSSDVTSPORAGPLAGVTTFVALYDYSRTETDLSFKKGERLQIVNTRKV 120
 58 PKLFGFNSSDVTSPORAGPLAGVTTFVALYDYSRTETDLSFKKGERLQIVNTRKV 114
 121 DVREGDWMHLAHSLSGTQGTGYIPSNYVAPSDSIQAEEMVFGKITRRESERLLNENPRT 180
 115 ---EGDWMHLAHSLSGTQGTGYIPSNYVAPSDSIQAEEMVFGKITRRESERLLNENPRT 171
 181 FLVASETTKAGAYCLSYSDPNAKGLNVGHYKIRKLDGSGGYITSRTPNSLQOLVAAYS 240
 172 FLVASETTKAGAYCLSYSDPNAKGLNVGHYKIRKLDGSGGYITSRTPNSLQOLVAAYS 231
 241 KHADGLCHRLTTCVPTSKPQTQGLAKDAMEIPRSLRLVKKLGGCCFGEVMMGTWNGTTR 300
 232 KHADGLCHRLTTCVPTSKPQTQGLAKDAMEIPRSLRLVKKLGGCCFGEVMMGTWNGTTR 291
 301 VAITLKPGTMSPEAFLOEAQVMKKLRHEKLVOLYAVVSEBPIYIVTVMKSGSLDPLK 360
 292 VAITLKPGTMSPEAFLOEAQVMKKLRHEKLVOLYAVVSEBPIYIVTVMKSGSLDPLK 351
 361 GETGKYRLPOLYVMAAQIASGMAVVERMYVHDLRAANILVGENILCVKADFGIARLI 420
 352 GETGKYRLPOLYVMAAQIASGMAVVERMYVHDLRAANILVGENILCVKADFGIARLI 411

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421 EDNEYTAQGAKEPKIKWTAPBAALYGRFTIKSDVMSFGILLTETLTGKRVYPGVNREV 480
412 EDNEYTAQGAKEPKIKWTAPBAALYGRFTIKSDVMSFGILLTETLTGKRVYPGVNREV 471
481 LDQYERGYNMPCPECECSLHDMQCQWRKPEPERPTEFYLOAFLEDFYFSTEPQYQGE 540
472 LDQYERGYNMPCPECECSLHDMQCQWRKPEPERPTEFYLOAFLEDFYFSTEPQYQGE 531
541 NL 542
532 NL 533

RESULT 14
US-08-426-509A-14
Sequence 14, Application US/08426509A
Patent No. 6326469
GENERAL INFORMATION:
APPLICANT: Ulrich, Axel
APPLICANT: Gishizaky, Mikhail
APPLICANT: Sures, Iman G.
TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York,
STATE: NY
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/426,509A
FILING DATE: 21-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/232,545
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-0074-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 543 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: No. 6326469e
US-08-426-509A-14

Query Match 73.7%; Score 2110.5; DB 2; Length 543;
Best Local Similarity 73.7%; Pred. No. 6.6e-158;
Matches 407; Conservative 51; Mismatches 75; Indels 19; Gaps 5;

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1 MGSNKRPKDASQRRSLPEAENVHAGAG--GAFPASQTPSKPASADGHRGSAAPAAFA 57
 1 MGSNKRPKDASQRRSLPEAENVHAGAG--GAFPASQTPSKPASADGHRGSAAPAAFA 57
 58 AABP-----KLFGFNSSDVTSPORAGPLAGVTTFVALYDYSRTETDLSFKKGER 110
 58 AABP-----KLFGFNSSDVTSPORAGPLAGVTTFVALYDYSRTETDLSFKKGER 110
 58 SMTPFGSSGVTTPFGASSSFSVPSYPAGLTGVTILFVALYDYEARTETDLSFKKGER 117
 111 LQIVNTRKVDVREGDWMHLAHSLSGTQGTGYIPSNYVAPSDSIQAEEMVFGKITRRESERL 170

Db 118 FQIINNT-----EGDWMEARSITATGNGYIPSNYVAPADSIQAEEMVFGMKGRKDAERL 171
Qy 171 LINAENPRGFLVRESSTTGAYCLSVSDPNNAKGLNVKHVKIRKLDGSGFYITSRTOFN 230
Db 172 LIMPNGORGIFLVRESSTTGAYSLSRDWEIRGDNVKKYKIRKLDNGGYITTRAQFD 231
Qy 231 SLQOLVAAYYSKHADGLCHRLTTVCPTSPOTQGLAKDAMEIPRESRLBVLVGGGCGFGEV 290
Db 232 TLQOLVAHYTHHADGLCHKLITVCPTVKPOTQGLAKDAMEIPRESRLBVLVGGGCGFGEV 291
Qy 291 WMGTNNGTTVAIKTLKPGTMSPEAFLOEAQVMKKLRHEKLVOLYAVVSEEPYIYTEYM 350
Db 292 WMGTNNGTTVAIKTLKPGTMSPEAFLOEAQVMKKLRHDKLVLYAVVSEEPYIYTEFM 351
Qy 351 SKGSLDLFLKGGGKTKLRPOLVDMAAQIASGMAVYERMYVHRDLRAANILVGENLVCK 410
Db 352 SKGSLDLFLKGGGKTKLRPOLVDMAAQIADGMAVIERMYVHRDLRAANILVGENLVCK 411
Qy 411 VADFGARLIEDNEYTAROGAKPFIKMTAPBAALYGRFTIKSDVMSFGILITELTTKGRV 470
Db 412 IADFGARLIEDNEYTAROGAKPFIKMTAPBAALYGRFTIKSDVMSFGILITELVTXGRV 471
Qy 471 PYGMYNREVLDOVERGYRMPCEPCEPSLHDMCQCRKEPERPTEFYLOAFLEDYFT 530
Db 472 PYGMYNREVLDOVERGYRMPCEPCEPSLHDMCQCRKEPERPTEFYLOAFLEDYFT 531
Qy 531 STEPQYQPGENTL 542
Db 532 ATEPQYQPGENTL 543

RESULT 15

US-08-232-545-14
Sequence 14, Application US/08232545
Patent No. 6506578
GENERAL INFORMATION:
APPLICANT: Ulrich, Axel
APPLICANT: Gishizky, Mikhail
APPLICANT: Sures, Iman G.
TITLE OF INVENTION: No. 6506578e1 Megakaryocytic Protein Tyrosine
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,545
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Cornuzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-050
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
TELEFAX: (212)869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 543 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown

MOLECULE TYPE: protein
US-08-232-545-14

Query Match 73.7%; Score 2110.5; DB 2; Length 543;
Best Local Similarity 73.7%; Pred. No. 6,6e-158;
Matches 407; Conservative 51; Mismatches 75; Indels 19; Gaps 5;

Qy 1 MGSNKSMP-KDASQRRBSLEPAENVAGAG--GAPPASQPSKAPASADGHRGSAAPAPA 57
Db 1 MGCISKENKSPAIKTRPENTPEPVSTSVSHYAEPTVSPCCSSA--KGTAVNFSLL 57
Qy 58 AAE-----KLFGFNSSDVTYSPORAGPLAGVTFVALYDYSRRTDLSFKKGR 110
Db 58 SMPFGSSSVTPFGGASSFSVPSYPAGLGGVITIPALVDYARTTEDLSFKKGR 117
Qy 111 LQIVNTRKVDVREGDWMLAHSLSTQGTGIPSNYVAPSDSIQAEEMVFGKTRRESERL 170
Db 118 FQIINNT-----EGDWMEARSITATGNGYIPSNYVAPADSIQAEEMVFGMKGRKDAERL 171
Qy 171 LINAENPRGFLVRESSTTGAYCLSVSDPNNAKGLNVKHVKIRKLDGSGFYITSRTOFN 230
Db 172 LIMPNGORGIFLVRESSTTGAYSLSRDWEIRGDNVKKYKIRKLDNGGYITTRAQFD 231
Qy 231 SLQOLVAAYYSKHADGLCHRLTTVCPTSPOTQGLAKDAMEIPRESRLBVLVGGGCGFGEV 290
Db 232 TLQOLVAHYTHHADGLCHKLITVCPTVKPOTQGLAKDAMEIPRESRLBVLVGGGCGFGEV 291
Qy 291 WMGTNNGTTVAIKTLKPGTMSPEAFLOEAQVMKKLRHEKLVOLYAVVSEEPYIYTEYM 350
Db 292 WMGTNNGTTVAIKTLKPGTMSPEAFLOEAQVMKKLRHDKLVLYAVVSEEPYIYTEFM 351
Qy 351 SKGSLDLFLKGGGKTKLRPOLVDMAAQIASGMAVYERMYVHRDLRAANILVGENLVCK 410
Db 352 SKGSLDLFLKGGGKTKLRPOLVDMAAQIADGMAVIERMYVHRDLRAANILVGENLVCK 411
Qy 411 VADFGARLIEDNEYTAROGAKPFIKMTAPBAALYGRFTIKSDVMSFGILITELTTKGRV 470
Db 412 IADFGARLIEDNEYTAROGAKPFIKMTAPBAALYGRFTIKSDVMSFGILITELVTXGRV 471
Qy 471 PYGMYNREVLDOVERGYRMPCEPCEPSLHDMCQCRKEPERPTEFYLOAFLEDYFT 530
Db 472 PYGMYNREVLDOVERGYRMPCEPCEPSLHDMCQCRKEPERPTEFYLOAFLEDYFT 531
Qy 531 STEPQYQPGENTL 542
Db 532 ATEPQYQPGENTL 543

Search completed: June 5, 2006, 17:18:19
Job time : 33.134 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 5, 2006, 17:37:14 ; Search time 108.467 Seconds
(without alignments)
2314.645 Million cell updates/sec

Title: US-10-691-079-1

Perfect score: 2863

Sequence: 1 MGSNKSXPKQASQRRSLRP.....AFLEDYRTSTPEYQPGENL 542

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Published Applications AA Main:*

1: /EMC_CeJerra_SIDS3/prodata/2/pubppaa/US07_PUBCOMB.pep:*

2: /EMC_CeJerra_SIDS3/prodata/2/pubppaa/US08_PUBCOMB.pep:*

3: /EMC_CeJerra_SIDS3/prodata/2/pubppaa/US09_PUBCOMB.pep:*

4: /EMC_CeJerra_SIDS3/prodata/2/pubppaa/US10A_PUBCOMB.pep:*

5: /EMC_CeJerra_SIDS3/prodata/2/pubppaa/US10B_PUBCOMB.pep:*

6: /EMC_CeJerra_SIDS3/prodata/2/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2863	100.0	542	4	US-10-691-079-1
2	2823	98.6	542	5	US-10-732-923-13447
3	2821	98.5	536	3	US-09-977-260-13
4	2821	98.5	536	3	US-09-929-266-10
5	2821	98.5	536	3	US-09-977-261-13
6	2821	98.5	536	4	US-10-691-079-2
7	2821	98.5	536	5	US-10-887-588-2
8	2821	98.5	536	5	US-10-497-641-2
9	2821	98.5	536	5	US-10-825-568-10
10	2821	98.5	536	5	US-10-821-231-C-1
11	2821	98.5	536	5	US-10-469-469-273
12	2821	98.5	536	6	US-11-233-510-24
13	2821	98.5	541	4	US-10-691-079-3
14	2816	98.4	535	4	US-10-394-322A-56
15	2816	98.4	535	4	US-10-814-109-4
16	2788	97.4	530	5	US-10-887-588-4
17	2754	96.2	530	5	US-10-330-773-749
18	2653.5	92.7	533	4	US-10-276-633-1
19	2653.5	92.6	533	5	US-10-732-923-13652
20	2650.5	92.6	533	5	US-10-732-923-13654
21	2650.5	92.6	533	6	US-11-230-995-3
22	2648.5	92.5	533	4	US-10-732-923-13650
23	2628.5	91.8	533	4	US-10-276-633-2
24	2608.5	91.1	587	5	US-10-732-923-13472
25	2601.5	90.9	568	5	US-10-732-923-13474
26	2595.5	90.7	587	5	US-10-732-923-13469
27	2586.5	90.3	557	5	US-10-732-923-13475

28	2520.5	88.0	526	5	US-10-732-923-13499	Sequence 13499, A
29	2503.5	87.4	526	5	US-10-732-923-13484	Sequence 13484, A
30	2503.5	87.4	772	5	US-10-732-923-13485	Sequence 13485, A
31	2484.5	86.8	526	5	US-10-732-923-13483	Sequence 13483, A
32	2478.5	86.6	526	5	US-10-732-923-13497	Sequence 13497, A
33	2475.5	86.5	537	5	US-10-732-923-13636	Sequence 13636, A
34	2472.5	86.4	526	5	US-10-732-923-13493	Sequence 13493, A
35	2472.5	86.4	526	5	US-10-732-923-13498	Sequence 13498, A
36	2471.5	86.3	526	5	US-10-732-923-13489	Sequence 13489, A
37	2470.5	86.3	526	5	US-10-732-923-13486	Sequence 13486, A
38	2469	86.2	525	5	US-10-732-923-13488	Sequence 13488, A
39	2469	86.2	535	5	US-10-732-923-13495	Sequence 13495, A
40	2468.5	86.2	526	5	US-10-732-923-13491	Sequence 13491, A
41	2457.5	85.8	526	5	US-10-732-923-13487	Sequence 13487, A
42	2453.5	85.7	526	5	US-10-732-923-13482	Sequence 13482, A
43	2450	85.6	532	5	US-10-732-923-13633	Sequence 13633, A
44	2449	85.5	532	5	US-10-732-923-13635	Sequence 13635, A
45	2446	85.4	532	5	US-10-732-923-13637	Sequence 13637, A

ALIGNMENTS

RESULT 1
US-10-691-079-1
Sequence 1, Application US/10691079
Publication No. US20040176313A1
GENERAL INFORMATION:
APPLICANT: AVENTIS PHARMA S.A.
TITLE OF INVENTION: Inhibitors of SRC kinase for use in Alzheimer's disease
FILE REFERENCE: PRAV002/00030
CURRENT APPLICATION NUMBER: US/10/691,079
CURRENT FILING DATE: 2003-10-22
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 542
TYPE: PRT
ORGANISM: Homo sapiens
US-10-691-079-1

Query Match 100.0%; Score 2863; DB 4; Length 542;
Best Local Similarity 100.0%; Pred. No. 7.6e-179;
Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MGSNKSXPKQASQRRSLRP	PAENVHAGGAF	PASQTPSKPASADGHRGSAFAFAAAE	60
DB	1	MGSNKSXPKQASQRRSLRP	PAENVHAGGAF	PASQTPSKPASADGHRGSAFAFAAAE	60
QY	61	PKLFGGNSDPTTSPQ	PACPLAGGVTTFVAL	LYESRTETDLSFKKGERLQIVNTRKV	120
DB	61	PKLFGGNSDPTTSPQ	PACPLAGGVTTFVAL	LYESRTETDLSFKKGERLQIVNTRKV	120
QY	121	DVREGDMMHLSSTG	GTGTPSNYVA	PSDSIOAEEMVFGKITRRESERLLNENPRT	180
DB	121	DVREGDMMHLSSTG	GTGTPSNYVA	PSDSIOAEEMVFGKITRRESERLLNENPRT	180
QY	181	FLVASESTTKGAYCL	SVSDPDNAKGLVVKYKIRKLD	SGGFYITRTOFNSLQDLVAYYS	240
DB	181	FLVASESTTKGAYCL	SVSDPDNAKGLVVKYKIRKLD	SGGFYITRTOFNSLQDLVAYYS	240
QY	241	KHADGLCHRLTTVC	PTSPKPTQGLAKDAWEI	PRBSLRLVYKGGCCGGEVMMGTNGTTR	300
DB	241	KHADGLCHRLTTVC	PTSPKPTQGLAKDAWEI	PRBSLRLVYKGGCCGGEVMMGTNGTTR	300
QY	301	VAITKLKPGTMSPA	FIQOAVMKLRHEKLV	QYAVVSEEPYITVEYNSKSLDPLK	360
DB	301	VAITKLKPGTMSPA	FIQOAVMKLRHEKLV	QYAVVSEEPYITVEYNSKSLDPLK	360
QY	361	GETGKYRLPOLVMA	QIAISGNAVYRMYVHRDL	PAANILVGENTVCKVADEGLARLI	420
DB	361	GETGKYRLPOLVMA	QIAISGNAVYRMYVHRDL	PAANILVGENTVCKVADEGLARLI	420

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QY 421 EDNEYTAROGAKPPIKMTAPEALYGRFTIKSDVMSFGILLTELTGKRVYPCGMVNRREV 480
|||
DB 421 EDNEYTAROGAKPPIKMTAPEALYGRFTIKSDVMSFGILLTELTGKRVYPCGMVNRREV 480
QY 481 LDQVERGYRMPCCPECPESLHDLMOCCMRKEPERPTFEYLQAFLEDYFTSTEPQYOPGE 540
|||
DB 481 LDQVERGYRMPCCPECPESLHDLMOCCMRKEPERPTFEYLQAFLEDYFTSTEPQYOPGE 540
QY 541 NL 542
|||
DB 541 NL 542

RESULT 2
US-10-732-923-13447
; Sequence 13447, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ. ID NOS: 24149
; SEQ. ID NO 13447
; LENGTH: 542
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-732-923-13447
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Query Match 98.6%; Score 2823; DB 5; Length 542;
Best Local Similarity 98.9%; Pred. No. 3,1e-176;
Matches 537; Conservative 3; Mismatches 1; Indels 2; Gaps 2;

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QY 1 MGSNKSXPQDASQRRSLBPAENVHAGGAFPASQTPSKPASADGHRGSAFAFAFAA 59
|||
DB 1 MGSNKSXPQDASQRRSLBPAENVHAGGAFPASQTPSKPASADGHRGSAFAFAFAA 59
QY 60 EPLKFGFNSSDVTYSPQRAGPLAGVTTFFVALYDYESRTETDLSFKKGERLQIVNNTRK 119
|||
DB 60 EPLKFGFNSSDVTYSPQRAGPLAGVTTFFVALYDYESRTETDLSFKKGERLQIVNNTRK 119
QY 60 EPLKFGFNSSDVTYSPQRAGPLAGVTTFFVALYDYESRTETDLSFKKGERLQIVNNTRK 119
|||
DB 60 EPLKFGFNSSDVTYSPQRAGPLAGVTTFFVALYDYESRTETDLSFKKGERLQIVNNTRK 119
QY 120 VDVBEGDWMLAHSLSGTQGTGYPNSNYAPSDSIOAEWYFGKTRRESERLLNAENPRG 179
|||
DB 120 VDVBEGDWMLAHSLSGTQGTGYPNSNYAPSDSIOAEWYFGKTRRESERLLNAENPRG 179
QY 180 TFLVRESSETTKGAYCISVSPDNAGKLVNKHVKIRKLDGSGFYITTSRTQFNSLQOLVAYY 239
|||
DB 180 TFLVRESSETTKGAYCISVSPDNAGKLVNKHVKIRKLDGSGFYITTSRTQFNSLQOLVAYY 239
QY 240 SKHADGICHRLTTCPTSKPQTQGLADAMEIPRESLRLEVKLGQCGFGEVMMGTWNGTT 299
|||
DB 240 SKHADGICHRLTTCPTSKPQTQGLADAMEIPRESLRLEVKLGQCGFGEVMMGTWNGTT 299
QY 300 RVALIKLKPGTMSPEAFLOEAQVWKLRHKKLVQVYAVVSEBPIYIYTEVMSKSLDPLK 359
|||
DB 300 RVALIKLKPGTMSPEAFLOEAQVWKLRHKKLVQVYAVVSEBPIYIYTEVMSKSLDPLK 359
QY 360 KSGTGYKLRLPOLVDMAAOIASGMAVYERNNVYHRDLRAANILVGENLVCKVADFGIARL 419
|||
DB 360 KSGTGYKLRLPOLVDMAAOIASGMAVYERNNVYHRDLRAANILVGENLVCKVADFGIARL 419
QY 420 IEDNEYTAROGAKPPIKMTAPEALYGRFTIKSDVMSFGILLTELTGKRVYPCGMVNR 479
|||
DB 420 IEDNEYTAROGAKPPIKMTAPEALYGRFTIKSDVMSFGILLTELTGKRVYPCGMVNR 479
QY 480 VLDQVERGYRMPCCPECPESLHDLMOCCMRKEPERPTFEYLQAFLEDYFTSTEPQYOPG 539
|||
DB 480 VLDQVERGYRMPCCPECPESLHDLMOCCMRKEPERPTFEYLQAFLEDYFTSTEPQYOPG 539
QY 540 ENL 542
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DB 540 ENL 542

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RESULT 3
US-09-977-260-13
; Sequence 13, Application US/09977260
; Publication No. US20020192790A1
; GENERAL INFORMATION:
; APPLICANT: ULBRICH, AXEL
; APPLICANT: GISHIZKY, MIKHAEL
; APPLICANT: SURES, IRMINGARD
; TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES
; FILE REFERENCE: 038602/1260
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 08/232,545
; PRIOR FILING DATE: 1994-04-22
; NUMBER OF SEQ. ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ. ID NO 13
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-977-260-13
```

Query Match 98.5%; Score 2821; DB 3; Length 536;
Best Local Similarity 98.9%; Pred. No. 4,2e-176;
Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

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QY 1 MGSNKSXPQDASQRRSLBPAENVHAGGAFPASQTPSKPASADGHRGSAFAFAFAA 60
|||
DB 1 MGSNKSXPQDASQRRSLBPAENVHAGGAFPASQTPSKPASADGHRGSAFAFAFAA 60
QY 61 PKLFGFNSSDVTYSPQRAGPLAGVTTFFVALYDYESRTETDLSFKKGERLQIVNNTKV 120
|||
DB 61 PKLFGFNSSDVTYSPQRAGPLAGVTTFFVALYDYESRTETDLSFKKGERLQIVNNTKV 120
QY 121 DVVBEGDWMLAHSLSGTQGTGYPNSNYAPSDSIOAEWYFGKTRRESERLLNAENPRG 180
|||
DB 121 DVVBEGDWMLAHSLSGTQGTGYPNSNYAPSDSIOAEWYFGKTRRESERLLNAENPRG 180
QY 181 FLVRESSETTKGAYCISVSPDNAGKLVNKHVKIRKLDGSGFYITTSRTQFNSLQOLVAYY 240
|||
DB 181 FLVRESSETTKGAYCISVSPDNAGKLVNKHVKIRKLDGSGFYITTSRTQFNSLQOLVAYY 240
QY 241 KHADGICHRLTTCPTSKPQTQGLADAMEIPRESLRLEVKLGQCGFGEVMMGTWNGTT 300
|||
DB 241 KHADGICHRLTTCPTSKPQTQGLADAMEIPRESLRLEVKLGQCGFGEVMMGTWNGTT 300
QY 301 VALIKLKPGTMSPEAFLOEAQVWKLRHKKLVQVYAVVSEBPIYIYTEVMSKSLDPLK 360
|||
DB 301 VALIKLKPGTMSPEAFLOEAQVWKLRHKKLVQVYAVVSEBPIYIYTEVMSKSLDPLK 360
QY 361 GETGKTLRLPOLVDMAAOIASGMAVYERNNVYHRDLRAANILVGENLVCKVADFGIARL 420
|||
DB 361 GETGKTLRLPOLVDMAAOIASGMAVYERNNVYHRDLRAANILVGENLVCKVADFGIARL 420
QY 420 IEDNEYTAROGAKPPIKMTAPEALYGRFTIKSDVMSFGILLTELTGKRVYPCGMVNR 474
|||
DB 420 IEDNEYTAROGAKPPIKMTAPEALYGRFTIKSDVMSFGILLTELTGKRVYPCGMVNR 474
QY 481 LDQVERGYRMPCCPECPESLHDLMOCCMRKEPERPTFEYLQAFLEDYFTSTEPQYOPG 540
|||
DB 481 LDQVERGYRMPCCPECPESLHDLMOCCMRKEPERPTFEYLQAFLEDYFTSTEPQYOPG 540
QY 541 NL 542
|||
DB 541 NL 542
```

RESULT 4
US-09-929-266-10

```
; Sequence 10, Application US/09929266
; Publication No. US20030045694A1
; GENERAL INFORMATION:
; APPLICANT: Brian T. Chait
; APPLICANT: Darin R. Latimer
; APPLICANT: Paul M. Izard
; APPLICANT: Eric R. Kershner
; APPLICANT: Jon S. Morrow
; APPLICANT: Matthew E. Roth
; APPLICANT: Kevin J. McConnell
; TITLE OF INVENTION: ULTRA-SENSITIVE DETECTION SYSTEMS
; FILE REFERENCE: 01173.000302
; CURRENT APPLICATION NUMBER: US/09/929,266
; CURRENT FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/224,939
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/283,498
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-929-266-10
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Query Match 98.5%; Score 2821; DB 3; Length 536;

Best Local Similarity 98.9%; Pred. No. 4.2e-176;

Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

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QY 1 MGSNKSXPKASQRRRLSEPAENVHAGGAGFPASQTPSKASADGHRGSPAAPAAAE 60
DB 1 MGSNKSXPKASQRRRLSEPAENVHAGGAGFPASQTPSKASADGHRGSPAAPAAAE 60
QY 61 PKLFGFNSSDPTVTSPPRAGPLAGGVTTFVALDYESTRTDLSFKKGERIQIYNNTRKV 120
DB 61 PKLFGFNSSDPTVTSPPRAGPLAGGVTTFVALDYESTRTDLSFKKGERIQIYNNTRKV 120
QY 121 DVREGDWMLAHSLSGTGTGYIPSNVYAPSDSIQAEWYFGKITRRESERLLNENPRT 180
DB 118 ---BGDWMLAHSLSGTGTGYIPSNVYAPSDSIQAEWYFGKITRRESERLLNENPRT 174
QY 181 FLVRESEITTGAYCLSYSDPDNAKGLNVKHKIRKLDGSGFYITSRQFNSLQOLVAYYS 240
DB 175 FLVRESEITTGAYCLSYSDPDNAKGLNVKHKIRKLDGSGFYITSRQFNSLQOLVAYYS 234
QY 241 KHADGLCHRLTTVCPTSKPOTQGLAKDAMEIPRESLBLEVKGCGCGEVMGTMNGTTR 300
DB 235 KHADGLCHRLTTVCPTSKPOTQGLAKDAMEIPRESLBLEVKGCGCGEVMGTMNGTTR 294
QY 301 VAIKTLKPGTMSPEAFLOEAQVMKGLRHEKLVQLYAVVSEBPIYIVTEYMSKSLDPLFK 360
DB 295 VAIKTLKPGTMSPEAFLOEAQVMKGLRHEKLVQLYAVVSEBPIYIVTEYMSKSLDPLFK 354
QY 361 GETGKYRLPOLVDMAAQIASGMAVYERMYVHRDLPAANILVGENIVCKYADGLARLI 420
DB 355 GETGKYRLPOLVDMAAQIASGMAVYERMYVHRDLPAANILVGENIVCKYADGLARLI 414
QY 421 EDNEYTRAGAKPFIKMTAPBAALYGRFTIKSDVWSGILLTELTTTGRVVPYPMVNRREV 480
DB 415 EDNEYTRAGAKPFIKMTAPBAALYGRFTIKSDVWSGILLTELTTTGRVVPYPMVNRREV 474
QY 481 LDQVERGYRMPCEPCEBSLHDLMCQCRKEPBERPTFEYLQAFLEBDYFTSTBPQYQGE 540
DB 475 LDQVERGYRMPCEPCEBSLHDLMCQCRKEPBERPTFEYLQAFLEBDYFTSTBPQYQGE 534
QY 541 NL 542
DB 535 NL 536
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RESULT 5

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US-09-977-261-13
; Sequence 13, Application US/09977261
; Publication No. US20030054527A1
; GENERAL INFORMATION:
; APPLICANT: ULIRICH, AXEL
; APPLICANT: GISHIZKY, MICHAIL
; APPLICANT: SURES, IRMINGARD
; TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES
; FILE REFERENCE: 038602/1259
; CURRENT APPLICATION NUMBER: US/09/977,261
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 08/232,545
; PRIOR FILING DATE: 1994-04-22
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-977-261-13
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Query Match 98.5%; Score 2821; DB 3; Length 536;

Best Local Similarity 98.9%; Pred. No. 4.2e-176;

Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

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QY 1 MGSNKSXPKASQRRRLSEPAENVHAGGAGFPASQTPSKASADGHRGSPAAPAAAE 60
DB 1 MGSNKSXPKASQRRRLSEPAENVHAGGAGFPASQTPSKASADGHRGSPAAPAAAE 60
QY 61 PKLFGFNSSDPTVTSPPRAGPLAGGVTTFVALDYESTRTDLSFKKGERIQIYNNTRKV 120
DB 61 PKLFGFNSSDPTVTSPPRAGPLAGGVTTFVALDYESTRTDLSFKKGERIQIYNNTRKV 117
QY 121 DVREGDWMLAHSLSGTGTGYIPSNVYAPSDSIQAEWYFGKITRRESERLLNENPRT 180
DB 118 ---BGDWMLAHSLSGTGTGYIPSNVYAPSDSIQAEWYFGKITRRESERLLNENPRT 174
QY 181 FLVRESEITTGAYCLSYSDPDNAKGLNVKHKIRKLDGSGFYITSRQFNSLQOLVAYYS 240
DB 175 FLVRESEITTGAYCLSYSDPDNAKGLNVKHKIRKLDGSGFYITSRQFNSLQOLVAYYS 234
QY 241 KHADGLCHRLTTVCPTSKPOTQGLAKDAMEIPRESLBLEVKGCGCGEVMGTMNGTTR 300
DB 235 KHADGLCHRLTTVCPTSKPOTQGLAKDAMEIPRESLBLEVKGCGCGEVMGTMNGTTR 294
QY 301 VAIKTLKPGTMSPEAFLOEAQVMKGLRHEKLVQLYAVVSEBPIYIVTEYMSKSLDPLFK 360
DB 295 VAIKTLKPGTMSPEAFLOEAQVMKGLRHEKLVQLYAVVSEBPIYIVTEYMSKSLDPLFK 354
QY 361 GETGKYRLPOLVDMAAQIASGMAVYERMYVHRDLPAANILVGENIVCKYADGLARLI 420
DB 355 GETGKYRLPOLVDMAAQIASGMAVYERMYVHRDLPAANILVGENIVCKYADGLARLI 414
QY 421 EDNEYTRAGAKPFIKMTAPBAALYGRFTIKSDVWSGILLTELTTTGRVVPYPMVNRREV 480
DB 415 EDNEYTRAGAKPFIKMTAPBAALYGRFTIKSDVWSGILLTELTTTGRVVPYPMVNRREV 474
QY 481 LDQVERGYRMPCEPCEBSLHDLMCQCRKEPBERPTFEYLQAFLEBDYFTSTBPQYQGE 540
DB 475 LDQVERGYRMPCEPCEBSLHDLMCQCRKEPBERPTFEYLQAFLEBDYFTSTBPQYQGE 534
QY 541 NL 542
DB 535 NL 536
```

RESULT 6

US-10-691-079-2

; Sequence 2, Application US/10691079

; Publication No. US2004017631A1

; GENERAL INFORMATION:

; APPLICANT: AVENTIS PHARMA S.A.

; TITLE OF INVENTION: Inhibitors of SRC kinase for use in Alzheimer's disease

FILE REFERENCE: PRAV2002/0030
CURRENT APPLICATION NUMBER: US/10/691,079
CURRENT FILING DATE: 2003-10-22
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 536
TYPE: PRT
ORGANISM: Homo sapiens
US-10-691-079-2

Query Match 98.5%; Score 2821; DB 4; Length 536;
Best Local Similarity 98.9%; Pred. No. 4,2e-176;
Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

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QY 1 MGSNKKPXDASORRSLPEAENVHAGGAFPAASQTPSKPASADGHRPSAFAFAAAE 60
DB 1 MGSNKKPXDASORRSLPEAENVHAGGAFPAASQTPSKPASADGHRPSAFAFAAAE 60
QY 61 PKLFGFNSSDVTSPORAGPLAGVTFVALYDYESRTETDLSFKKGERLQIVNNTKRY 120
DB 61 PKLFGFNSSDVTSPORAGPLAGVTFVALYDYESRTETDLSFKKGERLQIVNNTKRY 117
QY 121 DVREGDMWLAHSLSTGQGYIPSNVYAPSDSIQAEEMYPGKITRRESERLLNAENPRGT 180
DB 118 ---EGDMWLAHSLSTGQGYIPSNVYAPSDSIQAEEMYPGKITRRESERLLNAENPRGT 174
QY 181 FLVRESETTKGAYCLSVSPDNAGKLVKIKRLDSGCFYITTSRTQFNSLQQLVAYYS 240
DB 175 FLVRESETTKGAYCLSVSPDNAGKLVKIKRLDSGCFYITTSRTQFNSLQQLVAYYS 234
QY 241 KPADGCHRLTTCPTSPKPTQGLAKDAWEIPRESLRLEVKLGQCGFGEVWMTGNTTR 300
DB 235 KPADGCHRLTTCPTSPKPTQGLAKDAWEIPRESLRLEVKLGQCGFGEVWMTGNTTR 294
QY 301 VAIKTLKPGTMSPEAFLOEAQVMKCLRHEKLVOLYAVSEBPIYITEVMSKSLDPLK 360
DB 295 VAIKTLKPGTMSPEAFLOEAQVMKCLRHEKLVOLYAVSEBPIYITEVMSKSLDPLK 354
QY 361 GETGKTLRLPOLVDMAAOIASGMAVYERNNYHRDLRAANIIVGENLVCKVADFGARLI 420
DB 355 GETGKTLRLPOLVDMAAOIASGMAVYERNNYHRDLRAANIIVGENLVCKVADFGARLI 414
QY 421 EDNEYTAROGAKFPIMTAPBALYGRFTIKSDVMSFGILLTELTTKGRVPYGMVNRREV 480
DB 415 EDNEYTAROGAKFPIMTAPBALYGRFTIKSDVMSFGILLTELTTKGRVPYGMVNRREV 474
QY 481 LDQVERGYMPCPPECBSLHDMCCMKRKEBERPTFEYLQAFLEDTSTSTEPYOQGE 540
DB 475 LDQVERGYMPCPPECBSLHDMCCMKRKEBERPTFEYLQAFLEDTSTSTEPYOQGE 534
QY 541 NL 542
DB 535 NL 536
```

RESULT 7
US-10-887-588-2
Sequence 2, Application US/10887588
Publication No. US20040261142A1
GENERAL INFORMATION:
APPLICANT: Yeatman, Timothy J.
TITLE OF INVENTION: Mutated SRC Oncogene Composition and Methods
FILE REFERENCE: USF-T136
CURRENT FILING DATE: 2004-07-09
PRIOR APPLICATION NUMBER: US/09/444,711
PRIOR FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 536

TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (1)-(536)
OTHER INFORMATION: amino acid sequence of non-receptor tyrosine kinase encoded
US-10-887-588-2

Query Match 98.5%; Score 2821; DB 5; Length 536;
Best Local Similarity 98.9%; Pred. No. 4,2e-176;
Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

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QY 1 MGSNKKPXDASORRSLPEAENVHAGGAFPAASQTPSKPASADGHRPSAFAFAAAE 60
DB 1 MGSNKKPXDASORRSLPEAENVHAGGAFPAASQTPSKPASADGHRPSAFAFAAAE 60
QY 61 PKLFGFNSSDVTSPORAGPLAGVTFVALYDYESRTETDLSFKKGERLQIVNNTKRY 120
DB 61 PKLFGFNSSDVTSPORAGPLAGVTFVALYDYESRTETDLSFKKGERLQIVNNTKRY 117
QY 121 DVREGDMWLAHSLSTGQGYIPSNVYAPSDSIQAEEMYPGKITRRESERLLNAENPRGT 180
DB 118 ---EGDMWLAHSLSTGQGYIPSNVYAPSDSIQAEEMYPGKITRRESERLLNAENPRGT 174
QY 181 FLVRESETTKGAYCLSVSPDNAGKLVKIKRLDSGCFYITTSRTQFNSLQQLVAYYS 240
DB 175 FLVRESETTKGAYCLSVSPDNAGKLVKIKRLDSGCFYITTSRTQFNSLQQLVAYYS 234
QY 241 KPADGCHRLTTCPTSPKPTQGLAKDAWEIPRESLRLEVKLGQCGFGEVWMTGNTTR 300
DB 235 KPADGCHRLTTCPTSPKPTQGLAKDAWEIPRESLRLEVKLGQCGFGEVWMTGNTTR 294
QY 301 VAIKTLKPGTMSPEAFLOEAQVMKCLRHEKLVOLYAVSEBPIYITEVMSKSLDPLK 360
DB 295 VAIKTLKPGTMSPEAFLOEAQVMKCLRHEKLVOLYAVSEBPIYITEVMSKSLDPLK 354
QY 361 GETGKTLRLPOLVDMAAOIASGMAVYERNNYHRDLRAANIIVGENLVCKVADFGARLI 420
DB 355 GETGKTLRLPOLVDMAAOIASGMAVYERNNYHRDLRAANIIVGENLVCKVADFGARLI 414
QY 421 EDNEYTAROGAKFPIMTAPBALYGRFTIKSDVMSFGILLTELTTKGRVPYGMVNRREV 480
DB 415 EDNEYTAROGAKFPIMTAPBALYGRFTIKSDVMSFGILLTELTTKGRVPYGMVNRREV 474
QY 481 LDQVERGYMPCPPECBSLHDMCCMKRKEBERPTFEYLQAFLEDTSTSTEPYOQGE 540
DB 475 LDQVERGYMPCPPECBSLHDMCCMKRKEBERPTFEYLQAFLEDTSTSTEPYOQGE 534
QY 541 NL 542
DB 535 NL 536
```

RESULT 8
US-10-497-641-2
Sequence 2, Application US/10497641
Publication No. US20050037446A1
GENERAL INFORMATION:
APPLICANT: Schmitt and Stork
TITLE OF INVENTION: AGENTS THAT RECOGNIZE SRC WHEN PHOSPHORYLATED AT SERINE 17
FILE REFERENCE: 65064-02
CURRENT FILING DATE: US/10/497,641
CURRENT FILING DATE: 2004-06-04
PRIOR APPLICATION NUMBER: PCT/US02/41564
PRIOR FILING DATE: 2002-12-27
PRIOR APPLICATION NUMBER: 60/345,888
PRIOR FILING DATE: 2001-12-28
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 536
TYPE: PRT

ORGANISM: Homo sapiens
US-10-497-641-2

Query Match 98.5%; Score 2821; DB 5; Length 536;
Best Local Similarity 98.9%; Pred. No. 4.2e-176;
Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

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QY 1 MGSNKSXPKDASQRRRSLEPAENVHAGGAFPPASQTPSKASADGHRGSPAAFAPAAB 60
DB 1 MGSNKSXPKDASQRRRSLEPAENVHAGGAFPPASQTPSKASADGHRGSPAAFAPAAB 60
QY 61 PKLFGFNSSDPTVTSPPQAGPLAGGVTTFVALIYVESRTEITDLSFKKGERLQIVNTRKV 120
DB 61 PKLFGFNSSDPTVTSPPQAGPLAGGVTTFVALIYVESRTEITDLSFKKGERLQIVNTRKV 117
QY 121 DVREGDWMLAHSLSGTQGYI PSNYVAPSDSIQAEWYFGKITRRESERLLNENPRGT 180
DB 118 --BGDWMLAHSLSGTQGYI PSNYVAPSDSIQAEWYFGKITRRESERLLNENPRGT 174
QY 181 FLVRESSETTKAYCLSVDFPNAGLANVGHYKIRKLDGSGFYITSRTQFNSLQOLVAYYS 240
DB 175 FLVRESSETTKAYCLSVDFPNAGLANVGHYKIRKLDGSGFYITSRTQFNSLQOLVAYYS 234
QY 241 KHADGLCHRLTTVCPTSKPOTQGLAKDAWEIPRESLRLEVTLGGCCFGEVMMGTNGTTR 300
DB 235 KHADGLCHRLTTVCPTSKPOTQGLAKDAWEIPRESLRLEVTLGGCCFGEVMMGTNGTTR 294
QY 301 VAITKLKPGTMSPEAFIOEAVMKKLREHKL VOLIYAVSEBPIYIVTEYMSKSLDPLK 360
DB 295 VAITKLKPGTMSPEAFIOEAVMKKLREHKL VOLIYAVSEBPIYIVTEYMSKSLDPLK 354
QY 361 GETGKYLRPLQVDMAAQIASGMAVERMNVYHRDLPAANILVGENLVCKVADGRLALI 420
DB 355 GETGKYLRPLQVDMAAQIASGMAVERMNVYHRDLPAANILVGENLVCKVADGRLALI 414
QY 421 EDNEYTARQAKFPKKTAPALYGRFTIKSDVMSFGILLTELTTKGRVVPYPGVNRREV 480
DB 415 EDNEYTARQAKFPKKTAPALYGRFTIKSDVMSFGILLTELTTKGRVVPYPGVNRREV 474
QY 481 LDQVERGYRMPCEPCESLHDLMCQCRKSEPEERPFVEYLQAFLEDYFSTEPQYQGE 540
DB 475 LDQVERGYRMPCEPCESLHDLMCQCRKSEPEERPFVEYLQAFLEDYFSTEPQYQGE 534
QY 541 NL 542
DB 535 NL 536
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RESULT 9
US-10-825-568-10

Sequence 10, Application US/10825568
Publication No. US20050069916A1
GENERAL INFORMATION:
APPLICANT: Brian T. Chait
APPLICANT: Darin R. Latimer
APPLICANT: Paul M. Lizardi
APPLICANT: Eric R. Keremnar
APPLICANT: Jon S. Morrow
APPLICANT: Matthew B. Roth
APPLICANT: Martin J. Matthesich
APPLICANT: Kevin J. McConnell
TITLE OF INVENTION: ULTRA-SENSITIVE DETECTION SYSTEMS
FILE REFERENCE: 01173.000302
CURRENT FILING DATE: US/10/825.568
CURRENT FILING DATE: 2004-04-14
PRIOR APPLICATION NUMBER: US/09/929.266
PRIOR FILING DATE: 2001-08-13
PRIOR APPLICATION NUMBER: 60/224.939
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/283.498
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 10
LENGTH: 536
TYPE: PRT
ORGANISM: Homo sapiens
US-10-825-568-10

Query Match 98.5%; Score 2821; DB 5; Length 536;
Best Local Similarity 98.9%; Pred. No. 4.2e-176;
Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

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QY 1 MGSNKSXPKDASQRRRSLEPAENVHAGGAFPPASQTPSKASADGHRGSPAAFAPAAB 60
DB 1 MGSNKSXPKDASQRRRSLEPAENVHAGGAFPPASQTPSKASADGHRGSPAAFAPAAB 60
QY 61 PKLFGFNSSDPTVTSPPQAGPLAGGVTTFVALIYVESRTEITDLSFKKGERLQIVNTRKV 120
DB 61 PKLFGFNSSDPTVTSPPQAGPLAGGVTTFVALIYVESRTEITDLSFKKGERLQIVNTRKV 117
QY 121 DVREGDWMLAHSLSGTQGYI PSNYVAPSDSIQAEWYFGKITRRESERLLNENPRGT 180
DB 118 --BGDWMLAHSLSGTQGYI PSNYVAPSDSIQAEWYFGKITRRESERLLNENPRGT 174
QY 181 FLVRESSETTKAYCLSVDFPNAGLANVGHYKIRKLDGSGFYITSRTQFNSLQOLVAYYS 240
DB 175 FLVRESSETTKAYCLSVDFPNAGLANVGHYKIRKLDGSGFYITSRTQFNSLQOLVAYYS 234
QY 241 KHADGLCHRLTTVCPTSKPOTQGLAKDAWEIPRESLRLEVTLGGCCFGEVMMGTNGTTR 300
DB 235 KHADGLCHRLTTVCPTSKPOTQGLAKDAWEIPRESLRLEVTLGGCCFGEVMMGTNGTTR 294
QY 301 VAITKLKPGTMSPEAFIOEAVMKKLREHKL VOLIYAVSEBPIYIVTEYMSKSLDPLK 360
DB 295 VAITKLKPGTMSPEAFIOEAVMKKLREHKL VOLIYAVSEBPIYIVTEYMSKSLDPLK 354
QY 361 GETGKYLRPLQVDMAAQIASGMAVERMNVYHRDLPAANILVGENLVCKVADGRLALI 420
DB 355 GETGKYLRPLQVDMAAQIASGMAVERMNVYHRDLPAANILVGENLVCKVADGRLALI 414
QY 421 EDNEYTARQAKFPKKTAPALYGRFTIKSDVMSFGILLTELTTKGRVVPYPGVNRREV 480
DB 415 EDNEYTARQAKFPKKTAPALYGRFTIKSDVMSFGILLTELTTKGRVVPYPGVNRREV 474
QY 481 LDQVERGYRMPCEPCESLHDLMCQCRKSEPEERPFVEYLQAFLEDYFSTEPQYQGE 540
DB 475 LDQVERGYRMPCEPCESLHDLMCQCRKSEPEERPFVEYLQAFLEDYFSTEPQYQGE 534
QY 541 NL 542
DB 535 NL 536
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RESULT 10
US-10-821-231C-1

Sequence 1, Application US/10821231C
Publication No. US20050275837A1
GENERAL INFORMATION:
APPLICANT: Zhang, Dongmano
APPLICANT: Ben-Ametz, Dor
APPLICANT: Xie, Yong
APPLICANT: Davison, Vincent J.
APPLICANT: Mrozek, Melissa
APPLICANT: Ortiz, Corasi
TITLE OF INVENTION: PROCESS AND APPARATUS FOR SEGREGATION AND TESTING BY SPECTRAL
FILE REFERENCE: 12264/17
CURRENT FILING DATE: US/10/821.231C
CURRENT FILING DATE: 2004-04-08
PRIOR APPLICATION NUMBER: US 60/462.083
PRIOR FILING DATE: 2003-04-11
PRIOR APPLICATION NUMBER: US 60/462.472
PRIOR FILING DATE: 2003-04-11
PRIOR APPLICATION NUMBER: US 60/490.057
PRIOR FILING DATE: 2003-07-25

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 24
LENGTH: 536
TYPE: PRT
ORGANISM: Homo sapiens
US-11-233-510-24

Query Match 98.5%; Score 2821; DB 6; Length 536;
Best Local Similarity 98.9%; Pred. No. 4.2e-176;
Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

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QY 1 MGSNKSQPKDASQRRRSLEPAENVHAGCGGAFPPASQTPSKPASADGHRGSPAAAPAAAE 60
   |||
DB 1 MGSNKSQPKDASQRRRSLEPAENVHAGCGGAFPPASQTPSKPASADGHRGSPAAAPAAAE 60
   |||
QY 61 PKLFGFNSSDPTVTSPPQAGPLAGGVTTFVALDYESTETDLSFKKGERLQIVNNTKV 120
   |||
DB 61 PKLFGFNSSDPTVTSPPQAGPLAGGVTTFVALDYESTETDLSFKKGERLQIVNNTKV 117
   |||
QY 121 DVREGDWWLAHSLSTGTGYIPSNVVA PSDSIOABEWYFGKITRRESERLLLNENPRGT 180
   |||
DB 121 DVREGDWWLAHSLSTGTGYIPSNVVA PSDSIOABEWYFGKITRRESERLLLNENPRGT 174
   |||
QY 181 FLVRESSTKGAAYCLSYSDPDNAGLVNKHAKIRKLDGSGFYITSRQFNSLQOLVAYYS 240
   |||
DB 175 FLVRESSTKGAAYCLSYSDPDNAGLVNKHAKIRKLDGSGFYITSRQFNSLQOLVAYYS 234
   |||
QY 241 KHADELCHRLTTVPTSKPTQGLAKDAMEIPRESLRLEVKGCGCFGEVMMGTWGTTR 300
   |||
DB 235 KHADELCHRLTTVPTSKPTQGLAKDAMEIPRESLRLEVKGCGCFGEVMMGTWGTTR 294
   |||
QY 301 VAITLKPWTSPPAFLQEAQVMKKLRHEKLVQYAVVSEPIYIVTEYMSKSLDPLK 360
   |||
DB 295 VAITLKPWTSPPAFLQEAQVMKKLRHEKLVQYAVVSEPIYIVTEYMSKSLDPLK 354
   |||
QY 361 GETGKYRLPOLVMAAQIASGMAYVERMNVVHDLRAANILVGENLVCKVADGRLALI 420
   |||
DB 355 GETGKYRLPOLVMAAQIASGMAYVERMNVVHDLRAANILVGENLVCKVADGRLALI 414
   |||
QY 421 EDNEYTAROGAKFPDKMTAPPAALYGRFTIKSDVMSFGILLTELTTKGRVYPCGVNREV 480
   |||
DB 415 EDNEYTAROGAKFPDKMTAPPAALYGRFTIKSDVMSFGILLTELTTKGRVYPCGVNREV 474
   |||
QY 481 LDQVERGRMPCPECEBSLHDLMCQCKRKEPERPTFEYIQAFLQEDYFTSTEPQYQGE 540
   |||
DB 475 LDQVERGRMPCPECEBSLHDLMCQCKRKEPERPTFEYIQAFLQEDYFTSTEPQYQGE 534
   |||
QY 541 NL 542
   |||
DB 535 NL 536
```

RESULT 13

US-10-691-079-3
Sequence 3, Application US/10691079
Publication No. US2004017631A1
GENERAL INFORMATION:
APPLICANT: AVENTIS PHARMA S.A.
TITLE OF INVENTION: Inhibitors of SRC kinase for use in Alzheimer's disease
FILE REFERENCE: PRAV002/0030
CURRENT APPLICATION NUMBER: US/10/691.079
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 541
TYPE: PRT
ORGANISM: Murinae gen. sp.
US-10-691-079-3

Query Match 98.5%; Score 2820.5; DB 4; Length 541;
Best Local Similarity 98.7%; Pred. No. 4.6e-176;
Matches 535; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

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QY 1 MGSNKSQPKDASQRRRSLEPAENVHAGCGGAFPPASQTPSKPASADGHRGSPAAAPAAAE 60
   |||
DB 1 MGSNKSQPKDASQRRRSLEPAENVHAGCGGAFPPASQTPSKPASADGHRGSPAAAPAAAE 59
   |||
QY 61 PKLFGFNSSDPTVTSPPQAGPLAGGVTTFVALDYESTETDLSFKKGERLQIVNNTKV 120
   |||
DB 60 PKLFGFNSSDPTVTSPPQAGPLAGGVTTFVALDYESTETDLSFKKGERLQIVNNTKV 119
   |||
QY 121 DVREGDWWLAHSLSTGTGYIPSNVVA PSDSIOABEWYFGKITRRESERLLLNENPRGT 180
   |||
DB 120 DVREGDWWLAHSLSTGTGYIPSNVVA PSDSIOABEWYFGKITRRESERLLLNENPRGT 179
   |||
QY 181 FLVRESSTKGAAYCLSYSDPDNAGLVNKHAKIRKLDGSGFYITSRQFNSLQOLVAYYS 240
   |||
DB 180 FLVRESSTKGAAYCLSYSDPDNAGLVNKHAKIRKLDGSGFYITSRQFNSLQOLVAYYS 239
   |||
QY 241 KHADELCHRLTTVPTSKPTQGLAKDAMEIPRESLRLEVKGCGCFGEVMMGTWGTTR 300
   |||
DB 240 KHADELCHRLTTVPTSKPTQGLAKDAMEIPRESLRLEVKGCGCFGEVMMGTWGTTR 299
   |||
QY 301 VAITLKPWTSPPAFLQEAQVMKKLRHEKLVQYAVVSEPIYIVTEYMSKSLDPLK 360
   |||
DB 300 VAITLKPWTSPPAFLQEAQVMKKLRHEKLVQYAVVSEPIYIVTEYMSKSLDPLK 359
   |||
QY 361 GETGKYRLPOLVMAAQIASGMAYVERMNVVHDLRAANILVGENLVCKVADGRLALI 420
   |||
DB 360 GETGKYRLPOLVMAAQIASGMAYVERMNVVHDLRAANILVGENLVCKVADGRLALI 419
   |||
QY 421 EDNEYTAROGAKFPDKMTAPPAALYGRFTIKSDVMSFGILLTELTTKGRVYPCGVNREV 480
   |||
DB 420 EDNEYTAROGAKFPDKMTAPPAALYGRFTIKSDVMSFGILLTELTTKGRVYPCGVNREV 479
   |||
QY 481 LDQVERGRMPCPECEBSLHDLMCQCKRKEPERPTFEYIQAFLQEDYFTSTEPQYQGE 540
   |||
DB 480 LDQVERGRMPCPECEBSLHDLMCQCKRKEPERPTFEYIQAFLQEDYFTSTEPQYQGE 539
   |||
QY 541 NL 542
   |||
DB 540 NL 541
```

RESULT 14

US-10-394-322A-56
Sequence 56, Application US/10394322A
Publication No. US2003023391A1
GENERAL INFORMATION:
APPLICANT: SUNESIS PHARMACEUTICALS, INC.
TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
FILE REFERENCE: 39750-0006 US
CURRENT APPLICATION NUMBER: US/10/394.322A
PRIOR FILING DATE: 2003-03-20
PRIOR APPLICATION NUMBER: US 60/366,892
NUMBER OF SEQ ID NOS: 70
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 56
LENGTH: 535
TYPE: PRT
ORGANISM: Homo sapiens
US-10-394-322A-56

Query Match 98.4%; Score 2816; DB 4; Length 535;
Best Local Similarity 98.9%; Pred. No. 8.9e-176;
Matches 535; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

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QY 2 GSNKSQPKDASQRRRSLEPAENVHAGCGGAFPPASQTPSKPASADGHRGSPAAAPAAAE 61
   |||
DB 1 GSNKSQPKDASQRRRSLEPAENVHAGCGGAFPPASQTPSKPASADGHRGSPAAAPAAAE 60
   |||
QY 62 KLFGEFNSSDPTVTSPPQAGPLAGGVTTFVALDYESTETDLSFKKGERLQIVNNTKVD 121
   |||
```

Db 61 KLFQGFNSDVTYSPQAGPLAGGVTTFVALYDYESRTERTDLSFKKGERLQIVNNT---- 116
Qy 122 VREGDWMLAHSLSGTGQGYI PSNYVAPSDSIQAEEMVFGKITRRESRLILNENPRTGF 181
Db 117 --BGDWMLAHSLSGTGQGYI PSNYVAPSDSIQAEEMVFGKITRRESRLILNENPRTGF 174
Qy 182 LVRESSETTKGAYCLSVSDFDNAGLANVHKYKIRKLDGSGFYITSRTQFNSLQOLVAYYSK 241
Db 175 LVRESSETTKGAYCLSVSDFDNAGLANVHKYKIRKLDGSGFYITSRTQFNSLQOLVAYYSK 234
Qy 242 HADGLCHRLTTVCPTSPKPTQGLAKDAWEI PRESRLLEVKLGGCGCFGEVWMTNGTTRV 301
Db 235 HADGLCHRLTTVCPTSPKPTQGLAKDAWEI PRESRLLEVKLGGCGCFGEVWMTNGTTRV 294
Qy 302 AITTLKPGTMSPEAFLOEAQVMKKLRHEKLVOLYAVVSEBPIYIVTEYMSKSLDPLKG 361
Db 295 AITTLKPGTMSPEAFLOEAQVMKKLRHEKLVOLYAVVSEBPIYIVTEYMSKSLDPLKG 354
Qy 362 ETGKYLRLPOLVMAAQIASGMAYVERMNYVHRDLRAANILVGENLVCKVADFGLARLIE 421
Db 355 ETGKYLRLPOLVMAAQIASGMAYVERMNYVHRDLRAANILVGENLVCKVADFGLARLIE 414
Qy 422 DNEYTAROGAKFPKWTAPPAALYGRFTIKSDVMSFGILLTELTTKGRVPYPGMVRREV 481
Db 415 DNEYTAROGAKFPKWTAPPAALYGRFTIKSDVMSFGILLTELTTKGRVPYPGMVRREV 474
Qy 482 DVERGYRMPCEPCEBSLHDLMOCCWKKEPBERPFEYLOAFLEDFYFSTEPQYOGEN 541
Db 475 DVERGYRMPCEPCEBSLHDLMOCCWKKEPBERPFEYLOAFLEDFYFSTEPQYOGEN 534
Qy 542 L 542
Db 535 L 535

RESULT 15
US-10-814-109-4
; Sequence 4, Application US/10814109
; Publication No. US20050222042A1
; GENERAL INFORMATION:
; APPLICANT: Salter, Michael
; APPLICANT: Gingrich, Jeffrey
; TITLE OF INVENTION: Method for Modification of NMDA Receptors Through Inhibition of S
; FILE REFERENCE: 2560.004
; CURRENT APPLICATION NUMBER: US/10/814,109
; CURRENT FILING DATE: 2004-03-30
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 535
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-814-109-4

Query Match 98.4%; Score 2816; DB 5; Length 535;
Best Local Similarity 98.9%; Pred. No. 8,9e-176;
Matches 535; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

Qy 2 GSNKSKPKDASQRRRSLEPAENVHAGGGAFPASQTPSKPASADGHRGSAAPAPAAAP 61
Db 1 GSNKSKPKDASQRRRSLEPAENVHAGGGAFPASQTPSKPASADGHRGSAAPAPAAAP 60
Qy 62 KLFQGFNSDVTYSPQAGPLAGGVTTFVALYDYESRTERTDLSFKKGERLQIVNNTRKVD 121
Db 61 KLFQGFNSDVTYSPQAGPLAGGVTTFVALYDYESRTERTDLSFKKGERLQIVNNT---- 116
Qy 122 VREGDWMLAHSLSGTGQGYI PSNYVAPSDSIQAEEMVFGKITRRESRLILNENPRTGF 181
Db 117 --BGDWMLAHSLSGTGQGYI PSNYVAPSDSIQAEEMVFGKITRRESRLILNENPRTGF 174
Qy 182 LVRESSETTKGAYCLSVSDFDNAGLANVHKYKIRKLDGSGFYITSRTQFNSLQOLVAYYSK 241
Db 175 LVRESSETTKGAYCLSVSDFDNAGLANVHKYKIRKLDGSGFYITSRTQFNSLQOLVAYYSK 234

Qy 242 HADGLCHRLTTVCPTSPKPTQGLAKDAWEI PRESRLLEVKLGGCGCFGEVWMTNGTTRV 301
Db 235 HADGLCHRLTTVCPTSPKPTQGLAKDAWEI PRESRLLEVKLGGCGCFGEVWMTNGTTRV 294
Qy 302 AITTLKPGTMSPEAFLOEAQVMKKLRHEKLVOLYAVVSEBPIYIVTEYMSKSLDPLKG 361
Db 295 AITTLKPGTMSPEAFLOEAQVMKKLRHEKLVOLYAVVSEBPIYIVTEYMSKSLDPLKG 354
Qy 362 ETGKYLRLPOLVMAAQIASGMAYVERMNYVHRDLRAANILVGENLVCKVADFGLARLIE 421
Db 355 ETGKYLRLPOLVMAAQIASGMAYVERMNYVHRDLRAANILVGENLVCKVADFGLARLIE 414
Qy 422 DNEYTAROGAKFPKWTAPPAALYGRFTIKSDVMSFGILLTELTTKGRVPYPGMVRREV 481
Db 415 DNEYTAROGAKFPKWTAPPAALYGRFTIKSDVMSFGILLTELTTKGRVPYPGMVRREV 474
Qy 482 DVERGYRMPCEPCEBSLHDLMOCCWKKEPBERPFEYLOAFLEDFYFSTEPQYOGEN 541
Db 475 DVERGYRMPCEPCEBSLHDLMOCCWKKEPBERPFEYLOAFLEDFYFSTEPQYOGEN 534
Qy 542 L 542
Db 535 L 535

Search completed: June 5, 2006, 17:43:03
Job time : 110.467 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 5, 2006, 17:37:49 ; Search time 7.03027 Seconds

(without alignments)
891.618 Million cell updates/sec

Title: US-10-691-079-1

Perfect score: 2863
Sequence: 1 MGSNKSXPKASQRRSLRP.....AFLEDYFTSTPPOXPGENTL 542

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 58871 seqs, 11565156 residues

Total number of hits satisfying chosen parameters: 58871

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- Published Applications AA New:*
- 1: /EMC_Celerra_SIDS3/prodata/1/pubppa/US09_NEW_PUB.pep:*
 - 2: /EMC_Celerra_SIDS3/prodata/1/pubppa/US06_NEW_PUB.pep:*
 - 3: /EMC_Celerra_SIDS3/prodata/1/pubppa/US07_NEW_PUB.pep:*
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 - 7: /EMC_Celerra_SIDS3/prodata/1/pubppa/US12_NEW_PUB.pep:*
 - 8: /EMC_Celerra_SIDS3/prodata/1/pubppa/US60_NEW_PUB.pep:*

* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1525.5	53.3	505	6	US-10-511-937-2991 Sequence 2991, App
2	1461	51.0	512	6	US-10-505-928-353 Sequence 353, App
3	1461	51.0	512	6	US-10-511-937-2492 Sequence 2492, App
4	1458	50.9	509	6	US-10-511-937-2467 Sequence 2467, App
5	834	29.1	659	6	US-10-511-937-2593 Sequence 2593, App
6	829.5	29.0	631	7	US-11-312-958-60 Sequence 60, App1
7	787.5	27.5	620	6	US-10-511-937-2959 Sequence 2959, App
8	589	20.6	983	7	US-11-302-678-2 Sequence 2, App1
9	571	19.9	994	7	US-11-303-935-12 Sequence 12, App1
10	569.5	19.9	993	7	US-11-303-935-11 Sequence 11, App1
11	569	19.9	998	7	US-11-303-935-2 Sequence 2, App1
12	556.5	19.4	1130	7	US-11-312-958-52 Sequence 52, App1
13	489	17.1	894	7	US-11-251-465-21 Sequence 21, App1
14	482.5	16.9	885	6	US-10-505-928-432 Sequence 432, App
15	482.5	16.9	885	7	US-11-251-465-20 Sequence 20, App1
16	482	16.8	843	7	US-11-251-465-20 Sequence 20, App1
17	481	16.8	806	7	US-11-251-465-22 Sequence 22, App1
18	477.5	16.7	346	7	US-11-251-465-22 Sequence 22, App1
19	477.5	16.7	348	7	US-11-251-465-22 Sequence 22, App1
20	476.5	16.6	422	7	US-11-251-465-67 Sequence 67, App1
21	476.5	16.6	422	7	US-11-251-465-70 Sequence 70, App1
22	469	16.4	972	7	US-11-255-147-8 Sequence 8, App1
23	459	16.0	1308	7	US-11-248-122-2 Sequence 2, App1
24	448	15.6	999	6	US-10-196-749-434 Sequence 434, App
25	442	15.4	391	7	US-11-223-945-38 Sequence 38, App1

26	442	15.4	1259	7	US-11-223-945-40 Sequence 40, App1
27	441	15.4	550	6	US-10-538-066-757 Sequence 757, App
28	441	15.4	1255	6	US-10-538-066-364 Sequence 364, App
29	441	15.4	1255	7	US-11-223-945-43 Sequence 43, App1
30	439	15.3	993	6	US-10-511-937-2463 Sequence 2463, App
31	432	15.1	976	6	US-10-511-937-2423 Sequence 2423, App
32	427	14.9	1006	6	US-10-511-937-2425 Sequence 2425, App
33	427	14.6	1338	6	US-10-505-928-634 Sequence 634, App
34	417.5	14.6	1338	6	US-10-505-928-657 Sequence 657, App
35	413	14.4	953	7	US-11-312-958-56 Sequence 56, App1
36	408.5	14.3	1298	7	US-10-505-928-274 Sequence 274, App
37	403	14.1	374	6	US-10-953-349-3910 Sequence 3910, App
38	403	14.1	374	6	US-10-953-349-3909 Sequence 3909, App
39	403	14.1	412	6	US-10-511-814-2 Sequence 3908, App
40	397	13.9	648	6	US-10-511-814-14 Sequence 2, App1
41	397	13.9	648	6	US-10-511-814-14 Sequence 2, App1
42	367.5	12.8	272	6	US-10-370-959-27 Sequence 27, App1
43	367.5	12.8	278	6	US-10-370-959-17 Sequence 17, App1
44	367.5	12.8	278	6	US-10-370-959-31 Sequence 31, App1
45	367	12.8	247	7	US-11-251-465-75 Sequence 75, App1

ALIGNMENTS

RESULT 1
US-10-511-937-2991
Sequence 2991, Application US/10511937
Publication No. US20060088836A1
GENERAL INFORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
APPLICANT: Prentice, James
APPLICANT: Morris, Macdonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
FILE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
FILE REFERENCE: 506612000104
CURRENT APPLICATION NUMBER: US/10/511.937
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR FILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2991
LENGTH: 505
TYPE: PRT
ORGANISM: Homo sapiens
US-10-511-937-2991
Query Match 53.3%; Score 1525.5; DB 6; Length 505;
Best Local Similarity 55.6%; Pred. No. 3e+76;
Matches 299; Conservative 86; Mismatches 116; Indels 37; Gaps 6;
QY 1 MGSNKSXPKASQRRSLRP...AFLEDYFTSTPPOXPGENTL 542
DB 1 MGSNKSXPKASQRRSLRP...AFLEDYFTSTPPOXPGENTL 542
QY 61 PKLGFNSPTVTSPOAGPLAGVTTT--VALDYSSRTETDPSFKKSGRLQIVNTRK 119
DB 61 PKLGFNSPTVTSPOAGPLAGVTTT--VALDYSSRTETDPSFKKSGRLQIVNTRK 119
QY 41 -----GNSHNSNTPTGIR--AGSEDIYVALDYELIHEDLSFQKGDQMVLEBS-- 90
DB 41 -----GNSHNSNTPTGIR--AGSEDIYVALDYELIHEDLSFQKGDQMVLEBS-- 90
QY 120 VDVEGDMWLALHSLSTGQGYIPSNVYAPSDLSIOAEEMWYFKITRRSEBRLLLNAENRG 179
DB 120 VDVEGDMWLALHSLSTGQGYIPSNVYAPSDLSIOAEEMWYFKITRRSEBRLLLNAENRG 179
QY 91 -----GEMWKRSLATKREGYIPSNVYARVDSLTETEMFPGISRKQAEQLLPGNMLG 145
DB 91 -----GEMWKRSLATKREGYIPSNVYARVDSLTETEMFPGISRKQAEQLLPGNMLG 145

Qy	180	1FLVARESETTKAYCCLSVSDPDMNAGLANVKKYIKRLKLDSCGFITTSRTQNSLQOLVAY	239
Db	146	SEPMIDSEITTKGSSYSLSVADYDPRQDITVKKYIKRLDNGGFYISPRSTFSTLOELVDHY	205
Qy	240	SKHADGLCHRLTTVTPETSKPOTQGLAKDAMEI.PRESLRLTEVKLGOCQFGEVMMGTNNGTT	299
Db	206	KKGNDGLCOOKLSVPCMSKRPQ--KPEMKDAMEI.PRESLKUBKLGAGQFGEVMMATYNNKAT	264
Qy	300	RVALITKLPGTMSPEAFLOEAOVMKKLRHKKLVQLAVAVSEBPIYIVTEWMSKGSLLDFL	359
Db	265	KVAVTKMFGSSVSEAFLEAVNVMTLGHQDKLVKLAVVTKBEIYIITTEWMAKGSLLDFL	324
Qy	360	KGETGKYLRLLPOLVDMAAQIASGMAYVERMNVYHRDLRAANIIIVGNLVCKVADFGIARL	419
Db	325	KSEDSKQPL.PGLIDPFSQAIDAGMAFIEQRNYIHRDLRAANIIIVSASLVCKIADFGIARV	384
Qy	420	IEDNEYTARQAKKFPFKMTAPEALYGRITISDWSFGILLTELTTKGRVPPGMVNR	479
Db	385	IEDNEYTAREGAKFPFKMTAPEALINFGSTIKSDWSFGILLMEIYVGRIPPGMSNPE	444
Qy	480	VLDQVERGRMCCPEBCPESLDLMQCMRKXPEERPTFEYLQAFLEDVFTSTNEPQY	537
Db	445	VIRALERGRMRPENCPEELYNIMRCKMNRPEEPTEYELIQSVLDDPFAATESQY	502

RESULT 2
 US-10-505-928-353
 ; Sequence 353, Application US/10505928
 ; Publication No. US20060088532A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ludwig Institute for Cancer Research et al.
 ; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
 ; PTL REFERENCE: 28967/39178
 ; CURRENT APPLICATION NUMBER: US/10/505,928
 ; CURRENT FILING DATE: 2004-08-27
 ; PRIOR APPLICATION NUMBER: US 60/363,019
 ; PRIOR FILING DATE: 2002-03-07
 ; NUMBER OF SEQ ID NOS: 866
 ; SOFTWARE: PatentIn 3.2
 ; SEQ ID NO 353
 ; LENGTH: 512
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-505-928-353

Query Match	Score	DB	Length
Best Local Similarly	51.0%	1461	512
Match 287; Conservative	52.5%	Pred. NO. 9.4e-73	
	87	Mismatches 125;	Indels 48; Gaps 9

Qy	1	MGSMKSRPKDA-----SQRBSLEPAENVHAGGGAFAPSQTPSKPASMADGHRG9S	51
Db	1	MGCTISKGRDSSDDGVLDKTPVPRNTEFTIYRD-----PFSNKQQRV-----PE	47
Qy	52	AAFAFAAAEPKLFGGFNSSDYTSPQAPPLAGVTVFVALYDYESRTETDLSFKKGERL	111
Db	48	SQLPQGR-----FQTKD-----PEQGDIY-----VALPYDGIHPDDLSFKKGEKX	90
Qy	112	QIVNTRKVDYREDGMWLAHSITQGTGYPBNVYAPRSDIOAEEMVYFGKITPRSEBRLL	171
Db	91	KVLE-----EHGEMWMAKSSLLTKKEGFTPSNYAKATLTLEEBWFFQDITKMDERQD	143
Qy	172	LNAPNPGTFLVRESEETTKGAYCLSVSDPDNNAKGLNKKVYKIRKLDSGGFYISRQFNS	231
Db	144	LAPGNSAFAFLIRESEETLKGSFSLSRDPDPVHGVDIKYKIRSLDNGGYISPRITFPIC	203
Qy	232	LQQLVAVYSKHADGCHRLTTCPSKPTQOGLADAMERIPRESLAEVXKCGCCGGEVW	291
Db	204	ISDMTKHQQKQADGSCRRIEKAICISPKPQ-KPMDXDAWMEIPBSICLVKRLGAGQGEVW	262
Qy	292	MGYNNGTTRVAILKTLPGTMSPEAFLQEAQVMMKKLAREKLVDLYAVVS-EBPIYITEVW	350
Db	263	MGYNNSRKVAVKTLPGTMSVQAFLEBANLAKTKLOHDCLVLYAVVTRREBPYIITEVW	322

QY	351	3KGSLLDPLDKBETGKCYLLPOLVDMAAQJASGMAYVERNNYHROLRANIIIVGELJYCK	410
Db	323	AKGSLDLDEKDEGGKVLPLKLIIDSAQIAEGMAVIERKNYTHRDRLRANVLVSSLMCK	382
QY	411	VADFGIATLIEDNETYARQAGAKFPIKMTAPBAALYGRFPIKSDVMSFGILLTELTRYGHV	470
Db	383	IADRLANVIEDNETTAREGAKFPIKMTAPBALINNGCFPIKSDVMSFGILLVETIYGYKI	442
QY	471	PYPGKVNREVLDOVERGYRMPCCPEPCBSLHDLQCMCKRKEBERPTFYLOAFLEDYFT	530
Db	443	PYPGGTADNVMTATASQGYRMPREVENCPELVIYIMCMCKEKAERBPTFDYLOSVLDDPYT	502
QY	531	STEPQYQ	537
Db	503	ATEGQYQ	509

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RESULT 3
US-10-511-937-2492
; Sequence 2492, Application US/10511937
; Publication NO. US2006008836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2492
; LENGTH: 512
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2492

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Query Match	51.0%;	Score 1461;	DB 6;	Length 512;
Best Local Similarity	52.5%;	Prod. No. 9.4e-73;		
Matches 287;	Conservative	87;	Mismatches 125;	Indels 48; Gaps 9;
Qy	1	MSNKSAPKDA-----SQRRSLEPAENHAGAGGARPASQTESKPASADGHRPS	51	
Db	1	MGCIKSGKSDLDGDVLTQIPVRNTERITYVD-----PTSNKQGRPV-----PE	47	
Qy	52	AAFPAAAEPLFCGFSSDPTVTSFPGAAGPLAGVTFVVALYDSEKTEPDLSPKGRRL	111	
Db	48	SQLEPGR-----FQTKD-----PEEQGDIV-----VALYPDGGIHPDLSFKGSKM	90	
Qy	112	QIVANTRKVDVREGDWMIAHSLSTGQGYGYPISNVAAEDSIOAEWYFGKITRSEERLL	171	
Db	91	KYLE-----EHGEMWKAASLTLTKEGGEFIPSNVAKLNTLETREWFPKDITRDAERQL	143	
Qy	172	LMANPRGTPLYRSEFTTKGAYCISVSDPNAKLANLHYKIRLDDGGEFTTSTRTQNS	231	
Db	144	LAPNSAGAFILIRSETLKSFSLSVDFDVFHDVILKHVIRSLDMNGYIISPIITPC	203	
Qy	232	LOQLVAVYSKADGLCHRLITTVCPFSKPTQGLAKDAMEIPRESLRLEVKLGQGCFGEW	291	
Db	204	ISDIKHYKQADDLGRLEKACISPPKQ-KPMKDAMEIPRESILKVTKRGAGQFGKVV	262	

Qy	292	MGYNMGTRVAVIKTLKPGTMSDEAFLOZQVNMKJLHEKLVOLYAVS - BEPIYIITEYM	350
Dp	263	MGYNNSTKRVAKVTLKPGTMSVOAFLEBANIKTLQHDCLVRYIAVYTBEPYIITEYM	322
Qy	351	SKGSLIDPLKGETGYKLRLPOLVDMAOIASGMAVYERNMYVHRDIPAAIIVGENULVCK	410
Dp	323	AKGSLIDPLKPSDEGGKVLLPKLIDFSAQIAREGMAVYERKXVYIHRDIPAAIIVLSSESIMCK	382
Qy	411	VADFELARLIBENEXTAROGAKFPIKMTAPEALYGRFTIKSPVMSFGILLTLYLTTRKGRV	470
Dp	383	IADBELAVIBENEXTAROGAKFPIKMTAPEALINBCFPIIKSPVMSFGILLIYIVYVYKGI	442
Qy	471	PYPCGVNNEBVLDOVERGYRMPCCPBCBSLHIDMCCQMKREPERPTFEYLQAFLEDDYFT	530
Dp	443	PYPCGTNADVMYALOGYRMPREVENCPDELYDIMQCMKREKREPTFDYLOSVDLDFYT	502
Qy	531	STEPQYO 537	
Dp	503	ATEGOYO 509	

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RESULT 4
US-10-511-937-2467
: Sequence 2467, Application US/10511937
: Publication No. US20060088836A1
: GENERAL INFORMATION:
: APPLICANT: EXPRESSION DIAGNOSTICS, INC.
: APPLICANT: Mohlemuth, Jay
: APPLICANT: Fry, Kirk
: APPLICANT: Woodward, Robert
: APPLICANT: Ly, Ngoc
: APPLICANT: Prentice, James
: APPLICANT: Morris, Macdonald
: APPLICANT: Rosenberg, Steven
: TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
: TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
: FILE REFERENCE: 506612000104
: CURRENT APPLICATION NUMBER: US/10/511,937
: CURRENT FILING DATE: 2004-10-19
: PRIOR APPLICATION NUMBER: PCT/US2003/012946
: PRIOR FILING DATE: 2003-04-24
: PRIOR APPLICATION NUMBER: US 10/131,831
: PRIOR FILING DATE: 2002-04-24
: PRIOR APPLICATION NUMBER: US 10/325,899
: PRIOR FILING DATE: 2002-12-20
: NUMBER OF SEQ ID NOS: 3117
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 2467
: LENGTH: 509
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-10-511-937-2467

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	Query Match	Similarity	Score	DB	Length
Best Local	59.1%	Pred. No. 1	4e-72		509
Matches	272	Conservative	80	Mismatches	98
				Indels	10
				Gaps	3

Qy	31	EAOVWCKLHREKXVOLYXAVSEEPYIYTEWSSKSLDPFKGRTGXLRJLPCILVMDAAQ	378
Qy	288	EALWMLQLOHQLVRLXVAVYQEPYIYITTEWMSGLVDFKTESGIKLITINKLMDMAAQ	347
Qy	379	IASGMAVERMXYVHRDLPAANIIVGENLVCKVADFGIARLIIDNEYTAROGAKFPKWT	438
Db	348	IAGMGAFIERRNYIRHDLPAANIIVSDPLTSLCKIADFGLARLIIDNEYTAROGAKFPKWT	407
Qy	433	APBPAALYGRFTLKSDWWSFGILLTETLTTKGRVAPVPGMWREVLDOVGRGYMPCBPCE	498
Db	408	APBPAALYGFITLKSDWWSFGILLTETLVTHGRIIPGGMNPEVIONLERGYMVARPDNCPB	467
Qy	499	SLHDLMLCQCRKKEPBEERPFPEYLAQAFLEDYTSTPEQYOP	538
Db	468	EUYQMLRLOCKERPEDRPFTDLRSLVLEDFPAAIDGQYOP	507

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RESULT 5
US-10-511-937-2593
; Sequence 2593, Application US/10511937
; Publication No. US2006008836A1
GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fey, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
FILE REFERENCE: 506612000104
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR FILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 317
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2593
;
LENGTH: 659
;
TYPE: PRT
;
ORGANISM: Homo sapiens
US-10-511-937-2593

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	Query Match	29.1%	Score 834;	DB 6;	Length 659;
	Best Local Similarity	36.7%	Pred. No. 1e-38;		
	Matches 184;	Conservative	96;	Mismatches 184;	Indels 38; Gaps 14
Qy	40	KPLSADGHRGCPAAFPAPAAEPKLFEGGRNSDVTYSPPQAGPLAGVTT-----FVALYD	94		
Db	176	KPSS--HKRTKKPLPPPTPEEDQI-----LKKPLPPPPAAPASTSELKTVALLYD	224		
Qy	95	YESRTETDSFPKKGERTQIVNTRKADYVREGDMWLHLSLSTGQGTGYPSNVAFS-DSIQ	153		
Db	225	YPMNANDQLTKRGDGYFLLESNL-----PWRARD-KNGQGGIYIPSNVTEAEDSE	277		
Qy	154	AEFWYTGKTKTRRESERLLINAEINPGTVLVRESSETTKAYCLSL--SDFDNAKLINVKY	211		
Db	278	MYWYSKAMTRSOAQR-LTKQGGKGGFIVDS-SKAGKYIVSYPAKSTGDPQGV-IRHY	334		
Qy	212	KIRKLDSGGFYITSRTPQSLQQLAAVYKSKADGLCHRLTTCVCTSK-----POTQGLAK	266		
Db	335	WVCSPTQSQDYLAEKHLFTETIDELINHYQHSAGLISRLK--YFVSQONKVAPESTAGIGY	392		
Qy	267	DANEIRRESLRLEVNLGGCCGEGEYVMGMVNGTTRNATIKLPGMSBAPLQAEQVWKLL	326		
Db	393	GSWEIDPKULTPLKELGEGTGQFGVYVYGGMRQGYDALIMIKGSMSEBFLFEKAKVMNL	452		

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Oy 327 SHEKLVOLYAAVSEB--PIYIVTEWSSKSLDFELKGETSKYRLPLDYMAQIASGMXY 385
Db 453 SHEKLVOLYGVCTKCRPIFIITEYMANGLLWYLR--ENRHRQTOQLLCKDCOVCEAMY 511
Oy 386 VERNMYVHRDILRAANILVGENLVCKVADFGLARLIEDNEYTAROGAKPEIKWTAPEALY 445
Db 512 LESQOFLHRDLAARNCVLNVDDGVVAVSDPGLSRVYLDDEYTSVSGKFFVRMSPEVLMY 571
Oy 446 GRFTTKSVMSFGILLTELTTKGRVPYPRGMVNRVLDQVERGYRMPCEPCESLHLMC 505
Db 572 SKFSKSDSIMAFGVLMWEIYSLGKMPYERFTNSEAHEIAOGLRLVRPHASEKVTIMY 631
Oy 506 QCMRKEPERPTEYLOAFLED 527
Db 632 SCWEKADERPTFKILLSNILD 653

RESULT 6
US-11-312-958-60
: Sequence 60, Application US/11312958
: Publication No. US20060100152A1
: GENERAL INFORMATION:
: APPLICANT: Millennium Pharmaceuticals, Inc.
: APPLICANT: Rosenfeld, Julie Beth
: APPLICANT: Sinos-Santiago, Immaculada
: TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
: TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 9949, 14230, 760, 62553,
: TITLE OF INVENTION: 12216, 17719, 41897, 47174, 33408, 10002, 16209, 314, 636,
: TITLE OF INVENTION: 27410, 33260, 619, 15985, 69112, 2158, 224, 615, 44373,
: TITLE OF INVENTION: 95431, 22245, 2387, 16658, 55054, 16314, 1613, 1675, 9569 OR
: TITLE OF INVENTION: 13424 MOLECULES
: FILE REFERENCE: MP102-027P1RNONMIM
: CURRENT APPLICATION NUMBER: US/11/312,958
: CURRENT FILING DATE: 2005-12-20
: PRIOR APPLICATION NUMBER: US/10/369,022
: PRIOR FILING DATE: 2003-02-19
: PRIOR APPLICATION NUMBER: US 60/360,495
: PRIOR FILING DATE: 2002-02-28
: PRIOR APPLICATION NUMBER: US 60/370,121
: PRIOR FILING DATE: 2002-04-04
: PRIOR APPLICATION NUMBER: US 60/373,010
: PRIOR FILING DATE: 2002-04-16
: PRIOR APPLICATION NUMBER: US 60/373,908
: PRIOR FILING DATE: 2002-04-19
: PRIOR APPLICATION NUMBER: US 60/377,717
: PRIOR FILING DATE: 2002-05-03
: PRIOR APPLICATION NUMBER: US 60/379,949
: PRIOR FILING DATE: 2002-05-13
: PRIOR APPLICATION NUMBER: US 60/382,409
: PRIOR FILING DATE: 2002-05-21
: PRIOR APPLICATION NUMBER: US 60/385,280
: PRIOR FILING DATE: 2002-06-03
: PRIOR APPLICATION NUMBER: US 60/386,879
: PRIOR FILING DATE: 2002-06-06
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 64
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 60
: LENGTH: 631
: TYPE: PRT
: ORGANISM: Homo sapiens
US-11-312-958-60

Query Match 29.0%; Score 829.5; DB 7; Length 631;
Best Local Similarity 39.6%; Pred. No. 1.7e-38;
Matches 177; Conservative 90; Mismatches 161; Indels 19; Gaps 11;

Oy 90 VALYDYSRTTDSFKKGERLQIVNTRKVDYREGDWLAHSLSTGQTGYIPSNVA-- 147
Db 185 VAMVDYQAAEGHGGDRLRERGOEYLIL--EKNDVH--WWRARD-KYGNEGYIPSNVYTGK 237
Oy 148 PSDSIQAEWYFGKTRRESERLLLAENPNRGTFLVRSEETTKGAYCLSV--SDPNACKL 206
Db 148 PSDSIQAEWYFGKTRRESERLLLAENPNRGTFLVRSEETTKGAYCLSV--SDPNACKL 206

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Db      KSNMLDQEWYCRAMNRSKAEQ-LLRSBDKCGFVNRDS-SQGLYTVSLYTKFGGEGSS 295
Qy      207 NVKHYIKRKLDSG--GFYITRTQFNSIQOLVAYYSKADGLCHRL--TTYCPISKQOT 261
Db      296 GFRHYHIKETTPSKRYYLAKRHAFGS:PEIIEYHKHNAAGLVTRLRYPVASKGNAPTT 355
Qy      262 QGLKDAWEIPRESILRLBVKLGOCGFGVWNGTNGTRVALIKTLKPTMSPEALQEAQ 321
Db      356 AGFSYEKKELINPSELTFRRELJGSLFGVVLGKRRAGYKVAIKAIRGAMCEBDPIEBAK 415
Qy      322 VMKULRHEKLVOLVAVVSEB-PYIVTEYMSKSGSLDLFKGETGKYRLPOLVDMAAQIA 380
Db      416 VMKULTHPKVLQVLGVCTQKQKPIYIVTEFEMRGCLANFLRQGHFSR-DVLLSMCQDVC 474
Qy      381 SGMAIYERMYVHDLRLAANILVGENLYCKRADGLARLIEDNETTAQGAFFPKIWPAP 440
Db      475 EGMWEYLENNSIHRDLAARCLVSBAGVAKVSDGMAVYFLDDOYTSSSGAKFPVKWCP 534
Qy      441 EALYGRFTISDWSFGIILTELTITKGRVDPGVWVREVLDOYRGYRMCPCPECSL 500
Db      535 EVFYSRFSASDWSRGVLWMEYFTBGRMFEKXTNYEVVWYTRGRLYQPKLASNY 594
Qy      501 HDLMCQCWRKEPERPTFEYLQAEFL 527
Db      595 YEWLRCWQKEGRBGRPSFEDLRTIDE 621

RESULT 7
US-10-511-937-2959
; Sequence 2959, Application US/10511937
; Publication No. US20060088036A1
GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR FILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2959
LENGTH: 620
TYPE: PRT
ORGANISM: Homo sapiens
US-10-511-937-2959

Query Match      27.5%; Score 787.5; DB 6; Length 620;
Beet Local Similarity 34.4%; Pred. No. 3.2e-36;
Matches 177; Conservative 90; Mismatches 183; Indels 65; Gaps 15

Qy      19 EPAENVGAGGAGPASCOTSPSKPASADGHRGSPSAFAAPAALEPKLFGGFNSSDTVTSFOR 78
Db      147 DPTGN-----AKKKLPRLPPEDNRR-----PLMEEBE 173
Qy      79 AGPIAGVTTFFVALYDYESRTETDLSFKKGRLOIVANNTRKVDVREGDWMLAHSLSGQT 138
Db      174 -----TVVIALYDYQTNDDPDELALRNBEYCL-----LDSEIHWTVVOD-RINCH 218
Qy      139 GYISNVAVS--DSIQAEWYFGKIRRBSEERLLNAENRGTFIVRESEFTTGAYCLS 196
Db      139 GYISNVAVS--DSIQAEWYFGKIRRBSEERLLNAENRGTFIVRESEFTTGAYCLS 196

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Db 219 GYVPSYLVKSPNNLETFEYWNKSI SRDKAEKLLDPT-GKEGAFVWRDSRTA-GTYTVS 276
Qy 197 VSDPDNA----KGLNVGHYKIRKLDSC--GFTYTSRQFNSLQOLVAVYSKADGLCHRL 250
Db 277 V--FTKAVSENNPCIGHYHKEITNDPKRYVAEKVFDSPILLIYHQNHGGLVTRL 334
Qy 251 T-TYCC--PTSKPOTQGLAKAMEIPRESLRLEVLGCGCFGEVMMGTWNGTTRVAITLK 307
Db 335 RYVCFGRQAPVTAJRLRYKMWIDPSELFTFVQEISGGQGLVHLGWLAKDKVAITIR 394
Qy 308 PGTMSPEAPLOEAQVMMKLRHEKLVOLYAVVSE-PIYIYEVNYSKSLDPLFGTGY 366
Db 395 EGAMSEEDPIEBEAVMMKLSHPLVOLYGVCLGEQCLVFEFMEHGLSDYLTQGLF 454
Qy 367 LRLPOLYDMAQIAGNAYVERNNYHRDLPAANILVGENLVCAVDGRLAILEDNEYT 426
Db 455 -AAETLLGMCLDVECEGAYIEACVHIRDLAARNCLVGENQVIVSFGMTFPYLDQYT 513
Qy 427 ARQAKPEIKMTAEALYGRFTIKSDVMSFGILLTETTKGRVPYDGMVREVLDQYER 486
Db 514 SSTGKTPVWMASEVPSFSKSDVMSFGVLMMEVPSGKLPYENRSSEVEDIST 573
Qy 487 GYRMPCEPCEPSLHDMCOCWRKEPERPTEYL 521
Db 574 GFRLYKRLASTHYQIMNHCWKERPEDRAFSRL 608

RESULT 8
US-11-302-678-2
; Sequence 2, Application US/11302678
; Publication No. US20060088881A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Sileo-Santiago, Immaculada
; APPLICANT: Venkateswarlu, Karichecki
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46556, 62553, 302, 323,
; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
; FILE REFERENCE: MP102-012P1NMM OMNI
; CURRENT APPLICATION NUMBER: US/11/302, 678
; CURRENT FILING DATE: 2005-12-14
; PRIOR APPLICATION NUMBER: US/10/345, 680
; PRIOR FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/349, 511
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/360, 500
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/365, 041
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/374, 063
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/403, 468
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 60/414, 262
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/419, 986
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/423, 809
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/429, 797
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 983
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-302-678-2

Query Match 20.6%; Score 589; DB 7; Length 983;
Best Local Similarity 31.3%; Pred. No. 2.8e-25;
Matches 171; Conservative 80; Mismatches 164; Indels 132; Gaps 19;

Qy 61 PKLFGFNSSDYTVSPQRAEPLAGVYTFVALVDYESTETDLSFKKGERLQIVNNTRKV 120
Db 384 PRQGLTNTVTVY-----DLIANTTYTPEI 409
Qy 121 DVREGDWMILASHSTGQGY----IPSNVYAPSDSIQAEWYFGKIRRESERLLNAEN 176
Db 410 DAVNG-----VSELSPPRQPAVASITNQAAPSVLTIKK---DRTSRNLSISWQPEH 462
Qy 177 PRGTF-----VBSSETKAYCLSVDFNAGLANV-----HKIRLDSGCF 221
Db 463 PNGIILDEYEVKYEKQOETSYYTL-----RAGTNVITISLKEDTIYVQIRARTAGY 517
Qy 222 YITSRT-QFNS-----LQOLVAYYSKH-AD 244
Db 518 GYNSRKEFEFTSPDSFSISSESSQVMAISAVALIITLVIVYVLIGRFGYKSGKAD 577
Qy 245 -----GLCHRLTTCV-TSKPOTQGLADAMEIPRESLRLEVKLGQCGFGE 289
Db 578 EKRLHFGNGHLKLPGL---RTYVDPTHYEDPTQAVHFAKELDATNISIDKVGAGSFG 634
Qy 290 VMNGTWNGTTR---VAIKTLKPGTMSPEA--FLQEAQVKKLRHEKLVOLYAVVSE-EP 342
Db 635 VCSGRLKLPKKEISVAIKTLKGYTEKQRRDFEGEASINGQFDPHPIIRLEGVYTKSKP 694
Qy 343 IYIVTEYMSKSLDPLKGETGKYRLPOLVDMAAQIASGMAYVERNNYHRDLRAANIL 402
Db 695 VMIVTEYMSKSLDPLKRDHQAQPTVI-QLVGMIRGIASGMKLYSDMGVYHRDLAANIL 753
Qy 403 VGENLVCKVADFGIARLIEDN---EYARQAKPEIKMTAEALYGRFTIKSDVMSFGI 459
Db 754 INSNLVCKVSDFGLSRLEDDPEAAITTR-GGKIPIRMTPEALAYAKKFSASVSYGI 812
Qy 460 LTELTTKGRVPYPGVNVREVLDQVERGYMPCEPCEPSLHDMCOCWRKEPERPTE 519
Db 813 VLMEVMSYGRPYWMSNGQVIAKVDGRLPRPMDPALYOLMDCMQKDRNNRBFKE 872
Qy 520 YLQAFLE 526
Db 873 QIVSILD 879

RESULT 9
US-11-303-935-12
; Sequence 12, Application US/11303935
; Publication No. US20060099708A1
; GENERAL INFORMATION:
; APPLICANT: Closssek, Thomas
; APPLICANT: Ullrich, Axel
; TITLE OF INVENTION: METHODS FOR DIAGNOSIS
; AND TREATMENT OF MDK1
; SIGNAL TRANSDUCTION
; DISORDERS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/303, 935
; FILING DATE: 19-Dec-2005
; CLASSIFICATION: 435


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QY 203 AKGLNVAHKYIKRLKDSG-----FYTSRTPQNSLQOLVAVYSKADGLCH 248
D 573 ---IGRHCGYSKADQGBDELYHFHFKPGTKYIDET-YEDNRVAHQPAKELDSC- 627
QY 249 RLTTVCPTSKPOTGLAKDAWEIPRESIRLEVKLGOCGFEVWNG---TWNGTTRVAIK 304
D 628 -----IKIERVIGABEFGVCSGRKLKPGQRVAVAIK 660
QY 305 TLKPGTSPFA--FLQBAQVNAKLRHEKLVQIYAVSE-EPYIVTEYMSKSLDPLKG 361
D 661 TLKGVYTEKORRDLCEASITGCFDHPNVHLBEGVTRGKVMIVIEFMENGALDAFLRK 720
QY 362 ETGKYALPOLVYMAADIASGMAYVERMYHRDLRANILVGNLVCKVADPGLARLIE 421
D 721 HDGQFTVI-QLVGMRLGIAAGMRYLADMGVYHRDLAARNILVNSLVCKVSDPGLSRVIE 779
QY 422 DNE---YTARQAKFPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVPYGVNR 478
D 780 DDEPAVYTT-TGSKIPTVMTAPEALQYRKFTSADVMSYGIYVMEVMSYGERPFTMDMSNQ 838
QY 479 EVIDQVERGYRMPCCPPECESLDMCCQWKEKEPERPTEFYLOAFLE 526
D 839 DVIAIEGAYRLPAPMDCPAGLHQMLDMCQKDBAERPKFQIYGIID 886

RESULT 11
US-11-303-935-2
; Sequence 2, Application US/11303935
; Publication No. US20060099708A1
; GENERAL INFORMATION:
; APPLICANT: Closeek, Thomas
; Ullrich, Axel
; Millaer, Birgit
; TITLE OF INVENTION: METHODS FOR DIAGNOSIS
; AND TREATMENT OF MXL
; SIGNAL TRANSDUCTION
; DISORDERS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 613 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/303,935
; FILING DATE: 19-Dec-2005
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/073,064
; FILING DATE: 12-Feb-2002
; APPLICATION NUMBER: US/08/438,265
; FILING DATE: MAY 9, 1995
; APPLICATION NUMBER: US/08/368,776
; FILING DATE: January 3, 1995
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510

```

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; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 998 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-11-303-935-2

Query Match 19.3%; Score 569; DB 7; Length 998;
Best Local Similarity 28.7%; Pred. No. 3.5e-24;
Matches 180; Conservative 84; Mismatches 196; Indels 168; Gaps 22;

QY 31 AFAASQTPSPKPAADG-HRGP-----AFAAPAARKEKLEFGNSSDPTVSPQAGPLAG 84
D 300 SFEDRESSSRCECEDGYRAPSDPPYACTRPSAPQNL-FNINQTVLSLEMSPADN 357
QY 85 GVTFVALVDYBSRTETDLSFKKGE-----RLQIVANTR 118
D 358 GGRNDVYRILCKR---CSWQGEVCYPCGSNIGMPQQTLEDNYTVNDLHANVTF 413
QY 119 KVDV-----REGDWMLASLSTGQGYIPSNVAPS--DSIQAEWYFGKTRRESE 168
D 414 EVEAVNGVSDLSRSQRLFAVSLITGQ-----AAPQGVSGVWKE-----RVLGRSVQ 460
QY 169 RLILMAENPRG-----TLVRESERTKAYCLSYSDPNAKGLANVAY 211
D 461 LSWQEPHPNGVITVEYIKYERKQDRETYSTLTKVST-----ASINLKGTYVVF 513
QY 212 KIRLDSGCF-YITSRQFNSLQOLVAVYSKADGLCHRLTTV----- 253
D 514 QIRAVTAAGYGNVSPRLDAVLE-----ASGKMEATVAVSSEQNPVITIAVAVAG 565
QY 254 -----CPTSKPOTG-----LAKDAWEIPRES----- 275
D 566 TIIVFVWPGFIIGRHCGYSKADQGBDELYHFHFKPGTKYIDETPYEDPNRAVHQA 625
QY 276 -----LRLEVKLGOCGFEVWNG---TWNGTTRVAIKLKPGTSPFA--FLQBAQV 322
D 626 KELDASCIKIERVIGABEFGVCSGRKLKPGQRVAVAIKTLKGVYTEKORRDLCEASI 685
QY 323 MKKLHEKLVQIYAVSE-EPYIVTEYMSKSLDPLKSBETGKYLLPOLVMAAQIAS 381
D 686 MGQFDHPNVVHLBEGVTRGKVMIVIEFMENGALDAFLRHGQFTVI-QLVGMRLGIAA 744
QY 382 GMAVERMYHRDLRANILVGNLVCKVADPGLARLIEDNE---YTARQAKFPIKMT 438
D 745 GMRYLADMGYHRDLAARNILVNSLVCKVSDPGLSRVIEDDEPAVYTT-TGSKIPTVMT 803
QY 439 APEALYGRFTIKSDVMSFGILLTELTTKGRVPYGVNREVIDQVERGYRMPCCPE 498
D 804 APEALQYRKFTSADVMSYGIYVMEVMSYGERPFTMDMSNQDVIAIEGAYRLPAPMDCPA 863
QY 499 SLHDMCCQWKEKEPERPTEFYLOAFLE 526
D 864 GLHQLMDMCQKDBAERPKFQIYGIID 891

RESULT 12
US-11-312-958-52
; Sequence 52, Application US/11312958
; Publication No. US20060100152A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Rosenfeld, Julie Beth
; APPLICANT: Slios-Santiago, Immaculada
; TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
; PAIN AND PAINFUL DISORDERS USING 9949, 14230, 760, 62553,
; 12216, 17719, 41897, 47174, 33408, 10002, 16209, 314, 636,
; 27410, 33260, 619, 15985, 69112, 2158, 224, 615, 44373,
; 95431, 22245, 2387, 16658, 55054, 16314, 1613, 1675, 9569 OR
; TITLE OF INVENTION: 13424 MOLECULES

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LENGTH: 885
TYPE: PRT
ORGANISM: Homo sapiens
US-10-505-928-432

Query Match 16.9% Score 482.5; DB 6; Length 885;
Best Local Similarity 28.6%; Pred. No. 1.5e-19;
Matches 160; Conservative 72; Mismatches 212; Indels 115; Gaps 20;

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QY 18 LEPANVHGA--GGGAPASQTPSKPASADGHRPSAFAFA---AAEPKLFGGFNSSDT 72
D 334 LGPPENISATRNSQAQVHMEPPAPL-----QSTLLGYRLAYGQDTPVLMIDIGLRQE 388
QY 73 VTSFQRAGPLAGGVTTFVALYDYESRTETDLSFKKGERLQIVNTRKVDVREGDMWLAHS 132
D 389 VTLELQDGDGSVSNLTVCVAAY-----TAAODGGMSLPVP 422
QY 133 LSTGQGTGYPNSNYVAPSDSIQAEEMV--FGKITRRESEBRLLNANENRGTFVY--RSET 188
D 423 LEAMRPVKERS-----TPAFSMPWVYLLGAVVAAACVLLI-----ALFLVHRRKKE 470
QY 189 TKGAYCISVDFDNAKGLNVGHYKIRKLDGSGFYITSRTQFNSIQOLVAYYSKADGLCH 248
D 471 RYG---EVEEPTVERGELVYRVRKYSNR--TTEATLNSL----- 507
QY 249 RLTTVCTSKPQTQGLAKDAME-----IPRESLRLEVKLGQCGFGEVMMGTNN--GTT 299
D 508 -----GISELKEKLRDVMVDHRKVALGKTIGEGFQVMEGQLNQDSDIL 553
QY 300 RVALKTLKPG--TWSP-EAFLQEAQVWKLRHEKLVQLYAVV---SEEPY---ITYEY 349
D 554 KVAVKTKMIAICTRSELEDFLSEAVCKEFDHPVMMRLIGVCFQGSERESPAPVILPF 613
QY 350 MSKGSLLDFL---KGETGKYLRLPOLVDMAAQASGMAYYERNNYVHRDLRAANILVGE 405
D 614 MKHGDLSFLYSRLGQPYLLPTQMLVKFMADIASGMEYLSYSTRFTHRDIAARNCLME 673
QY 406 NLVCKVADFGIARLIEDNEYTARQG--AKPPIKWTAPBAALYGRFTIKSDVMSFGILLTE 463
D 674 NMSVCVADFGLSKTIYGDY-YRQGRIAKMPVKMIAIESLADRYTTSKSDVMSFGVTWME 732
QY 464 LTTKGRVYPGMMVNRVLDQVERGYRMPCEPECESLHDLMOCKWRKEPERPFEVYLA 523
D 733 IATRGQTPYPGVENSEIYDYLROGNRLKQPADCLDGYALMSRCWELNPDORPSFTELRE 792
QY 524 FLEDYFTSTEPQYOGENTL 542
D 793 DLENTLKALPPAQEPDEIL 811
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RESULT 15
US-11-251-465-20
Sequence 20, Application US/11251465
Publication No. US20060094061A1
GENERAL INFORMATION:
APPLICANT: Blys, Reginald
APPLICANT: Vandeghinete, Nick
APPLICANT: Tomme, Peter
APPLICANT: Klaassen, Hubertus
TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The
TITLE OF INVENTION: Same, Useful In The Treatment Of Joint Degenerative And
FILE REFERENCE: P30,172-A USA
CURRENT APPLICATION NUMBER: US/11/251,465
PRIOR APPLICATION NUMBER: 60/619,384
PRIOR FILING DATE: 2004-10-15
NUMBER OF SEQ ID NOS: 880
SOFTWARE: PatentIn version 3.3
SEQ ID NO 20
LENGTH: 885
TYPE: PRT
ORGANISM: Homo sapiens

US-11-251-465-20

Query Match 16.9% Score 482.5; DB 7; Length 885;
Best Local Similarity 28.6%; Pred. No. 1.5e-19;
Matches 160; Conservative 72; Mismatches 212; Indels 115; Gaps 20;

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QY 18 LEPANVHGA--GGGAPASQTPSKPASADGHRPSAFAFA---AAEPKLFGGFNSSDT 72
D 334 LGPPENISATRNSQAQVHMEPPAPL-----QSTLLGYRLAYGQDTPVLMIDIGLRQE 388
QY 73 VTSFQRAGPLAGGVTTFVALYDYESRTETDLSFKKGERLQIVNTRKVDVREGDMWLAHS 132
D 389 VTLELQDGDGSVSNLTVCVAAY-----TAAODGGMSLPVP 422
QY 133 LSTGQGTGYPNSNYVAPSDSIQAEEMV--FGKITRRESEBRLLNANENRGTFVY--RSET 188
D 423 LEAMRPVKERS-----TPAFSMPWVYLLGAVVAAACVLLI-----ALFLVHRRKKE 470
QY 189 TKGAYCISVDFDNAKGLNVGHYKIRKLDGSGFYITSRTQFNSIQOLVAYYSKADGLCH 248
D 471 RYG---EVEEPTVERGELVYRVRKYSNR--TTEATLNSL----- 507
QY 249 RLTTVCTSKPQTQGLAKDAME-----IPRESLRLEVKLGQCGFGEVMMGTNN--GTT 299
D 508 -----GISELKEKLRDVMVDHRKVALGKTIGEGFQVMEGQLNQDSDIL 553
QY 300 RVALKTLKPG--TWSP-EAFLQEAQVWKLRHEKLVQLYAVV---SEEPY---ITYEY 349
D 554 KVAVKTKMIAICTRSELEDFLSEAVCKEFDHPVMMRLIGVCFQGSERESPAPVILPF 613
QY 350 MSKGSLLDFL---KGETGKYLRLPOLVDMAAQASGMAYYERNNYVHRDLRAANILVGE 405
D 614 MKHGDLSFLYSRLGQPYLLPTQMLVKFMADIASGMEYLSYSTRFTHRDIAARNCLME 673
QY 406 NLVCKVADFGIARLIEDNEYTARQG--AKPPIKWTAPBAALYGRFTIKSDVMSFGILLTE 463
D 674 NMSVCVADFGLSKTIYGDY-YRQGRIAKMPVKMIAIESLADRYTTSKSDVMSFGVTWME 732
QY 464 LTTKGRVYPGMMVNRVLDQVERGYRMPCEPECESLHDLMOCKWRKEPERPFEVYLA 523
D 733 IATRGQTPYPGVENSEIYDYLROGNRLKQPADCLDGYALMSRCWELNPDORPSFTELRE 792
QY 524 FLEDYFTSTEPQYOGENTL 542
D 793 DLENTLKALPPAQEPDEIL 811
```

Search completed: June 5, 2006, 17:43:30
Job time : 9.03027 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 5, 2006, 17:01:34 ; Search time 117.529 Seconds
(without alignments)
2085.165 Million cell updates/sec

Title: US-10-691-079-2

Perfect score: 2834
Sequence: 1 MGSNKSXPADASQRRSLRP.....AFLEDTFTSTPEQYQENL 536

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

- 1: A_Geneseq_8:*
- 2: geneseqp19808:*
- 3: geneseqp19808:*
- 4: geneseqp20008:*
- 5: geneseqp20028:*
- 6: geneseqp20038:*
- 7: geneseqp20038:*
- 8: geneseqp20048:*
- 9: geneseqp20058:*
- 10: geneseqp20068:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2834	100.0	536	2 AAR39706	AAR39706 Human pp6
2	2834	100.0	536	2 ABG95123	ABG95123 Human v-s
3	2834	100.0	536	5 AAU78678	AAU78678 Human SH2
4	2834	100.0	536	6 ABP57260	ABP57260 Human src
5	2834	100.0	536	7 ADI20072	ADI20072 Human c-s
6	2834	100.0	536	8 ADL22904	ADL22904 Human MP2
7	2834	100.0	536	8 ADQ88400	ADQ88400 Human wil
8	2834	100.0	536	8 ADQ97772	ADQ97772 Human can
9	2834	100.0	536	8 ADU04517	ADU04517 Protein t
10	2834	100.0	536	8 ADY84076	ADY84076 Human Src
11	2834	100.0	536	9 ADV94834	ADV94834 Human wil
12	2834	100.0	536	9 AEA35914	AEA35914 Human Src
13	2834	100.0	549	8 ADY84080	ADY84080 Human Src
14	2829	99.8	535	7 ADP45087	ADP45087 Human kin
15	2829	99.8	535	9 AED21154	AED21154 Human non
16	2821	99.5	542	8 ABB97339	ABB97339 Novel hum
17	2821	99.5	542	8 ADY84075	ADY84075 Human Src
18	2801	98.8	530	8 ADQ88402	ADQ88402 Human mut
19	2801	98.8	530	8 ADV94836	ADV94836 Human mut
20	2778.5	98.0	541	6 ABP57261	ABP57261 Mouse src
21	2778.5	98.0	541	8 ADY84077	ADY84077 Murine Src
22	2663.5	94.0	533	3 AAY44447	AAY44447 Wild-type
23	2663.5	94.0	533	4 AAB84661	AAB84661 Amino aci

24	2663.5	94.0	533	9 AEB07192	AEB07192 Chicken c
25	2659.5	93.8	533	3 AAY44449	AAY44449 Mutant ch
26	2658.5	93.8	533	2 AAR39705	AAR39705 Chicken p
27	2657.5	93.8	533	3 AAY44451	AAY44451 Mutant ch
28	2482	87.6	523	9 AEB07190	AEB07190 Rous sarc
29	2408.5	85.0	565	4 ABG23778	ABG23778 Novel hum
30	2225	78.5	423	8 ADQ97769	ADQ97769 Mouse can
31	2123.5	74.9	543	4 AAB84663	AAB84663 Amino aci
32	2123.5	74.9	543	4 ABG10302	ABG10302 Novel hum
33	2123.5	74.9	543	6 ADA00843	ADA00843 Human Src
34	2123.5	74.9	543	7 ADP45099	ADP45099 Human kin
35	2123.5	74.9	543	8 ADL22913	ADL22913 Human MP2
36	2123.5	74.9	543	8 ADQ19329	ADQ19329 Human PRO
37	2123.5	74.9	543	8 ADQ19331	ADQ19331 Human PRO
38	2123.5	74.9	543	8 ADQ26047	ADQ26047 v-yes-1 y
39	2123.5	74.9	543	8 ADU06318	ADU06318 Novel bro
40	2123.5	74.9	543	9 ADW78761	ADW78761 Human Yam
41	2123.5	74.9	543	9 ADY19868	ADY19868 PRO polyP
42	2123.5	74.9	543	9 AEA35915	AEA35915 Human PRO
43	2123.5	74.9	543	9 AEA35915	AEA35915 Human Yeb
44	2123.5	74.9	543	9 AED01122	AED01122 Human c-y
45	2117.5	74.7	541	5 AAU74614	AAU74614 Pertinucle

ALIGNMENTS

RESULT 1
ID AAR39706 standard; protein; 536 AA.
AAAR39706;
AC AAR39706;
XX 25-MAR-2003 (revised)
DT 23-DEC-1993 (first entry)
XX 22-JUL-1993.
XX 05-JAN-1993; 93WO-US00445.
XX 06-JAN-1992; 92US-00820011.
XX (UYTA) UNIV YALE.
XX Bell L, Madri JA, Warren SL, Luthringer DJ;
PI WPI; 1993-243209/30.
XX P-PSDB; AAR39705.
XX Genetically engineered endothelial cells - which exhibit enhanced cell
PT migration, urokinase-type plasminogen activator activity, and reduced
PT mononuclear cell adhesion and fibronectin prodn.
XX Disclosure; Page 75-77; 91pp; English.
XX The DNA encoding a portion or (more preferably) the entire pp60 c-src
XX polypeptide (Given in AAQ46688) is used to transform endothelial cells.
XX Transformed cells produce increased amounts of pp60 c-src and have
XX improved therapeutic properties. They migrate at faster rates than non-
XX transformed counterparts; have an enhanced ability to inhibit the
XX formation of thrombi and/or dissolve thrombi once they have formed and
XX exhibit reduced mononuclear cell adhesion. They can also be used to
XX improve the success of surgical procedures such as coronary angioplasty,
XX heart bypass surgery, vessel graft and stent implantation. (Updated on 25
XX -MAR-2003 to correct FN field.)

XX	Sequence	536 AA;	100.0%;	Score 2834;	DB 2;	Length 536;
XX	Query Match		100.0%;			
XX	Beat Local Similarity		100.0%;			Pred. No. 1e-242;
XX	Matches 536;	Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;
QY	1	MGNSKSKPKDASQRRRLSEPAENVHAGGGAGFPAQSPQSPKASADGHRGSPAAFPAAAE	60			
DB	1	MGNSKSKPKDASQRRRLSEPAENVHAGGGAGFPAQSPQSPKASADGHRGSPAAFPAAAE	60			
QY	61	PKLREGFNSDPTVYSPORAGPLAGGVTFVALYDVESTETDLSFKKBERLOIVNNTGCD	120			
DB	61	PKLREGFNSDPTVYSPORAGPLAGGVTFVALYDVESTETDLSFKKBERLOIVNNTGCD	120			
QY	121	WMLAHSLSGTQGTGYIPSNVYVAPSDSIQAEEMWYFGKITRRESERLLLNENPGTELVRES	180			
DB	121	WMLAHSLSGTQGTGYIPSNVYVAPSDSIQAEEMWYFGKITRRESERLLLNENPGTELVRES	180			
QY	181	ETTGAAYCLVSYSDFDNAGLVNKHVKIRKLDSGGFYITSRTQFNSLQQLVAYYSGHADGL	240			
DB	181	ETTGAAYCLVSYSDFDNAGLVNKHVKIRKLDSGGFYITSRTQFNSLQQLVAYYSGHADGL	240			
QY	241	CHRLTTVPTSPKPOQVGLAKDAWEIPRESRLREVLGGGCGREVMWGTRNGTRVAIKTL	300			
DB	241	CHRLTTVPTSPKPOQVGLAKDAWEIPRESRLREVLGGGCGREVMWGTRNGTRVAIKTL	300			
QY	301	KPGTMSPAFIFOEAOVMKKLRHEKIVOLYAVVSEEPYIVTEVMSKSLDPLKGETGKY	360			
DB	301	KPGTMSPAFIFOEAOVMKKLRHEKIVOLYAVVSEEPYIVTEVMSKSLDPLKGETGKY	360			
QY	361	LRLPLVDMAAQIASGMAVVERBNVYVHDLRAANILVGENLVCKYADPGLARLLEDNEYT	420			
DB	361	LRLPLVDMAAQIASGMAVVERBNVYVHDLRAANILVGENLVCKYADPGLARLLEDNEYT	420			
QY	421	AROGAKKFKIKTAPPAALYGRFTTISDVMSFGILLTELTKGRVYPCGMVNRVILDQVER	480			
DB	421	AROGAKKFKIKTAPPAALYGRFTTISDVMSFGILLTELTKGRVYPCGMVNRVILDQVER	480			
QY	481	GYRMPCEPCEPSLHDLMCOCMRKSPERPTFEYLOAFLEDFYFSTEPYOYQGENL	536			
DB	481	GYRMPCEPCEPSLHDLMCOCMRKSPERPTFEYLOAFLEDFYFSTEPYOYQGENL	536			
RESULT 2						
ABG95123						
ID	ABG95123	standard;	protein;	536 AA.		
XX	ABG95123;					
XX	04-DEC-2002	(first entry)				
XX	Human v-src isoform.					
XX	Chromosome aberration; oncogenic fusion protein; cancer; oncogene;					
XX	proliferative disease; cellular protein isoform; heat shock protein 90;					
XX	HSP-90; rheumatoid arthritis; cancer; hematopoietic disorder;					
XX	T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CMV;					
XX	acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;					
XX	acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;					
XX	papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;					
XX	rhabdomyosarcoma; synovial sarcoma; viral infection.					
OS	Homo sapiens.					
XX	MO200269900-A2.					
XX	12-SEP-2002.					
XX	01-MAR-2002; 2002MO-US006518.					
XX	01-MAR-2001; 2001US-0272751P.					

Query Match	100.0%;	Score 2834;	DB 5;	Length 536;
Best Local Similarity	100.0%;	Pred. No. 1e-242;		
Matches 536;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY 1 MGSNKSRRKQKDSORRRRLSEPEENHNGAGGGAFPASQTPSKRPSADGHRGSPAAAPAAAE 60				
DB 1 MGSNKSRRKQKDSORRRRLSEPEENHNGAGGGAFPASQTPSKRPSADGHRGSPAAAPAAAE 60				
QY 61 PKLFCGFSSDPTVWSPORAGPLAGVTFVVALVYSESTREDLSFKKGERLOIVNNTGCD 120				
DB 61 PKLFCGFSSDPTVWSPORAGPLAGVTFVVALVYSESTREDLSFKKGERLOIVNNTGCD 120				
QY 121 WMLASHLSGTQGYI PSNYYVAPSDSIQAEWYFGKITRSEBRLLNLANENRGTFLVES 180				
DB 121 WMLASHLSGTQGYI PSNYYVAPSDSIQAEWYFGKITRSEBRLLNLANENRGTFLVES 180				
QY 181 ETTKCAVYCLSYSDPDNAKGLVAKYIKTRKLDSGGFYITSRQFNSLQOLVAYYSGHADGL 240				
DB 181 ETTKCAVYCLSYSDPDNAKGLVAKYIKTRKLDSGGFYITSRQFNSLQOLVAYYSGHADGL 240				
QY 241 CHRLLTVCPSTKPOQGLAKQAMELPRESLREYKLDGGCGGEVWGMGTNCTTRVAIKTL 300				
DB 241 CHRLLTVCPSTKPOQGLAKQAMELPRESLREYKLDGGCGGEVWGMGTNCTTRVAIKTL 300				
QY 301 KPGTMSPEAFQEAQVWVKLHHEKLVOLYAVVSEEPYITVTEWNSKSLDPLFGGETGKY 360				
DB 301 KPGTMSPEAFQEAQVWVKLHHEKLVOLYAVVSEEPYITVTEWNSKSLDPLFGGETGKY 360				
QY 361 LRLPOLVDMAQIISGMAVVERNMYVHRDLPAANILVGENLVCKVADFGRLRLIEDNEYT 420				
DB 361 LRLPOLVDMAQIISGMAVVERNMYVHRDLPAANILVGENLVCKVADFGRLRLIEDNEYT 420				
QY 421 ARQGAAPKIKTAAEALYGRFTIKSDVWSGILLTELTKGRVPRPYPMNVNRYVLDOVER 480				
DB 421 ARQGAAPKIKTAAEALYGRFTIKSDVWSGILLTELTKGRVPRPYPMNVNRYVLDOVER 480				
QY 481 GYRNPCEPCECESHLDLMCCMCKEPEERPFPEYLOAFLEDYFTYSTEBOYQGENL 536				
DB 481 GYRNPCEPCECESHLDLMCCMCKEPEERPFPEYLOAFLEDYFTYSTEBOYQGENL 536				

Db 481 GYRMPCEPCESLHDLMCQMKRKEPERPFEYLQAFLEBYFSTEQYQGENL 536
|||||
RESULT 3
AAU78678
ID AAU78678 standard; protein; 536 AA.
XX
AC AAU78678;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human SH2/SH3 domain containing protein, v-src.
XX
KM Protein profiling; c-src; SH2; SH3; antibody microarray;
KM protein microarray; DNA microarray; expression profiling; immunology;
KM protein analysis; proteome analysis; human; protein expression profiling.
XX
OS Homo sapiens.
XX
PN WO200214867-A2.
XX
PD 21-FEB-2002.
XX
PF 13-AUG-2001; 2001WO-US041709.
XX
PR 11-AUG-2000; 2000US-0224939P.
PR 12-APR-2001; 2001US-0283498P.
XX
PA (AGIL-) AGILIX CORP.
XX
PI Chait BT, Lattimer DR, Lizardi PM, Kershnar ER, Morrow JS;
PI Roth ME, Maltessich WJ, McConnell KJ;
XX
DR WPI; 2002-304072/34.
XX
PT Detecting multiple analytes by separating a set of reporter signals
PT having common property from molecules lacking common property, altering
PT signal, detecting and distinguishing altered forms of signal from each
PT other.
XX
PS Disclosure; Page 224; 341pp; English.
XX
XX The invention relates to detecting (M1) multiple analytes involving
XX separating a set of reporter signals (RS), where each RS has a common
XX property, from molecules lacking the common property, altering the RS,
XX and detecting and distinguishing the altered forms of the RS from each
XX other. The method (M1) is useful for detecting multiple analytes M1 is
XX useful for detection of analytes and biomolecules, (such as proteins,
XX peptides and protein fragments), preferably for multiplex detection and
XX analysis of analytes and biomolecules. M1 is useful to detect a specific
XX analyte (in a specific sample or in multiple samples) or multiple
XX analytes (in a single sample or multiple samples), and to gather and
XX catalogue information about unknown analytes. M1 is useful as a detection
XX system in a number of fields, including antibody or protein microarrays,
XX DNA microarrays, expression profiling, comparative genomics, immunology,
XX diagnostic assay and quality control. M1 is useful as a detection and
XX analysis system for protein analysis, proteome analysis, proteomic,
XX protein expression profiling, de novo protein discovery, functional
XX genomics and protein detection. M1 increases the sensitivity and accuracy
XX of detection of analytes of interest, and allows a complex sample of
XX analytes to be quickly and easily catalogued in a reproducible manner. M1
XX is compatible with techniques involving cleavage, treatment or
XX fragmentation of a bulk sample in order to simplify the sample prior to
XX introduction into the first stage of a multistage detection system. M1 is
XX also compatible with any desired sample, including raw extracts and
XX fractionated samples. The present sequence is human c-src whose SH2/SH3
XX domains are detected in a sample, using the method of the invention
XX
SQ Sequence 536 AA:
Query Match 100.0%; Score 2834; DB 5; Length 536;
Best Local Similarity 100.0%; Pred. No. 1e-242;

Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGSNKSXPKQASQRRRSLEPAMENVHAGGCAFPASQTPSKASADGRGSEAAAPAAAE 60
Db 1 MGSNKSXPKQASQRRRSLEPAMENVHAGGCAFPASQTPSKASADGRGSEAAAPAAAE 60
QY 61 PKLFGFNSSDTVNSPORAGPLAGVTFVVALDYESTETEDLSFKKGERLQIVNTEGD 120
Db 61 PKLFGFNSSDTVNSPORAGPLAGVTFVVALDYESTETEDLSFKKGERLQIVNTEGD 120
QY 121 WMLAHSLSGTQGYIPSNVYVAPSDIOAEEMYPFKITRRESERLLNANENRGTFVRES 180
Db 121 WMLAHSLSGTQGYIPSNVYVAPSDIOAEEMYPFKITRRESERLLNANENRGTFVRES 180
QY 181 ETTYGAYCLVSDPDNAKGLNVKIKRKLDGSGFYITSRQFNSLQQLVAYYSKADGL 240
Db 181 ETTYGAYCLVSDPDNAKGLNVKIKRKLDGSGFYITSRQFNSLQQLVAYYSKADGL 240
QY 241 CHRLTTCPTSPKPTQGLAKDAMEIPRESLLEVKLGQCGEYVMGTMNGTTRVAIKTL 300
Db 241 CHRLTTCPTSPKPTQGLAKDAMEIPRESLLEVKLGQCGEYVMGTMNGTTRVAIKTL 300
QY 301 KPGTMSPEAFLOEAQVMKRLHEKLVOLYAVVSEEPITYVTEYMSKSLDPLKGETGKY 360
Db 301 KPGTMSPEAFLOEAQVMKRLHEKLVOLYAVVSEEPITYVTEYMSKSLDPLKGETGKY 360
QY 361 LRLPOLVMAAQIASGNAVYRMNYVHRDLPAANILVGENIVCYADFGRLIEDNEYT 420
Db 361 LRLPOLVMAAQIASGNAVYRMNYVHRDLPAANILVGENIVCYADFGRLIEDNEYT 420
QY 421 ARQAKFPKIKWTAREALVYGFETIKSDVWSGILLTETTKGRVPYPMGVNREVLDOVER 480
Db 421 ARQAKFPKIKWTAREALVYGFETIKSDVWSGILLTETTKGRVPYPMGVNREVLDOVER 480
QY 481 GYRMPCEPCESLHDLMCQMKRKEPERPFEYLQAFLEBYFSTEQYQGENL 536
Db 481 GYRMPCEPCESLHDLMCQMKRKEPERPFEYLQAFLEBYFSTEQYQGENL 536
RESULT 4
ABP57260
ID ABP57260 standard; protein; 536 AA.
XX
AC ABP57260;
XX
DT 17-APR-2003 (first entry)
XX
DE Human src-c protein SEQ ID NO:3.
XX
KW Human; src-c; tyrosine kinase; src-c inhibitor; cytosstatic; osteopathic;
KW antiinflammatory; antibacterial; antisense therapy; vaccine; cancer;
KW antisense oligonucleotide; aberrant bone remodeling; breast cancer;
KW hyperproliferative disorder; pancreatic cancer; lung cancer; tumour;
KW ovarian cancer; oesophageal cancer; neuroblastoma; retinoblastoma;
KW Kaposi's sarcoma; infection; inflammation; tumour formation.
XX
OS Homo sapiens.
XX
PN WO200295053-A2.
XX
PD 28-NOV-2002.
XX
PF 16-MAY-2002; 2002WO-US015684.
XX
PR 18-MAY-2001; 2001US-00860473.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett FC, Walt AT;
XX
XX WPI; 2003-120806/11.
XX
DR N-PSDB; ABZ59382.
XX

PT New antisense oligonucleotides targeted to nucleic acids encoding src-c,
PT useful for diagnosing, treating or preventing diseases associated with
PT the expression of src-c, e.g. cancer or inflammation, and in research
PT applications.

XX Example 13; Page 97-100; 137pp; English.

CC The present invention describes a compound (I) that is 8-50 nucleobases
CC in length targeted to a nucleic acid molecule encoding a 5'UTR, 3'UTR,
CC coding region, intron region, exon region, stop codon, intron:exon
CC junction, exon:exon junction, or 5' mRNA variant of src-c, and which
CC specifically hybridizes with and inhibits the expression of src-c. (I)
CC have cytostatic, antiinflammatory, osteopathic and antibacterial
CC activities, and can be used in antisense therapy and in vaccines. The
CC antisense compound (I) can be used for modulating the expression of src-
CC c and for treating diseases or conditions associated with expression of
CC src-c, e.g. aberrant bone remodeling or hyperproliferative disorders,
CC particularly cancer, such as breast cancer, pancreatic cancer, lung
CC cancer, ovarian cancer, oesophageal cancer, neuroblastoma, retinoblastoma
CC or Kaposi's sarcoma. (I) are also useful for diagnostic, therapeutic,
CC prophylaxis, e.g. to prevent or delay infection, inflammation or tumour
CC formation, as research reagents and kits, and in distinguishing between
CC functions of various members of a biological pathway. The present
CC sequence represents human src-c, which is used in an example from the
CC present invention

XX Sequence 536 AA;

Query Match 100.0%; Score 2834; DB 6; Length 536;
Best Local Similarity 100.0%; Pred. No. 1e-242;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSNKSQPDASQRRSLSPAENVHAGGAGFPASQTPSKPASADGHRGSAAPAPAAE 60
DB 1 MGSNKSQPDASQRRSLSPAENVHAGGAGFPASQTPSKPASADGHRGSAAPAPAAE 60
QY 61 PKLFGFNSSDVTYTSFQRAQPLAGVYTFVALYDRESRTETDLSFKKGERLQIVNTEGD 120
DB 61 PKLFGFNSSDVTYTSFQRAQPLAGVYTFVALYDRESRTETDLSFKKGERLQIVNTEGD 120
QY 121 WMLAHSLSGTQGYIPSNVVAAPSDSIQAEEMVFGKITRRESERLLNAENPRGTFVRES 180
DB 121 WMLAHSLSGTQGYIPSNVVAAPSDSIQAEEMVFGKITRRESERLLNAENPRGTFVRES 180
QY 181 ETTKGAICYLSDVDFDNAGKLVNHYKIRKLDGSGFYITSTQFNSIQQLVAYYSKADGL 240
DB 181 ETTKGAICYLSDVDFDNAGKLVNHYKIRKLDGSGFYITSTQFNSIQQLVAYYSKADGL 240
QY 241 CHRLLTVCTPSKQTOGLAKDAWEIPRESLRLEVKLGOCGCFEVMWGTNGTTRVAIKTL 300
DB 241 CHRLLTVCTPSKQTOGLAKDAWEIPRESLRLEVKLGOCGCFEVMWGTNGTTRVAIKTL 300
QY 301 KEGTMSPEAFLOBAQVMKCLRHEKLVQLYAVVSEBPIYIVTEYMSKSLDPLKGETGKY 360
DB 301 KEGTMSPEAFLOBAQVMKCLRHEKLVQLYAVVSEBPIYIVTEYMSKSLDPLKGETGKY 360
QY 361 LRLPOLVDMAAQIASGMAVYERBNVYHRDLRAANILVGENLVCKVADFGIARLIENDEYT 420
DB 361 LRLPOLVDMAAQIASGMAVYERBNVYHRDLRAANILVGENLVCKVADFGIARLIENDEYT 420
QY 421 AROGAKFPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVPPGVMNREVLDOVER 480
DB 421 AROGAKFPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVPPGVMNREVLDOVER 480
QY 481 GYRMPCEPCPSGLHLMCCQWRKEPERPTEFYLOAFLEDYTSSTEPQYQGENL 536
DB 481 GYRMPCEPCPSGLHLMCCQWRKEPERPTEFYLOAFLEDYTSSTEPQYQGENL 536

RESULT 5
AD120072
ID AD120072 standard; protein; 536 AA.
XX

AC AD120072;
XX
XX 22-APR-2004 (first entry)
XX

DE Human c-Src.

XX Specific-binding agent; Src; Cytostatic; Cardiant; Src-positive tumor;
XX heart disease.
XX

OS Homo sapiens.

PN WO2003057238-A1.

PD 17-JUL-2003.

PF 27-DEC-2002; 2002WO-US041564.

PR 28-DEC-2001; 2001US-034588P.

PA (UYOR-) UNIV OREGON HEALTH SCI.

PI Schmitt JM, Stork RJS;

XX WPI; 2003-587076/55.

DR N-PSDB; AD120071.

PT New specific-binding agent which specifically binds to Src when Src is
PT phosphorylated at serine-17 (Ser17) but does not detectably bind to Src
PT when Ser17 is not phosphorylated, useful for identifying abnormal cell
PT proliferation.

PS Disclosure; SEQ ID NO 2; 40pp; English.

CC The present invention relates to a specific-binding agent which
CC specifically binds to Src when Src is phosphorylated at serine at
CC position 17 (Ser17) but does not detectably bind to Src when Ser17 is not
CC phosphorylated. The specific-binding agent is useful as a diagnostic
CC agent. The agent and the methods may also be used for treating Src-
CC positive tumors or heart disease. The present sequence represents human c-
CC Src.

XX Sequence 536 AA;

Query Match 100.0%; Score 2834; DB 7; Length 536;
Best Local Similarity 100.0%; Pred. No. 1e-242;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSNKSQPDASQRRSLSPAENVHAGGAGFPASQTPSKPASADGHRGSAAPAPAAE 60
DB 1 MGSNKSQPDASQRRSLSPAENVHAGGAGFPASQTPSKPASADGHRGSAAPAPAAE 60
QY 61 PKLFGFNSSDVTYTSFQRAQPLAGVYTFVALYDRESRTETDLSFKKGERLQIVNTEGD 120
DB 61 PKLFGFNSSDVTYTSFQRAQPLAGVYTFVALYDRESRTETDLSFKKGERLQIVNTEGD 120
QY 121 WMLAHSLSGTQGYIPSNVVAAPSDSIQAEEMVFGKITRRESERLLNAENPRGTFVRES 180
DB 121 WMLAHSLSGTQGYIPSNVVAAPSDSIQAEEMVFGKITRRESERLLNAENPRGTFVRES 180
QY 181 ETTKGAICYLSDVDFDNAGKLVNHYKIRKLDGSGFYITSTQFNSIQQLVAYYSKADGL 240
DB 181 ETTKGAICYLSDVDFDNAGKLVNHYKIRKLDGSGFYITSTQFNSIQQLVAYYSKADGL 240
QY 241 CHRLLTVCTPSKQTOGLAKDAWEIPRESLRLEVKLGOCGCFEVMWGTNGTTRVAIKTL 300
DB 241 CHRLLTVCTPSKQTOGLAKDAWEIPRESLRLEVKLGOCGCFEVMWGTNGTTRVAIKTL 300
QY 301 KEGTMSPEAFLOBAQVMKCLRHEKLVQLYAVVSEBPIYIVTEYMSKSLDPLKGETGKY 360
DB 301 KEGTMSPEAFLOBAQVMKCLRHEKLVQLYAVVSEBPIYIVTEYMSKSLDPLKGETGKY 360
QY 361 LRLPOLVDMAAQIASGMAVYERBNVYHRDLRAANILVGENLVCKVADFGIARLIENDEYT 420
DB 361 LRLPOLVDMAAQIASGMAVYERBNVYHRDLRAANILVGENLVCKVADFGIARLIENDEYT 420

```
Db      361 LRLPOLVDMAAQIASGMAVYERMYVHRDLRAANIIVGENLVCKVADFGLARLIEDNEYT 420
Qy      421 AROGAKPPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVPYFGMNVREVLDOVER 480
Db      421 AROGAKPPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVPYFGMNVREVLDOVER 480
Qy      481 GYRMPCEPCEPESLHDMCQCKRKEPERPTFEYLQAFLEDYFTSTEPQYOPGENL 536
Db      481 GYRMPCEPCEPESLHDMCQCKRKEPERPTFEYLQAFLEDYFTSTEPQYOPGENL 536

RESULT 6
ADL22904
ID      ADL22904 standard; protein: 536 AA.
Xx      Xx
Ac      ADL22904;
Dx      20-MAY-2004 (first entry)
Dx      Xx
Dx      Human MP2153 polypeptide sequence SEQ ID NO: 24.
Dx      Xx
Dx      human; MP2153; p21; p53; cancer.
Xx      Xx
Xx      Homo sapiens.
Xx      Xx
Xx      MO2004015069-A2.
Xx      Xx
Xx      19-FEB-2004.
Xx      Xx
Xx      06-AUG-2003; 2003WC-US024505.
Xx      Xx
Xx      07-AUG-2002; 2002US-0401701P.
Xx      Pr      16-SEP-2002; 2002US-0411017P.
Xx      Pr      30-DEC-2002; 2002US-0437107P.
Xx      Xx
Xx      (EXEL-) EXELIXIS INC.
Xx      Pa
Xx      Francis-Liang H, Friedman L, Kidd T, Roche S, Belvin M;
Xx      Pl      Plozman GD, Lickteig K, Zhang H, Amundsen CD;
Xx      Xx
Xx      WPI; 2004-180653/17.
Xx      Dr      N-PSDB; ADL22887.
Xx      Xx
Xx      Identifying a candidate p21 or p53 pathway modulating agent using an
Xx      Pt      assay system having a modulator of p21 or p53 (MP2153) polypeptide or
Xx      Pt      nucleic acid, useful for diagnosing or treating cancer, such as colon or
Xx      Pt      breast cancer.
Xx      Xx
Xx      Example 3; Page 87-90; 110pp; English.
Xx      Xx
Xx      The present invention relates to a method of identifying a candidate p21
Xx      Cc      or p53 pathway modulating agent. This comprises providing an assay system
Xx      Cc      comprising a modulator of p21 or p53 (MP2153) polypeptide or nucleic
Xx      Cc      acid, contacting the assay system with a test agent, where in its
Xx      Cc      presence the system provides a reference activity, and detecting a test
Xx      Cc      agent-biased activity of the assay system, wherein a difference between
Xx      Cc      the test agent-biased activity and the reference activity identifies the
Xx      Cc      test agent as a candidate p21 or p53 pathway modulating agent. The
Xx      Cc      methods and compositions of the present invention are useful for the
Xx      Cc      diagnosis and/or treatment of diseases or conditions associated with
Xx      Cc      aberrant expression or activity of the p21 or p53 pathway, such as
Xx      Cc      cancer, preferably colon or head and neck cancer. The present sequence is
Xx      Cc      a human MP2153 protein sequence of the invention.
Xx      Xx
Xx      Sequence 536 AA;
Xx      S0

Query Match      100.0%; Score 2834; DB 8; Length 536;
Best Local Similarity 100.0%; Pred. No. 1e-242;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      61 PKLFGNSSDTVTSRORAGPLAGGVTTFVALVDYESTETDLSFKKGERLQIVNTEGD 120
Db      61 PKLFGGNSSDTVTSRORAPLAGGVTTFVALVDYESTETDLSFKKGERLQIVNTEGD 120
Qy      121 WMLAHSLSSTQGTGYIPSNVYAPSDSIQAEEMVFGKIRRESERLLNAENPRGTFVRES 180
Db      121 WMLAHSLSSTQGTGYIPSNVYAPSDSIQAEEMVFGKIRRESERLLNAENPRGTFVRES 180
Qy      181 ETTKGAAYCLSVSPDNKAGLVNKHYYKIRKLDSSGFTYTSRTQFNSLQOLVAYYSKADGL 240
Db      181 ETTKGAAYCLSVSPDNKAGLVNKHYYKIRKLDSSGFTYTSRTQFNSLQOLVAYYSKADGL 240
Qy      241 CHRLTYVCPTSKPTQGLADAMEIPRESLRLEVKLGQCGFGEVMTGNTKVAIKTL 300
Db      241 CHRLTYVCPTSKPTQGLADAMEIPRESLRLEVKLGQCGFGEVMTGNTKVAIKTL 300
Qy      301 KPGTMSPEAFLOEAQVKKLRHEKLVOLYVAVSEEPYIYITEVMSKSLDPLKGETGKY 360
Db      301 KPGTMSPEAFLOEAQVKKLRHEKLVOLYVAVSEEPYIYITEVMSKSLDPLKGETGKY 360
Qy      361 LRLPOLVDMAAQIASGMAVYERMYVHRDLRAANIIVGENLVCKVADFGLARLIEDNEYT 420
Db      361 LRLPOLVDMAAQIASGMAVYERMYVHRDLRAANIIVGENLVCKVADFGLARLIEDNEYT 420
Qy      421 AROGAKPPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVPYFGMNVREVLDOVER 480
Db      421 AROGAKPPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVPYFGMNVREVLDOVER 480
Qy      481 GYRMPCEPCEPESLHDMCQCKRKEPERPTFEYLQAFLEDYFTSTEPQYOPGENL 536
Db      481 GYRMPCEPCEPESLHDMCQCKRKEPERPTFEYLQAFLEDYFTSTEPQYOPGENL 536

RESULT 7
ADQ88400
ID      ADQ88400 standard; protein: 536 AA.
Xx      Xx
Xx      ADQ88400;
Xx      Xx
Xx      07-OCT-2004 (first entry)
Xx      Xx
Xx      Human wild-type tyrosine kinase protein pp60.
Xx      Ds
Xx      Cellular oncogene Src; c-Src; tyrosine kinase protein pp60; cancer;
Xx      Km      infection; inflammation; tumour; gene therapy; human.
Xx      Xx
Xx      Homo sapiens.
Xx      Os
Xx      Xx
Xx      US6764833-B1.
Xx      Pn
Xx      20-JUL-2004.
Xx      Pd
Xx      24-NOV-1999; 99US-00444711.
Xx      Pf
Xx      24-NOV-1999; 99US-00444711.
Xx      Pr
Xx      (UYSF-) UNIV SOUTH FLORIDA.
Xx      Pa
Xx      Yeastman TJ, Irby RB;
Xx      Pi
Xx      WPI; 2004-532511/51.
Xx      Dr      N-PSDB; ADQ88399.
Xx      Xx
Xx      New isolated c-Src tyrosine kinase polynucleotide, useful for treating
Xx      Pt      diseases associated or caused by mutant Src, cancer, or for preventing
Xx      Pt      infection, inflammation, or tumor formation.
Xx      Xx
Xx      Disclosure; SEQ ID NO 2; 29pp; English.
Xx      Xx
Xx      The invention relates to novel mutant cellular oncogene Src (c-Src) which
Xx      Cc      codes for mutant tyrosine kinase protein pp60. c-Src sequences are useful
Xx      Cc      for treating diseases which are associated or caused by mutant Src. They
```

CC are useful for treating cancer, to delay or prevent infection,
CC inflammation or tumour formation. The invention is also useful in gene
CC therapy. The present sequence is human wild-type tyrosine kinase protein
CC pp60.
XX

Sequence 536 AA;

Query Match 100.0%; Score 2834; DB 8; Length 536;
Best Local Similarity 100.0%; Pred. No. 1e-242;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSNKSXPXKASQRRSLLEPAENVHAGGAGFPAASQTPSKPASADGHRGSAAPAPAAE 60
DB 1 MGSNKSXPXKASQRRSLLEPAENVHAGGAGFPAASQTPSKPASADGHRGSAAPAPAAE 60
QY 61 PKLFGGNSSDVTSFORAGPLAGVTTFPALVDYBSRTETDLSFKKGERLQIVNNTGCD 120
DB 61 PKLFGGNSSDVTSFORAGPLAGVTTFPALVDYBSRTETDLSFKKGERLQIVNNTGCD 120
QY 121 WMLAHSLSGTQTYIPSNVYAPSDSIQAEEMVFGKTRRSERLLNAENPRGTFVRES 180
DB 121 WMLAHSLSGTQTYIPSNVYAPSDSIQAEEMVFGKTRRSERLLNAENPRGTFVRES 180
QY 181 ETTKGAIVCLSVSPFDNAKGLNVGHYKIRKLDSCGFYITTSRTQFNSLQOLVAAYYSKADGL 240
DB 181 ETTKGAIVCLSVSPFDNAKGLNVGHYKIRKLDSCGFYITTSRTQFNSLQOLVAAYYSKADGL 240
QY 241 CHRLLTVCPSPKQOTGLADAMEIPRESLRLEVKLGCGCFGEVMGTMGTTTVAIKTL 300
DB 241 CHRLLTVCPSPKQOTGLADAMEIPRESLRLEVKLGCGCFGEVMGTMGTTTVAIKTL 300
QY 301 KPGTMSPEAFLOEAQVMKLRHEKLVQLVAVVSEEPYIYITEVMSKSLDLFLKGETGKY 360
DB 301 KPGTMSPEAFLOEAQVMKLRHEKLVQLVAVVSEEPYIYITEVMSKSLDLFLKGETGKY 360
QY 361 LRLPOLVDMAAQIASGMAYVERMYVHRDLRAANIIVGENLVCKVADFGIARLIEDNEYT 420
DB 361 LRLPOLVDMAAQIASGMAYVERMYVHRDLRAANIIVGENLVCKVADFGIARLIEDNEYT 420
QY 421 ARGAKEPFIKMTAPEALYGRFTIKSDVMSFGILLTELTKGRVPYPGMNRREVLDOVER 480
DB 421 ARGAKEPFIKMTAPEALYGRFTIKSDVMSFGILLTELTKGRVPYPGMNRREVLDOVER 480
QY 481 GYMPCEPPECBSLHLMCCMKRKEPERPTFEYLOAFLEDYFTSTEPQYQPGENTL 536
DB 481 GYMPCEPPECBSLHLMCCMKRKEPERPTFEYLOAFLEDYFTSTEPQYQPGENTL 536

RESULT 8
ADQ97772
ID ADQ97772 standard; protein; 536 AA.

AC ADQ97772;

DT 07-OCT-2004 (first entry)

DE Human cancer associated sequence HPI0-043, SEQ ID 749.

KW Cytostatic; Gene Therapy; cancer; leukemia; lymphoma; Human.

OS Homo sapiens.

PN MO2004060304-A2.

PD 22-JUL-2004.

PF 22-DEC-2003; 2003MO-US041389.

PR 27-DEC-2002; 2002US-00330773.

PA (SAGR-) SAGRES DISCOVERY INC.

XX Moritz DW, Malandro MS; PI

XX WPI; 2004-543761/52.

PT New isolated cancer associated nucleic acids comprising at least 10
PT contiguous nucleotides, useful for diagnosing, preventing and/or treating
PT cancers such as leukemia and lymphoma.

PS Claim 1; SEQ ID NO 749; 199pp; English.

CC The present invention relates to cancer associated sequences (ADQ97025-
CC ADQ98004). The sequences are useful for the diagnosis, prevention and/or
CC treatment of cancer, such as leukemia and lymphoma. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 536 AA;

Query Match 100.0%; Score 2834; DB 8; Length 536;
Best Local Similarity 100.0%; Pred. No. 1e-242;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSNKSXPXKASQRRSLLEPAENVHAGGAGFPAASQTPSKPASADGHRGSAAPAPAAE 60
DB 1 MGSNKSXPXKASQRRSLLEPAENVHAGGAGFPAASQTPSKPASADGHRGSAAPAPAAE 60
QY 61 PKLFGGNSSDVTSFORAGPLAGVTTFPALVDYBSRTETDLSFKKGERLQIVNNTGCD 120
DB 61 PKLFGGNSSDVTSFORAGPLAGVTTFPALVDYBSRTETDLSFKKGERLQIVNNTGCD 120
QY 121 WMLAHSLSGTQTYIPSNVYAPSDSIQAEEMVFGKTRRSERLLNAENPRGTFVRES 180
DB 121 WMLAHSLSGTQTYIPSNVYAPSDSIQAEEMVFGKTRRSERLLNAENPRGTFVRES 180
QY 181 ETTKGAIVCLSVSPFDNAKGLNVGHYKIRKLDSCGFYITTSRTQFNSLQOLVAAYYSKADGL 240
DB 181 ETTKGAIVCLSVSPFDNAKGLNVGHYKIRKLDSCGFYITTSRTQFNSLQOLVAAYYSKADGL 240
QY 241 CHRLLTVCPSPKQOTGLADAMEIPRESLRLEVKLGCGCFGEVMGTMGTTTVAIKTL 300
DB 241 CHRLLTVCPSPKQOTGLADAMEIPRESLRLEVKLGCGCFGEVMGTMGTTTVAIKTL 300
QY 301 KPGTMSPEAFLOEAQVMKLRHEKLVQLVAVVSEEPYIYITEVMSKSLDLFLKGETGKY 360
DB 301 KPGTMSPEAFLOEAQVMKLRHEKLVQLVAVVSEEPYIYITEVMSKSLDLFLKGETGKY 360
QY 361 LRLPOLVDMAAQIASGMAYVERMYVHRDLRAANIIVGENLVCKVADFGIARLIEDNEYT 420
DB 361 LRLPOLVDMAAQIASGMAYVERMYVHRDLRAANIIVGENLVCKVADFGIARLIEDNEYT 420
QY 421 ARGAKEPFIKMTAPEALYGRFTIKSDVMSFGILLTELTKGRVPYPGMNRREVLDOVER 480
DB 421 ARGAKEPFIKMTAPEALYGRFTIKSDVMSFGILLTELTKGRVPYPGMNRREVLDOVER 480
QY 481 GYMPCEPPECBSLHLMCCMKRKEPERPTFEYLOAFLEDYFTSTEPQYQPGENTL 536
DB 481 GYMPCEPPECBSLHLMCCMKRKEPERPTFEYLOAFLEDYFTSTEPQYQPGENTL 536

RESULT 9
ADU04517
ID ADU04517 standard; peptide; 536 AA.

AC ADU04517;

DT 13-JAN-2005 (first entry)

DE Protein tyrosine kinase Src.

KW Protein tyrosine kinase; Src; proto-oncogene; phosphorylation;

KM protein structure; enzyme; EC_2.7.1.112.

XX Unidentified.

XX Key Location/Qualifiers
 FH Modified-site 216 /note= "Tyr phosphorylation site"
 FT Modified-site 419 /note= "Tyr phosphorylation site"
 FT Modified-site 530 /note= "Tyr phosphorylation site"
 FT Modified-site /note= "Tyr phosphorylation site"
 XX
 PN WO2004092703-A2.
 XX
 PD 28-OCT-2004.
 XX
 PF 09-APR-2004; 2004WO-US010834.
 XX
 PR 11-APR-2003; 2003US-0462083P.
 PR 11-APR-2003; 2003US-0462472P.
 PR 25-JUL-2003; 2003US-0490057P.
 PR 08-MAR-2004; 2004US-0551311P.
 PR 19-MAR-2004; 2004US-0554701P.
 PR 08-APR-2004; 2004US-00821231.
 XX
 PA (PURD) PURDUE RES FOUND.
 XX
 PI Zhang D, Amotz B, Xie Y, Davison VJ, Mrozek M, Ortiz C;
 XX WPI; 2004-784629/77.
 XX
 DR
 XX
 PT Obtaining structural characteristic information for separation and
 PT detection of e.g. proteins comprises irradiating a region formed by
 PT evaporating specimen-containing solvent in a droplet on planar solvo-
 PT phobic sample support.
 XX
 PS Example C; Page 25; 91pp; English.
 XX
 CC The present sequence is that of proto-oncogene protein tyrosine kinase
 CC Src (p60-src, c-src). The invention relates to the combined use of solid
 CC substrates, micro-deposition techniques, spectral imaging methods, and
 CC data processing to facilitate the concentration and separate detection of
 CC biological molecules including proteins, peptides, polysaccharides,
 CC glycans and nucleosides, in a liquid mixture, using spectral analysis
 CC such as normal Raman spectroscopy, infrared spectroscopy and matrix-
 CC assisted laser desorption/ionisation (MALDI) time-of-flight mass
 CC spectrometry. The methods were demonstrated in examples from the
 CC invention using peptide fragments of Src. These demonstrated the high
 CC level of analyte discrimination that can be achieved and that the method
 CC can be used to detect and quantify Tyr phosphorylation in tryptic digests
 CC of physiologically important proteins.
 CC
 XX Sequence 536 AA;
 SQ
 Query Match 100.0%; Score 2834; DB 8; Length 536;
 Best Local Similarity 100.0%; Pred. No. 1e-242;
 Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGSNKSXPDKASQRRSLRPAENVHAGGAFPAASQTPSPKASADGHRGSAAPAPAAE 60
 DB 1 MGSNKSXPDKASQRRSLRPAENVHAGGAFPAASQTPSPKASADGHRGSAAPAPAAE 60
 QY 61 PKLFGGNSSDTYTSPORAGPIAGGVTTFFVALYVBERSTEDLSFKKGERLQIVNNTBGD 120
 DB 61 PKLFGGNSSDTYTSPORAGPIAGGVTTFFVALYVBERSTEDLSFKKGERLQIVNNTBGD 120
 QY 61 PKLFGGNSSDTYTSPORAGPIAGGVTTFFVALYVBERSTEDLSFKKGERLQIVNNTBGD 120
 DB 61 PKLFGGNSSDTYTSPORAGPIAGGVTTFFVALYVBERSTEDLSFKKGERLQIVNNTBGD 120
 QY 121 WMLAHSISTGOTGYTIPSNYVAPSDSIQAEEMYPFKITRRESEKLLILNAENRGTFLVRES 180
 DB 121 WMLAHSISTGOTGYTIPSNYVAPSDSIQAEEMYPFKITRRESEKLLILNAENRGTFLVRES 180
 QY 121 WMLAHSISTGOTGYTIPSNYVAPSDSIQAEEMYPFKITRRESEKLLILNAENRGTFLVRES 180
 DB 121 WMLAHSISTGOTGYTIPSNYVAPSDSIQAEEMYPFKITRRESEKLLILNAENRGTFLVRES 180
 QY 181 ETTKGAYCLSVSDPDNAGKLVNKHVKIRKLDSSGGFYITSTRTOFNSLOQLVAVYKADGL 240
 DB 181 ETTKGAYCLSVSDPDNAGKLVNKHVKIRKLDSSGGFYITSTRTOFNSLOQLVAVYKADGL 240
 QY 241 CHRLTTCPTSPKPTQGLADAWMEIPRESLRLFEVKGCGCPGEVWGMGTNCTEVAIKTL 300
 DB 241 CHRLTTCPTSPKPTQGLADAWMEIPRESLRLFEVKGCGCPGEVWGMGTNCTEVAIKTL 300

DB 241 CHRLTTCPTSPKPTQGLADAWMEIPRESLRLFEVKGCGCPGEVWGMGTNCTEVAIKTL 300
 QY 301 KPGTMSPEAFLOEQVWKKLRHEKLVOLXAVSEEPYIYEWMSKSLDPLGEGCKY 360
 DB 301 KPGTMSPEAFLOEQVWKKLRHEKLVOLXAVSEEPYIYEWMSKSLDPLGEGCKY 360
 QY 361 LRLPOLVMAAQIASGNAVYERMYVHRDLRAANILVGENLVCKVADGLARLIEDNEYT 420
 DB 361 LRLPOLVMAAQIASGNAVYERMYVHRDLRAANILVGENLVCKVADGLARLIEDNEYT 420
 QY 421 ARQAKFPIKWTAPBAALYGRFTIKSDVWSPGILLTELTGKRVYPGMVNRVLDQYER 480
 DB 421 ARQAKFPIKWTAPBAALYGRFTIKSDVWSPGILLTELTGKRVYPGMVNRVLDQYER 480
 QY 481 GYRMPCEPCEPESLHDMCCMRKEPERPFEYLQAFLEBYFTSTEPQYQNGENTL 536
 DB 481 GYRMPCEPCEPESLHDMCCMRKEPERPFEYLQAFLEBYFTSTEPQYQNGENTL 536
 RESULT 10
 ADY84076
 ID ADY84076 standard; protein; 536 AA.
 XX
 AC ADY84076;
 XX
 DT 02-JUN-2005 (first entry)
 XX
 DE Human Src protein isoform 2 SEQ ID NO:2.
 XX
 KW pharmaceutical; Alzheimer's disease; neuroprotective; nootropic;
 KW Src tyrosine kinase.
 XX
 OS Homo sapiens.
 XX
 PN EPI413887-A1.
 XX
 PD 28-APR-2004.
 XX
 PR 22-OCT-2002; 2002EP-00292608.
 PR 22-OCT-2002; 2002EP-00292608.
 XX
 PA (AVENTIS PHARMA SA.
 XX
 PI Mercken L, Zambirano N, Russo T;
 XX WPI; 2004-332834/31.
 DR
 XX
 PT Identifying therapeutic compound for treating Alzheimer's disease,
 PT involves providing Src protein and determining inhibitory effect of
 PT compound on Src activity.
 XX
 PS Claim 4; SEQ ID NO 2; 45pp; English.
 XX
 CC The invention relates to a novel method for identifying (M1) a
 CC therapeutic compound for the treatment of Alzheimer's disease, involving
 CC providing a Src protein and determining the inhibitory effect of a
 CC compound on the Src activity. The method optionally involves providing a
 CC sequence which regulates Src expression and determining if a compound
 CC inhibits the expression of Src protein. A compound of the invention has
 CC neuroprotective and nootropic activity. The compound identified by the
 CC method of the invention is useful for preparing a pharmaceutical for
 CC treating Alzheimer's disease. The present sequence represents isoform 2
 CC of human Src protein.
 XX
 SQ Sequence 536 AA;
 Query Match 100.0%; Score 2834; DB 8; Length 536;
 Best Local Similarity 100.0%; Pred. No. 1e-242;
 Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGSNKSXPDKASQRRSLRPAENVHAGGAFPAASQTPSPKASADGHRGSAAPAPAAE 60
 DB 1 MGSNKSXPDKASQRRSLRPAENVHAGGAFPAASQTPSPKASADGHRGSAAPAPAAE 60

Db 1 MGSNKGKPDASQRRRSLEPAENVHAGGAFPASQTPSKPASADGHRGSAFAFAAAE 60
QY PKLFGFNSSDVTTSQORAGPLAGGVTTFVALDYESRTTDLSPFKGGERLQIVNTEGD 120
Db 61 PKLFGFNSSDVTTSQORAGPLAGGVTTFVALDYESRTTDLSPFKGGERLQIVNTEGD 120
QY 121 WMLAHSLSGTQGYIFSNVYVAPSDSIQAEEMWFGKTRRESERLLINAEPRGTFIVRES 180
Db 121 WMLAHSLSGTQGYIFSNVYVAPSDSIQAEEMWFGKTRRESERLLINAEPRGTFIVRES 180
QY 181 ETTKGAICYLSVSPFDNAKGLNVGHYKIRKLDGSGFYITSRTOFNSIQOLVAVYSKADGL 240
Db 181 ETTKGAICYLSVSPFDNAKGLNVGHYKIRKLDGSGFYITSRTOFNSIQOLVAVYSKADGL 240
QY 241 CHRLLTVCTPSKQOTGLAKDAWEIPRESLRLEVKLGQCFCGEVWNGTNGTTRVAIKTL 300
Db 241 CHRLLTVCTPSKQOTGLAKDAWEIPRESLRLEVKLGQCFCGEVWNGTNGTTRVAIKTL 300
QY 301 KPGTMSPEAFLOAQYMKLRHEKLVOLVAVSEBPIYITVEYMSKSLDPLKGETGKY 360
Db 301 KPGTMSPEAFLOAQYMKLRHEKLVOLVAVSEBPIYITVEYMSKSLDPLKGETGKY 360
QY 361 LRLPOLVDMAAQJASGMAYVERMNYVHRDLRAANILVGENLVCKVADFGIARLIEDNEYT 420
Db 361 LRLPOLVDMAAQJASGMAYVERMNYVHRDLRAANILVGENLVCKVADFGIARLIEDNEYT 420
QY 421 AROGAKFPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVPYPGMVRREVLDOVER 480
Db 421 AROGAKFPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVPYPGMVRREVLDOVER 480
QY 481 GYRMPCPPECPSLHLMQCCKRKEPERPTFEYLOAFLEDYFTSTBPQYQGENL 536
Db 481 GYRMPCPPECPSLHLMQCCKRKEPERPTFEYLOAFLEDYFTSTBPQYQGENL 536

RESULT 11

ADV94834
ID ADV94834 standard; protein; 536 AA.

XX ADV94834;

XX 10-MAR-2005 (first entry)

XX Human wild type c-Src protein.

XX cytostatic; gene therapy; mutagenesis; tumor; sarcoma; neuroblastoma;
KM breast carcinoma; c-Src; tyrosine kinase inhibitor; enzyme.

XX Homo sapiens.

XX US2004261142-A1.

XX 23-DEC-2004.

XX 09-JUL-2004; 2004US-00887588.

XX 24-NOV-1999; 99US-00444711.

XX (YEAT/) YEATMAN T J.

XX (IRBY/) IRBY R B.

XX Yeatman TJ, Irby RB;

XX MPI; 2005-038810/04.

XX N-PSDB; ADV94833.

XX New truncated c-Src polypeptide, useful for treating and/or preventing
PT clinical conditions associated with or caused by Src mutation, e.g.
PT tumors.

XX Disclosure; SEQ ID NO 2; 28pp; English.

XX The invention relates to a truncated c-Src polypeptide comprising a

CC sequence of 530 amino acids given in the specification. The polypeptide,
CC composition and method are useful for treating and/or preventing clinical
CC conditions associated with or caused by Src mutation e.g. tumors
CC (sarcoma, neuroblastoma, breast carcinoma). This sequence corresponds to
CC the wild type c-Src protein.

XX SQ Sequence 536 AA;

Query Match 100.0%; Score 2834; DB 9; Length 536;
Best Local Similarity 100.0%; Pred.No.1e-242;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSNKGKPDASQRRRSLEPAENVHAGGAFPASQTPSKPASADGHRGSAFAFAAAE 60
Db 1 MGSNKGKPDASQRRRSLEPAENVHAGGAFPASQTPSKPASADGHRGSAFAFAAAE 60
QY 61 PKLFGFNSSDVTTSQORAGPLAGGVTTFVALDYESRTTDLSPFKGGERLQIVNTEGD 120
Db 61 PKLFGFNSSDVTTSQORAGPLAGGVTTFVALDYESRTTDLSPFKGGERLQIVNTEGD 120
QY 121 WMLAHSLSGTQGYIFSNVYVAPSDSIQAEEMWFGKTRRESERLLINAEPRGTFIVRES 180
Db 121 WMLAHSLSGTQGYIFSNVYVAPSDSIQAEEMWFGKTRRESERLLINAEPRGTFIVRES 180
QY 181 ETTKGAICYLSVSPFDNAKGLNVGHYKIRKLDGSGFYITSRTOFNSIQOLVAVYSKADGL 240
Db 181 ETTKGAICYLSVSPFDNAKGLNVGHYKIRKLDGSGFYITSRTOFNSIQOLVAVYSKADGL 240
QY 241 CHRLLTVCTPSKQOTGLAKDAWEIPRESLRLEVKLGQCFCGEVWNGTNGTTRVAIKTL 300
Db 241 CHRLLTVCTPSKQOTGLAKDAWEIPRESLRLEVKLGQCFCGEVWNGTNGTTRVAIKTL 300
QY 301 KPGTMSPEAFLOAQYMKLRHEKLVOLVAVSEBPIYITVEYMSKSLDPLKGETGKY 360
Db 301 KPGTMSPEAFLOAQYMKLRHEKLVOLVAVSEBPIYITVEYMSKSLDPLKGETGKY 360
QY 361 LRLPOLVDMAAQJASGMAYVERMNYVHRDLRAANILVGENLVCKVADFGIARLIEDNEYT 420
Db 361 LRLPOLVDMAAQJASGMAYVERMNYVHRDLRAANILVGENLVCKVADFGIARLIEDNEYT 420
QY 421 AROGAKFPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVPYPGMVRREVLDOVER 480
Db 421 AROGAKFPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVPYPGMVRREVLDOVER 480
QY 481 GYRMPCPPECPSLHLMQCCKRKEPERPTFEYLOAFLEDYFTSTBPQYQGENL 536
Db 481 GYRMPCPPECPSLHLMQCCKRKEPERPTFEYLOAFLEDYFTSTBPQYQGENL 536

RESULT 12

AEA35914
ID AEA35914 standard; protein; 536 AA.

XX AEA35914;

XX 25-AUG-2005 (first entry)

XX Human Src kinase amino acid sequence SEQ ID NO:1.

XX Src family kinase; Src kinase.

XX Homo sapiens.

XX Key Location/Qualifiers

XX FT Misc-difference 298 /note= "constant amino acid K in domain SH2"

XX FT Misc-difference 341 /note= "constant amino acid T in domain SH2"

XX FT Misc-difference 530 /note= "constant amino acid Y in domain SH1"

XX EP1541694-A1.

PD 15-JUN-2005.
 XX
 PF 12-DEC-2003; 2003EP-00028713.
 XX
 PR 12-DEC-2003; 2003EP-00028713.
 XX
 PA (SIRE-) SIRENADE PHARM AG.
 XX
 PI Obermeier A, Bieger B;
 XX WPI; 2005-428084/44.
 DR
 XX
 PT Identifying compound which modulates Src family kinase (SFK) activity, by
 PT contacting cells expressed with SFK or mutated SFK with test compound,
 PT where change in phenotype of cells indicates that test compound modulates
 PT SFK activity.
 PS
 PS Disclosure; SEQ ID NO 1; 114pp; English.

CC The invention relates to a method (M1) for identifying, selecting and/or
 CC characterizing a compound which modulates Src family kinase (SFK)
 CC activity, by expressing nucleic acids encoding SFK or mutated SFK in
 CC cells, contacting cells with test compound and determining whether
 CC phenotype of cells is changed as compared with phenotype of cells not
 CC expressed with above nucleic acids, where difference in phenotype
 CC indicates that test compound modulate SFK activity. Also described: (1) a
 CC compound (I) identified, selected and/or characterized by (M1); and (2) a
 CC pharmaceutical composition (PCI) containing (1), and a carrier, adjuvant
 CC or vehicle. (1) is useful as a medicament, particularly for the treatment
 CC of diseases, which are at least in part caused by a Src family kinase.
 CC (1) and PCI are useful for producing a medicament for the treatment of
 CC diseases, which are at least in part caused by a Src family kinase,
 CC particularly by a dysfunction of a Src family kinase, in particular
 CC cancer, hypercalcaemia, restenosis, osteoporosis, osteoarthritis,
 CC symptomatic treatment of bone metastasis, rheumatoid arthritis,
 CC inflammatory bowel disease, multiple sclerosis, psoriasis, lupus, graft
 CC versus host disease, T-cell mediated hypersensitivity disease,
 CC Hashimoto's thyroiditis, Guillain-Barre syndrome, chronic obstructive
 CC pulmonary disorder, contact dermatitis, Paget's disease, asthma, ischemic
 CC or reperfusion injury, allergic disease, atopic dermatitis, transplant
 CC rejection or allergic rhinitis. The present sequence represents human Src
 CC kinase, which is given in the exemplification of the present invention.

XX
 SQ Sequence 536 AA;

Query Match 100.0%; Score 2834; DB 9; Length 536;
 Best Local Similarity 100.0%; Pred. No. 1e-242;

Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSNKSFKPCASQRRSLPEAENVHAGGAFPPASQTPSKPASADGHRGSAAPAPAAE 60
 DB 1 MGSNKSFKPCASQRRSLPEAENVHAGGAFPPASQTPSKPASADGHRGSAAPAPAAE 60
 QY 61 PKLFGGNSSDTVTSPPRAGPLAGGVTTFVALVYSERTEDLSFKKGERLQIYNNTGEGD 120
 DB 61 PKLFGGNSSDTVTSPPRAGPLAGGVTTFVALVYSERTEDLSFKKGERLQIYNNTGEGD 120
 QY 121 MWLAHSLSTGQTGYIPSNVYAPSDSIQAEWYFGKTRRESERILLNANRGTFVRES 180
 DB 121 MWLAHSLSTGQTGYIPSNVYAPSDSIQAEWYFGKTRRESERILLNANRGTFVRES 180
 QY 181 ETTKGAYCLSVSDPNAKGLNVKXKIRKLDGSGFYITTSRTQFNSLQOLVAYYSKADGL 240
 DB 181 ETTKGAYCLSVSDPNAKGLNVKXKIRKLDGSGFYITTSRTQFNSLQOLVAYYSKADGL 240
 QY 241 CHRLTTCPTSKPOTQGLADKAMEIPRESILAEVYKLGCGCGEYFMGMNNTTVAIKTL 300
 DB 241 CHRLTTCPTSKPOTQGLADKAMEIPRESILAEVYKLGCGCGEYFMGMNNTTVAIKTL 300
 QY 301 KPGTMSDEAPLQEAQWKKLREKLVOLYAVSEEPYIYVTEYMSKSGSLDLFGKETGKY 360
 DB 301 KPGTMSDEAPLQEAQWKKLREKLVOLYAVSEEPYIYVTEYMSKSGSLDLFGKETGKY 360

QY 361 LRLPOLYDMAQIASGMAVYERMYVHRDLPAANILVGENLVCKVADGRLARLEEDNEYT 420
 DB 361 LRLPOLYDMAQIASGMAVYERMYVHRDLPAANILVGENLVCKVADGRLARLEEDNEYT 420
 QY 421 ARQAKFPKWTABEALVGRFTIKSDVWSPGILLTTELTTKGRVYPGMVNRREVLDQYER 480
 DB 421 ARQAKFPKWTABEALVGRFTIKSDVWSPGILLTTELTTKGRVYPGMVNRREVLDQYER 480
 QY 481 GYRMPCEPCEPSLHDMCCQWRKPEBEPFPFETLQAFLEDFYFTSTEQYQGENYL 536
 DB 481 GYRMPCEPCEPSLHDMCCQWRKPEBEPFPFETLQAFLEDFYFTSTEQYQGENYL 536

RESULT 13

ID ADY84080 standard; protein; 549 AA.

AC ADY84080;

DT 02-JUN-2005 (first entry)

DE Human Src cDNA encoded amino acid #1.

KW pharmaceutical; Alzheimer's disease; neuroprotective; nootropic;
 KW Src tyrosine kinase.

OS Homo sapiens.

PN EPI413887-A1.

PD 28-APR-2004.

PF 22-OCT-2002; 2002EP-00292608.

PR 22-OCT-2002; 2002EP-00292608.

PA (AVET) AVENTIS PHARMA SA.

PI Mercken I, Zambrano N, Russo T;

DR WPI; 2004-332834/31.

DR N-PSDB; ADY84078.

PT Identifying therapeutic compound for treating Alzheimer's disease,
 PT involves providing Src protein and determining inhibitory effect of
 PT compound on Src activity.

PS Disclosure; SEQ ID NO 4; 45pp; English.

CC The invention relates to a novel method for identifying (M1) a
 CC therapeutic compound for the treatment of Alzheimer's disease, involving
 CC providing a Src protein and determining the inhibitory effect of a
 CC compound on the Src activity. The method optionally involves providing a
 CC sequence which regulates Src expression and determining if a compound
 CC inhibits the expression of Src protein. A compound identified by the
 CC neuroprotective and nootropic activity. The compound identified by the
 CC method of the invention is useful for preparing a pharmaceutical for
 CC treating Alzheimer's disease. The present sequence is encoded by the
 CC human Src cDNA. The sequence is represented as part of SEQ ID NO:4 in the
 CC sequence listing of the specification.

XX
 SQ Sequence 549 AA;

Query Match 100.0%; Score 2834; DB 8; Length 549;
 Best Local Similarity 100.0%; Pred. No. 1e-242;

Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSNKSFKPCASQRRSLPEAENVHAGGAFPPASQTPSKPASADGHRGSAAPAPAAE 60
 DB 14 MGSNKSFKPCASQRRSLPEAENVHAGGAFPPASQTPSKPASADGHRGSAAPAPAAE 73
 QY 61 PKLFGGNSSDTVTSPPRAGPLAGGVTTFVALVYSERTEDLSFKKGERLQIYNNTGEGD 120
 DB 61 PKLFGGNSSDTVTSPPRAGPLAGGVTTFVALVYSERTEDLSFKKGERLQIYNNTGEGD 120

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Db      74 PKLFGFNSSDVTSPQAGPLAGVTTFVALYDYESRTETDLSFKKGERLQIVNNTGEGD 133
Qy      121 WMLAHSLSGTGTGYIPSNYVAPSDSIQAEEMYPGKITRRBSERLLNAENPRGTFVRES 180
Db      134 WMLAHSLSGTGTGYIPSNYVAPSDSIQAEEMYPGKITRRBSERLLNAENPRGTFVRES 193
Qy      181 ETTKGAYCLSVSPFDNAKGLNVKHYKIRKLDSSGFFYITSRTQFNSLQQLVAAYYSKHADGL 240
Db      194 ETTKGAYCLSVSPFDNAKGLNVKHYKIRKLDSSGFFYITSRTQFNSLQQLVAAYYSKHADGL 253
Qy      241 CHRLTYTCPTSKPQTQGLADAMEIPRESLRLEVKLGQGCFGSEVMGTWNGTTRVAIKTL 300
Db      254 CHRLTYTCPTSKPQTQGLADAMEIPRESLRLEVKLGQGCFGSEVMGTWNGTTRVAIKTL 313
Qy      301 KPGTMSPEAPLQEAQVWKKLRHEKLVQLYAVVSEEPYIYIVTEVMSKSLDPLKGETGKYL 360
Db      314 KPGTMSPEAPLQEAQVWKKLRHEKLVQLYAVVSEEPYIYIVTEVMSKSLDPLKGETGKYL 373
Qy      361 LRLPOLVDMAAOIASGMAVYERMYVHRDLRAANILVGENLVCKVADFGLARLIEDNEYT 420
Db      374 LRLPOLVDMAAOIASGMAVYERMYVHRDLRAANILVGENLVCKVADFGLARLIEDNEYT 433
Qy      421 AROGAKFPKWTAPBEALYGRFTIKSDVMSFGILLTELTKGRVPYPGMVRREVLDOVER 480
Db      434 AROGAKFPKWTAPBEALYGRFTIKSDVMSFGILLTELTKGRVPYPGMVRREVLDOVER 493
Qy      481 GRMPCPECPESLHDMCCMKRKEPERPTFEYLOAFLEDYFTSTEPQYQGENL 536
Db      494 GRMPCPECPESLHDMCCMKRKEPERPTFEYLOAFLEDYFTSTEPQYQGENL 549

RESULT 14
ADP45087
ID ADP45087 standard; protein; 535 AA.
AC ADP45087;
XX
XX 12-FEB-2004 (first entry)
DT
XX
XX Human kinase SRC.
DE
XX
XX Human; protein kinase; enzyme; inhibitor; SRC.
XX
XX Homo sapiens.
OS
XX
XX MO2003081210-A2.
PN
XX
XX 02-OCT-2003.
PD
XX
XX 20-MAR-2003; 2003WO-US008725.
PF
XX
XX 21-MAR-2002; 2002US-0366892P.
PR
XX
XX (SUNE-) SUNESIS PHARM INC.
PA
XX
XX Prescott JC, Braisted A;
PI
XX
XX WPI; 2003-865136/80.
DR
XX
XX Identifying ligand binding to inactive conformation of target protein
PT kinase (T) comprises contacting the conformation modified (T) which
PT contains reactive group at binding site, with ligands and detecting
PT kinase-ligand conjugate formation.
XX
XX Disclosure; SEQ ID NO 56; 260pp; English.
PS
XX
XX The present invention relates to a method for identifying a ligand (L),
CC which binds to an inactive conformation of target protein kinase (T). The
CC method involves contacting inactive conformation of (T), which contains
CC or is modified to contain a reactive group at or near a binding site of
CC interest, with one or more ligand candidates capable of covalently
CC bonding to the reactive group thus forming a kinase-(L) conjugate (C).
CC The method is useful for identifying protein kinase inhibitors that

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CC preferentially bind to inactive conformation of a target protein kinase.
CC The present sequence is a protein kinase which may be modified via an
CC amino acid substitution, for use in the method of the invention.
XX
XX Sequence 535 AA;
SQ
Query Match          99.8%; Score 2829; DB 7; Length 535;
Best Local Similarity 100.0%; Pred. No. 2, 8e-242;
Matches 535; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 GSNKSPKQASQRRRSLEPENVHAGGAPASQTPSKPASADGHRGSAAPAPAAAP 61
Db      1 GSNKSPKQASQRRRSLEPENVHAGGAPASQTPSKPASADGHRGSAAPAPAAAP 60
Qy      62 KLGGFPPSSDVTYSPQAGPLAGVTTFVALYYESRTETDLSFKKGERLQIVNNTGEGD 121
Db      61 KLGGFPPSSDVTYSPQAGPLAGVTTFVALYYESRTETDLSFKKGERLQIVNNTGEGD 120
Qy      122 WMLAHSLSGTGTGYIPSNYVAPSDSIQAEEMYPGKITRRBSERLLNAENPRGTFVRES 181
Db      121 WMLAHSLSGTGTGYIPSNYVAPSDSIQAEEMYPGKITRRBSERLLNAENPRGTFVRES 180
Qy      182 ETTKGAYCLSVSPFDNAKGLNVKHYKIRKLDSSGFFYITSRTQFNSLQQLVAAYYSKHADGL 241
Db      181 ETTKGAYCLSVSPFDNAKGLNVKHYKIRKLDSSGFFYITSRTQFNSLQQLVAAYYSKHADGL 240
Qy      242 HRITTYCPTSKPQTQGLADAMEIPRESLRLEVKLGQGCFGSEVMGTWNGTTRVAIKTL 301
Db      241 HRITTYCPTSKPQTQGLADAMEIPRESLRLEVKLGQGCFGSEVMGTWNGTTRVAIKTL 300
Qy      302 PGTMSPEAPLQEAQVWKKLRHEKLVQLYAVVSEEPYIYIVTEVMSKSLDPLKGETGKYL 361
Db      301 PGTMSPEAPLQEAQVWKKLRHEKLVQLYAVVSEEPYIYIVTEVMSKSLDPLKGETGKYL 360
Qy      362 RLPOLVDMAAOIASGMAVYERMYVHRDLRAANILVGENLVCKVADFGLARLIEDNEYT 421
Db      361 RLPOLVDMAAOIASGMAVYERMYVHRDLRAANILVGENLVCKVADFGLARLIEDNEYT 420
Qy      422 AROGAKFPKWTAPBEALYGRFTIKSDVMSFGILLTELTKGRVPYPGMVRREVLDOVER 481
Db      421 AROGAKFPKWTAPBEALYGRFTIKSDVMSFGILLTELTKGRVPYPGMVRREVLDOVER 480
Qy      482 YRMPCPECPESLHDMCCMKRKEPERPTFEYLOAFLEDYFTSTEPQYQGENL 536
Db      481 YRMPCPECPESLHDMCCMKRKEPERPTFEYLOAFLEDYFTSTEPQYQGENL 535

RESULT 15
AED21154
ID AED21154 standard; protein; 535 AA.
AC AED21154;
XX
XX 01-DEC-2005 (first entry)
DT
XX
XX Human non-receptor protein tyrosine kinase Src protein SEQ ID NO: 4.
DE
XX
XX Protein interaction; therapeutic; cerebrovascular ischemia;
XX cerebroprotective; vasotropic; hypoxia; ischemia; multiple sclerosis;
XX neuroprotective; Huntington's chorea; anticonvulsant; nootropic;
XX parkinson's disease; antiparkinsonian; Alzheimer's disease; hyperglycemia;
XX antidiabetic; diabetes; trauma; tranquilizer; vulnerability; epilepsy;
XX grand mal seizure; muscle hypertonia; muscle relaxant; paralytic;
XX muscular-gen.; asthma; antiasthmatic; cardiac arrest; cardiant;
XX macular degeneration; ophthalmological; psychiatric disorder;
XX neuroleptic; schizophrenia; AIDS dementia complex; dementia;
XX inflammation; antiinflammatory; pain; analgesic; opiate dependence;
XX antidiabetic; cocaine addiction; alcoholism; anticholinic;
XX anorexia nervosa; anabolic; eating-disorders-gen.; enzyme;
XX Src tyrosine kinase.
XX
XX Homo sapiens.
XX

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 5, 2006, 17:08:03 ; Search time 21.5195 Seconds

(without alignments)
2396.538 Million cell updates/sec

Title: US-10-691-079-2

Perfect score: 2834
Sequence: 1 MGSNKSXPXASQRRSLRP.....AFLEDYFTSTPEYQPGENL 536Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR 80:*

1: PIR1:.*
2: PIR2:.*
3: PIR3:.*
4: PIR4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the change being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2821	99.5	542	1	TVHUSC protein-tyrosine k
2	2778.5	98.0	541	1	AA3610 protein-tyrosine k
3	2661.5	93.9	533	1	TVCHS protein-tyrosine k
4	2621.5	92.5	587	1	TVFVPR protein-tyrosine k
5	2614.5	92.3	568	1	TVFVSL protein-tyrosine k
6	2599.5	91.7	557	1	TVFVSL protein-tyrosine k
7	2516.5	88.8	526	1	TVFV60 protein-tyrosine k
8	2497.5	88.1	526	2	S20808 protein-tyrosine k
9	2491.5	87.9	526	1	OKFVVR protein-tyrosine k
10	2484.5	87.7	526	2	S15562 protein-tyrosine k
11	2481.5	87.6	526	1	TVFVPR protein-tyrosine k
12	2466.5	87.0	526	2	S6420 protein-tyrosine k
13	2463	86.9	532	1	B34104 protein-tyrosine k
14	2462	86.9	532	1	AA34104 protein-tyrosine k
15	2453.5	86.6	545	2	S52313 protein-tyrosine k
16	2446.5	86.3	546	2	S52314 protein-tyrosine k
17	2418	85.3	523	1	TVFVMT protein-tyrosine k
18	2134.5	75.3	537	1	AA5501 protein-tyrosine k
19	2123.5	74.9	543	1	TVHUS protein-tyrosine k
20	2121.5	74.9	541	1	TVCHYS protein-tyrosine k
21	2118.5	74.8	541	2	S31645 protein-tyrosine k
22	2065.5	72.9	544	2	S15193 protein-tyrosine k
23	2052.5	72.4	528	1	TVFVGR protein-tyrosine k
24	1978	69.8	534	1	AA4991 protein-tyrosine k
25	1960.5	69.2	537	2	I51592 protein-tyrosine k
26	1956	69.0	534	1	S33568 protein-tyrosine k
27	1949	68.8	536	2	S33569 protein-tyrosine k
28	1932.5	68.2	537	1	TVHUSY protein-tyrosine k
29	1929.5	68.1	542	2	AA9114 protein-tyrosine k

30	1923	67.9	539	2	B49114 protein-tyrosine k
31	1921.5	67.8	537	1	A43806 protein-tyrosine k
32	1856	65.5	529	1	TVHUPR protein-tyrosine k
33	1845	65.1	517	2	A43807 protein-tyrosine k
34	1813	64.0	517	2	S24547 protein-tyrosine k
35	1600.5	56.5	509	1	TVHAST protein-tyrosine k
36	1594	56.2	663	1	TVHVR protein-tyrosine k
37	1573	55.5	392	2	S04205 protein-tyrosine k
38	1525.5	53.8	505	1	TVHUSC protein-tyrosine k
39	1520.5	53.7	503	1	QJ1321 protein-tyrosine k
40	1515.5	53.5	503	1	TVMSHC protein-tyrosine k
41	1494	52.7	507	1	A39939 protein-tyrosine k
42	1464	51.7	509	1	OKHULK protein-tyrosine k
43	1464	51.7	512	1	TVHULY protein-tyrosine k
44	1456	51.4	512	1	I56160 protein-tyrosine k
45	1455	51.3	509	1	I48845 protein-tyrosine k

ALIGNMENTS

RESULT 1

TVHUSC protein-tyrosine kinase (EC 2.7.1.112) src, neuronal - human

C:Species: Homo sapiens (man)

C>Date: 30-Jun-1989 #sequence_revision 07-Oct-1994 #text_change 05-Oct-2004

C/Accession: A26891; A61083; A23287; A28832; B34704

R/Tanaka, A.; Gibbs, C.P.; Arthur, R.R.; Anderson, S.K.; Kung, H.J.; Fujita, D.J.

Mol. Cell. Biol. 7, 1978-1983, 1987

A>Title: DNA sequence encoding the amino-terminal region of the human c-src protein: imp

A/Reference number: A26891; MUID:87257903; PMID:3299057

A/Accession: A26891

A/Molecule type: mRNA

A/Residues: 1-117;124-191 <TAN>

A/Cross-references: UNIPROT:P12931; UNIPARC:UPI0000172578; UNIPARC:UPI0000172579; GB:M16

J:Pyper, J.M.; Bolen, J.B.

J:Neurosci. Res. 24, 89-96, 1989

A>Title: Neuron-specific splicing of C-SRC RNA in human brain.

A/Reference number: A61083

A/Accession: A61083

A/Molecule type: mRNA

A/Residues: 98-145 <PYP>

A/Cross-references: UNIPARC:UPI0000172574

A/Molecule type: mRNA

A/Residues: 98-117;124-145 <PY2>

A/Cross-references: UNIPARC:UPI0000172574

R:Anderson, S.K.; Gibbs, C.P.; Tanaka, A.; Kung, H.J.; Fujita, D.J.

Mol. Cell. Biol. 5, 1122-1129, 1985

A>Title: Human cellular src gene: Nucleotide sequence and derived amino acid sequence of

A/Reference number: A23287; MUID:85213483; PMID:2582238

A/Accession: A23287

A/Molecule type: mRNA

A/Residues: 197-542 <AND>

A/Cross-references: UNIPARC:UPI000016H06; GB:X02647; NID:G36588; PIDN:CAA26485.1; PID:G

R:Parke, R.C.; Mardon, G.; Lebo, R.V.; Varnus, H.B.; Bishop, J.M.

Mol. Cell. Biol. 5, 831-838, 1985

A>Title: Isolation of duplicated human C-src genes located on chromosomes 1 and 20.

A/Reference number: A28832; MUID:85187981; PMID:2581127

A/Accession: A28832

A/Molecule type: mRNA

A/Residues: 382-542 <PAR>

A/Cross-references: UNIPARC:UPI000017257D

R:Pyper, J.M.; Bolen, J.B.

Mol. Cell. Biol. 10, 2035-2040, 1990

A>Title: Identification of a novel neuronal C-SRC exon expressed in human brain.

A/Reference number: A34704; MUID:90220588; PMID:1651439

A/Accession: B34704

A/Molecule type: mRNA

A/Residues: 118-123 <PY3>

A/Cross-references: UNIPARC:UPI000017257E

C/Genetics:

A/Gene: GDB:SRC

A:Cross-references: GDB:120750; OMIM:190090
A:Map position: 20q11.2-20q11.2
A:Introns: 84/1; 117/2; 123/2; 156/2; 191/1; 241/1; 293/1; 353/1; 378/3; 430/1; 474/1
C:Function:
A:Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
C/Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C/Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pld
F:1-542/Product: protein-tyrosine kinase src, neuronal #status predicted <Mat>
F:1-117,124-542/Product: protein-tyrosine kinase src, short form #status predicted <Mat>
F:91-146/Domain: SH3 homology <SH3>
F:157-254/Domain: SH2 homology <SH2>
F:774-532/Domain: protein kinase homology <KIN>
F:282-290/Region: protein kinase ATP-binding motif
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:104/Active site: Lys #status predicted
F:425,536/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 99.5%; Score 2821; DB 1; Length 542;
Best Local Similarity 98.9%; Pred. No. 7,1e-132;
Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

QY 1 MGSNKSXPDKASQRRSLPEAENVHAGGAFPASQTPSKPASADGHRGSAAFAPAAAE 60
DB 1 MGSNKSXPDKASQRRSLPEAENVHAGGAFPASQTPSKPASADGHRGSAAFAPAAAE 60
QY 61 PKLFGFNSSDVTSPOBAPLAGVTTFVALYDYSRRTDLSFKKGERLQIVNNT--- 117
DB 61 PKLFGFNSSDVTSPOBAPLAGVTTFVALYDYSRRTDLSFKKGERLQIVNNTKRV 120
QY 118 ---EGDWMHLAHSLSGTQGYIPSNVYAPSDSIQAEWYFGKITRRESEBLLLAENPRGT 174
DB 121 DVREGDWMHLAHSLSGTQGYIPSNVYAPSDSIQAEWYFGKITRRESEBLLLAENPRGT 180
QY 175 FLVRESEBTTKGAYCLSVSDPDNAKGLNVKHYKIRKLDGSGFYITTSRQFNSLQQLVAYYS 234
DB 181 FLVRESEBTTKGAYCLSVSDPDNAKGLNVKHYKIRKLDGSGFYITTSRQFNSLQQLVAYYS 240
QY 235 KHAADGICHLRTTYCPTSPKQTOGLADDAWEIPRESRLRLEVKLGQCGFGEVWMTNGTTR 294
DB 241 KHAADGICHLRTTYCPTSPKQTOGLADDAWEIPRESRLRLEVKLGQCGFGEVWMTNGTTR 300
QY 295 VALKTLKPGTMSPEALQEAQVWKKLRHEKLVQLYAVSEBPIYITEVWKSGLDPLK 354
DB 301 VALKTLKPGTMSPEALQEAQVWKKLRHEKLVQLYAVSEBPIYITEVWKSGLDPLK 360
QY 355 GETGKTLRLPOLVDMAAQIASGMAVYERVMYVHRDLRAANILVGENLVCKVADFGIARLI 414
DB 361 GETGKTLRLPOLVDMAAQIASGMAVYERVMYVHRDLRAANILVGENLVCKVADFGIARLI 420
QY 415 EDNEYTARQAGAPFIMTAPBALYGRFTIKSDVMSFGILLTELTTKGRVPYGMVNRREV 474
DB 421 EDNEYTARQAGAPFIMTAPBALYGRFTIKSDVMSFGILLTELTTKGRVPYGMVNRREV 480
QY 475 LDQVERGYMPCPECPESLHDLCCMKRKEBERPTFEYLQAFLEDYFTSTEPQYOPGE 534
DB 481 LDQVERGYMPCPECPESLHDLCCMKRKEBERPTFEYLQAFLEDYFTSTEPQYOPGE 540
QY 535 NL 536
DB 541 NL 542

RESULT 2
A43610
protein-tyrosine kinase (BC 2.7.1.112) src, neuronal [similarity] - mouse
N/Alternate names: Rouse sarcoma oncogene
C/Species: Mus musculus (house mouse)
C/Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 05-Oct-2004
C/Accession: A43610
R/Martinez, R.; Mathey-Prevot, B.; Bernard, A.; Baltimore, D.
Science 237, 411-415, 1987
A:Title: Neuronal pp60(c-src) contains a six-amino acid insertion relative to its non-mg
A:Reference number: A43610; MUID:87263406; PMID:2440106

A:Accession: A43610
A:Molecule type: mRNA
A:Residue: 1-541 <Mat>
A:Cross-references: UNIPROT:P05480; UNIPARC:UPI0000161D19; GB:M17011; NID:g201056; PIDN:
C/Comment: The neuronal c-src has an 6 residue insertion of RLVAVR within the amino-termi
C/Genetics:
A:Gene: Src
A:Cross-references: MGI:98397
A:Map position: 2:91.0
C/Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C/Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pld
F:156-253/Domain: SH3 homology <SH3>
F:156-253/Domain: SH2 homology <SH2>
F:273-531/Domain: protein kinase homology <KIN>
F:281-289/Region: protein kinase ATP-binding motif
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:103/Active site: Lys #status predicted
F:424,535/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 98.0%; Score 2778.5; DB 1; Length 541;
Best Local Similarity 97.6%; Pred. No. 8,7e-130;
Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;

QY 1 MGSNKSXPDKASQRRSLPEAENVHAGGAFPASQTPSKPASADGHRGSAAFAPAAAE 60
DB 1 MGSNKSXPDKASQRRSLPEAENVHAGGAFPASQTPSKPASADGHRGSAAFAPAAAE 59
QY 61 PKLFGFNSSDVTSPOBAPLAGVTTFVALYDYSRRTDLSFKKGERLQIVNNT--- 117
DB 61 PKLFGFNSSDVTSPOBAPLAGVTTFVALYDYSRRTDLSFKKGERLQIVNNTKRV 119
QY 118 ---EGDWMHLAHSLSGTQGYIPSNVYAPSDSIQAEWYFGKITRRESEBLLLAENPRGT 174
DB 120 DVREGDWMHLAHSLSGTQGYIPSNVYAPSDSIQAEWYFGKITRRESEBLLLAENPRGT 179
QY 175 FLVRESEBTTKGAYCLSVSDPDNAKGLNVKHYKIRKLDGSGFYITTSRQFNSLQQLVAYYS 234
DB 180 FLVRESEBTTKGAYCLSVSDPDNAKGLNVKHYKIRKLDGSGFYITTSRQFNSLQQLVAYYS 239
QY 235 KHAADGICHLRTTYCPTSPKQTOGLADDAWEIPRESRLRLEVKLGQCGFGEVWMTNGTTR 294
DB 240 KHAADGICHLRTTYCPTSPKQTOGLADDAWEIPRESRLRLEVKLGQCGFGEVWMTNGTTR 299
QY 295 VALKTLKPGTMSPEALQEAQVWKKLRHEKLVQLYAVSEBPIYITEVWKSGLDPLK 354
DB 300 VALKTLKPGTMSPEALQEAQVWKKLRHEKLVQLYAVSEBPIYITEVWKSGLDPLK 359
QY 355 GETGKTLRLPOLVDMAAQIASGMAVYERVMYVHRDLRAANILVGENLVCKVADFGIARLI 414
DB 360 GETGKTLRLPOLVDMAAQIASGMAVYERVMYVHRDLRAANILVGENLVCKVADFGIARLI 419
QY 415 EDNEYTARQAGAPFIMTAPBALYGRFTIKSDVMSFGILLTELTTKGRVPYGMVNRREV 474
DB 420 EDNEYTARQAGAPFIMTAPBALYGRFTIKSDVMSFGILLTELTTKGRVPYGMVNRREV 479
QY 475 LDQVERGYMPCPECPESLHDLCCMKRKEBERPTFEYLQAFLEDYFTSTEPQYOPGE 534
DB 480 LDQVERGYMPCPECPESLHDLCCMKRKEBERPTFEYLQAFLEDYFTSTEPQYOPGE 539
QY 535 NL 536
DB 540 NL 541

RESULT 3
T4VHS
protein-tyrosine kinase (BC 2.7.1.112) src - chicken
N/Alternate names: kinase-related transforming protein src
C/Species: Gallus gallus (chicken)
C/Date: 19-Feb-1984 #sequence_revision 07-Oct-1994 #text_change 05-Oct-2004
C/Accession: A00630; 150217; A41256; C35650; A32432
R/Takeya, T.; Hanafusa, H.
Cell 32, 881-890, 1983


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QY      181 ETTKGA YC LSVSDPNDAGKGLNVGHYKIRKLDSSGFYITSRTOFNSLQOLVAAYYSKADGL 240
DB      178 ETTKGA YC LSVSDPNDAGKGLNVGHYKIRKLDSSGFYITSRTOFNSLQOLVAAYYSKADGL 237
QY      241 CHRLTVVCPTSKPQTQGLAKDAWEIPRESLRLEVKLGQCGCFGEVMMGTNGTTRVAIKTL 300
DB      238 CHRLTVVCPTSKPQTQGLAKDAWEIPRESLRLEVKLGQCGCFGEVMMGTNGTTRVAIKTL 297
QY      301 KPGTMSPEAFLOEAQVMKKLRHEKLVOLYAVVSEBPIYITVEYMSKGSLLDFLKGETGKY 360
DB      298 KPGTMSPEAFLOEAQVMKKLRHEKLVOLYAVVSEBPIYITVEYMSKGSLLDFLKGETGKY 357
QY      361 LRLPOLVDMAAOIASGMAVVERMNYVHRDLRAANILVGENLVCKVADFGLARLIENDEY 420
DB      358 LRLPOLVDMAAOIASGMAVVERMNYVHRDLRAANILVGENLVCKVADFGLARLIENDEY 417
QY      421 ARQGAFFPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVPPYGMVNRBVLDOVER 480
DB      418 ARQGAFFPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVPPYGMVNRBVLDOVER 477
QY      481 GYRMPCCPPECPSLHDLMCQCKRKEBERPTEBYLOAFLEDYFTSTEP 528
DB      478 GYRMPCCPPECPSLHDLMCQCKRKEBERPTEBYLOAFLEDYFTSTEP 525

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RESULT 5

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TREVSI
protein-tyrosine kinase (EC 2.7.1.112) src - avian sarcoma virus S1
C:Species: avian sarcoma virus S1
C>Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 05-Oct-2004
C:Accession: A25375
R:Ikawa, S.; Hagino-Yamagishi, K.; Kawai, S.; Yamamoto, T.; Toyoshima, K.
Mol. Cell. Biol. 6, 2420-2428, 1986
A:Title: Activation of the cellular src gene by transducing retrovirus.
A:Reference number: A25375; PMID:87064539; PMID:3097513
A:Accession: A25375
A:Molecule type: DNA
A:Residues: 1-568 <1KA>
A:Cross-references: UNIPROT:P14084; UNIPARC:UPI0000135F25
C:Genetics:
C:Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C:Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; phc
F:148-245/Domain: SH2 homology <SH2>
F:265-523/Domain: protein kinase homology <KIN>
F:273-281/Region: protein kinase ATP-binding motif
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:295/Active site: Lys #status predicted
F:416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

```

```

Query Match      92.3%; Score 2614.5; DB 1; Length 568;
Best Local Similarity 93.8%; Pred. No. 1.1e-121;
Matches 495; Conservative 12; Mismatches 18; Indels 3; Gaps 1;

QY      1 MGSNSKRPDASORRRSLPEAEVNHGAGGAPPASQTPSKPASADGHRGSAFAFAAAE 60
DB      1 MGSNSKRPDASORRRSLPEAEVNHGAGGAPPASQTPSKPASADGHRGSAFAFAAAE 57
QY      61 PKLFGFNSDPVTSPQARAGPLAGVTTFFVALYDYDSRRTDLSFKKGERLQIVNTEGD 120
DB      58 PKLFGFNSDPVTSPQARAGPLAGVTTFFVALYDYDSRRTDLSFKKGERLQIVNTEGD 117
QY      121 NWLAHSLSTGQGYIPSNVAPSDSIQAEWYFGKITRRESRLLNLAENPRTGFLVRES 180
DB      118 NWLAHSLSTGQGYIPSNVAPSDSIQAEWYFGKITRRESRLLNLAENPRTGFLVRES 177
QY      181 ETTKGA YC LSVSDPNDAGKGLNVGHYKIRKLDSSGFYITSRTOFNSLQOLVAAYYSKADGL 240
DB      178 ETTKGA YC LSVSDPNDAGKGLNVGHYKIRKLDSSGFYITSRTOFNSLQOLVAAYYSKADGL 237
QY      241 CHRLTVVCPTSKPQTQGLAKDAWEIPRESLRLEVKLGQCGCFGEVMMGTNGTTRVAIKTL 300

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DB      238 CHRLTVVCPTSKPQTQGLAKDAWEIPRESLRLEVKLGQCGCFGEVMMGTNGTTRVAIKTL 297
QY      301 KPGTMSPEAFLOEAQVMKKLRHEKLVOLYAVVSEBPIYITVEYMSKGSLLDFLKGETGKY 360
DB      298 KPGTMSPEAFLOEAQVMKKLRHEKLVOLYAVVSEBPIYITVEYMSKGSLLDFLKGETGKY 357
QY      361 LRLPOLVDMAAOIASGMAVVERMNYVHRDLRAANILVGENLVCKVADFGLARLIENDEY 420
DB      358 LRLPOLVDMAAOIASGMAVVERMNYVHRDLRAANILVGENLVCKVADFGLARLIENDEY 417
QY      421 ARQGAFFPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVPPYGMVNRBVLDOVER 480
DB      418 ARQGAFFPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVPPYGMVNRBVLDOVER 477
QY      481 GYRMPCCPPECPSLHDLMCQCKRKEBERPTEBYLOAFLEDYFTSTEP 528
DB      478 GYRMPCCPPECPSLHDLMCQCKRKEBERPTEBYLOAFLEDYFTSTEP 525

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RESULT 6

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TREVSI
protein-tyrosine kinase (EC 2.7.1.112) src - avian sarcoma virus S2
C:Species: avian sarcoma virus S2
C>Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 05-Oct-2004
C:Accession: B25375
R:Ikawa, S.; Hagino-Yamagishi, K.; Kawai, S.; Yamamoto, T.; Toyoshima, K.
Mol. Cell. Biol. 6, 2420-2428, 1986
A:Title: Activation of the cellular src gene by transducing retrovirus.
A:Reference number: A25375; PMID:87064539; PMID:3097513
A:Accession: B25375
A:Molecule type: DNA
A:Residues: 1-557 <1KA>
A:Cross-references: UNIPROT:P14085; UNIPARC:UPI0000135F26
C:Genetics:
C:Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology;
C:Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; onc
F:148-245/Domain: SH2 homology <SH2>
F:265-523/Domain: protein kinase homology <KIN>
F:273-281/Region: protein kinase ATP-binding motif
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:295/Active site: Lys #status predicted
F:416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

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Query Match      91.7%; Score 2599.5; DB 1; Length 557;
Best Local Similarity 89.7%; Pred. No. 5.7e-121;
Matches 496; Conservative 14; Mismatches 22; Indels 21; Gaps 2;

QY      1 MGSNSKRPDASORRRSLPEAEVNHGAGGAPPASQTPSKPASADGHRGSAFAFAAAE 60
DB      1 MGSNSKRPDASORRRSLPEAEVNHGAGGAPPASQTPSKPASADGHRGSAFAFAAAE 57
QY      61 PKLFGFNSDPVTSPQARAGPLAGVTTFFVALYDYDSRRTDLSFKKGERLQIVNTEGD 120
DB      58 PKLFGFNSDPVTSPQARAGPLAGVTTFFVALYDYDSRRTDLSFKKGERLQIVNTEGD 117
QY      121 NWLAHSLSTGQGYIPSNVAPSDSIQAEWYFGKITRRESRLLNLAENPRTGFLVRES 180
DB      118 NWLAHSLSTGQGYIPSNVAPSDSIQAEWYFGKITRRESRLLNLAENPRTGFLVRES 177
QY      181 ETTKGA YC LSVSDPNDAGKGLNVGHYKIRKLDSSGFYITSRTOFNSLQOLVAAYYSKADGL 240
DB      178 ETTKGA YC LSVSDPNDAGKGLNVGHYKIRKLDSSGFYITSRTOFNSLQOLVAAYYSKADGL 237
QY      241 CHRLTVVCPTSKPQTQGLAKDAWEIPRESLRLEVKLGQCGCFGEVMMGTNGTTRVAIKTL 300
DB      238 CHRLTVVCPTSKPQTQGLAKDAWEIPRESLRLEVKLGQCGCFGEVMMGTNGTTRVAIKTL 297
QY      301 KPGTMSPEAFLOEAQVMKKLRHEKLVOLYAVVSEBPIYITVEYMSKGSLLDFLKGETGKY 360
DB      298 KPGTMSPEAFLOEAQVMKKLRHEKLVOLYAVVSEBPIYITVEYMSKGSLLDFLKGETGKY 357

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Qy 361 LRLPOLVDMAAQIASGMAVYERMYVHRDLAANILVGENLVCKVADPGLARLIEDNEYT 420
Db 358 LRLPOLVDMAAQIASGMAVYERMYVHRDLAANILVGENLVCKVADPGLARLIEDNEYT 417
Qy 421 ARQAKFPFKMTAEALYGRFTIKSDVWSFGILLTELTKGRVPYPGMVNREVLDQYER 480
Db 418 ARQAKFPFKMTAEALYGRFTIKSDVWSFGILLTELTKGRVPYPGMVNREVLDQYER 477
Qy 481 GYRMPCEPCEPSLHDMCCMRKEPERPFEYLQAFLEDDYF----- 523
Db 478 GYRMPCEPCEPSLHDMCCMRKOPPERPFEYLQAFLEDDYLGILAMTWMEDKQEGPRG 537
Qy 524 -TSTEPQYQGEN 535
Db 538 ETASNKQERPED 550

RESULT 7

protein-tyrosine kinase (EC 2.7.1.112) src - Rous sarcoma virus
C:Species: Rous sarcoma virus
C:Date: 22-May-1981 #sequence revision 17-Dec-1982 #text_change 05-Oct-2004
C:Accession: A38017; A00631; S02726; A38018
R:Cernilofsky, A.P.; Levinson, A.D.; Varmus, H.E.; Bishop, J.M.; Tischner, E.; Goodman, Nature 301, 736-738, 1983
A:Title: Corrections to the nucleotide sequence of the src gene of Rous sarcoma virus.
A:Reference number: A38017; MUID:83141780; PMID:6298633
A:Accession: A38017
A:Molecule type: DNA
A:Residues: 1-526 <CZB>
A:Cross-references: UNIPROT:P00524; UNIPARC:UPI0000170DC3; GB:L29199; GB:J02018; GB:J02020
R:Takeya, T.; Hanafusa, H.
Cell 32, 881-890, 1983
A:Title: Structure and sequence of the cellular gene homologous to the RSV sec gene and
A:Reference number: A00630; MUID:83155664; PMID:6299580
A:Accession: A00631
A:Molecule type: DNA
A:Residues: 1-62, 'D', 64-95, 'T', 97-123, 'V', 125-300, 'N', 302-526 <TAK>
A:Cross-references: UNIPARC:UPI0000172582
A:Experimental source: stratin Schmidt-Ruppin
R:Bernier, J.V.; Dezelic, P.; Marx, M.; Calochy, G.
Nucleic Acids Res. 17, 1252, 1989
A:Title: Nucleotide sequence of the src gene of the Schmidt-Ruppin strain of Rous Sarcom
A:Reference number: S02726; MUID:89160256; PMID:2537953
A:Accession: S02726
A:Molecule type: DNA
A:Residues: 1-9, 'G', 11-62, 'D', 64-123, 'V', 125-319, 'K', 321-495, 'S', 497-526 <BAR>
A:Cross-references: UNIPARC:UPI0000135F2C; EMBL:X13745; NID:961908; PIDN:CAA32012.1; PID
R:Takeya, T.; Feldman, R.A.; Hanafusa, H.
J. Virol. 44, 1-11, 1982
A:Title: DNA sequence of the viral and cellular src gene of chickens: I. Complete nucle
A:Reference number: A38018; MUID:83059858; PMID:6292477
A:Accession: A38018
A:Molecule type: DNA
A:Residues: 1-15, 'C', 17-94, 'RT', 97-116, 'D', 118-337, 'T', 339-526 <TA2>
A:Cross-references: UNIPARC:UPI0000135F24; GB:X00928; NID:9210187; PIDN:AAA42565.1; PID
A:Experimental source: stratin RASV441
R:Neil, J.C.; Ghydael, J.; Vogt, P.K.; Smart, J.E.
Nature 291, 675-677, 1981
A:Title: Homologous tyrosine phosphorylation sites in transformation-specific gene produ
A:Reference number: A38019; MUID:81220979; PMID:6264320
A:Contents: annotation; phosphorylation site
C:Comment: The sequence from the Schmidt-Ruppin strain is shown.
C:Genetics:
A:Gene: src
C:Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C:Keywords: ATP; autophosphorylation; blocked amino end; 11oprotein; myristylation; onc
F:88-137/Domain: SH3 homology <SH3>
F:148-245/Domain: SH2 homology <SH2>
F:265-523/Domain: protein kinase homology <KIN>
F:273-281/Region: protein kinase ATP-binding motif
F:273-281/Region: protein kinase ATP-binding motif

F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:295/Active site: Lys #status predicted
F:416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status experime

Query Match 88.8%; Score 2516.5; DB 1; Length 526;
Best Local Similarity 92.3%; Pred. No. 6.56-117;
Matches 479; Conservative 13; Mismatches 24; Indels 3; Gaps 1;

Qy 1 MGSNKSXPKQASQRRRLPEAENVHAGGAFPAISQTPSKASADGHRGSAAPAAAE 60
Db 1 MGSSKSKXPQPSQRRRLPEPDSTH--HGFPASQTPNKTAADTHTTPERSFGYATE 57
Qy 61 PKLFGFNSSDPTVTSPPRAGPLAGGYTTPVALVYRESRTENDLSFKKGERLQIVNNTGD 120
Db 58 PKLFGFNSSDPTVTSPPRAGPLAGGYTTPVALVYRESWIRTDLSFKKGERLQIVNNTGN 117
Qy 121 WMLAHSLSGTQGYIPENYVAPSDSIQAEWYFGKITRRESERLLNAENRGTFPVRES 180
Db 118 WMLAHSLSLTQGYIIPENYVAPSDSIQAEWYFGKITRRESERLLNPENRGTFPVRES 177
Qy 181 ETTGAYCLSVSPDNAGKLVKHYKIRKLDGSGFYITTSRTQFNSLQQLVAYYSKADGL 240
Db 178 ETTGAYCLSVSPDNAGKLVKHYKIRKLDGSGFYITTSRTQFNSLQQLVAYYSKADGL 237
Qy 241 CHRLTYCPNPKPQTQGLADAWRIPRESRLFEVKLGCGCEGYVMGTMTGTVAIKTL 300
Db 238 CHRLTYCPNPKPQTQGLADAWRIPRESRLFEVKLGCGCEGYVMGTMTGTVAIKTL 297
Qy 301 KPGTMSPEAFLOEAQWKKLRHEKLVQYAVVSEPIYIVENYKSGSLDPLKGSTGY 360
Db 298 KPGTMSPEAFLOEAQWKKLRHEKLVQYAVVSEPIYIVENYKSGSLDPLKGSTGY 357
Qy 361 LRLPOLVDMAAQIASGMAVYERMYVHRDLAANILVGENLVCKVADPGLARLIEDNEYT 420
Db 358 LRLPOLVDMAAQIASGMAVYERMYVHRDLAANILVGENLVCKVADPGLARLIEDNEYT 417
Qy 421 ARQAKFPFKMTAEALYGRFTIKSDVWSFGILLTELTKGRVPYPGMVNREVLDQYER 480
Db 418 ARQAKFPFKMTAEALYGRFTIKSDVWSFGILLTELTKGRVPYPGMVNREVLDQYER 477
Qy 481 GYRMPCEPCEPSLHDMCCMRKEPERPFEYLQAFLEDDYF 519
Db 478 GYRMPCEPCEPSLHDMCCMRKOPPERPFEYLQAFLEDDY 516

RESULT 8

protein-tyrosine kinase (EC 2.7.1.112) src - Rous sarcoma virus
C:Species: Rous sarcoma virus
C:Date: 20-Feb-1995 #sequence revision 20-Feb-1995 #text_change 05-Oct-2004
C:Accession: S20808; S32774
R:Bodor, J.; Rozkoc, F.; Svoboda, J.
submitted to the EMBL Data Library, May 1990
A:Description: Sequence organization of the adjacent chromosomal flanks the LTR.
A:Reference number: S20808
A:Accession: S20808
A:Molecule type: DNA
A:Residues: 1-526 <BD>
A:Cross-references: UNIPROT:Q06567; UNIPARC:UPI00001066B2; EMBL:X52822; NID:949656; PIDN
A:Experimental source: Mesocricetus auratus (golden hamster) provirus
C:Genetics:
A:Gene: src
C:Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C:Keywords: ATP; autophosphorylation; oncogene; phosphoprotein; phosphotransferase; tran
F:88-137/Domain: SH3 homology <SH3>
F:148-245/Domain: SH2 homology <SH2>
F:265-523/Domain: protein kinase homology <KIN>
F:273-281/Region: protein kinase ATP-binding motif
F:295/Active site: Lys #status predicted
F:416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 88.1%; Score 2497.5; DB 2; Length 526;
Best Local Similarity 91.7%; Pred. No. 5.66-116;

F:416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 87.7%; Score 2484.5; DB 2; Length 526;
Best Local Similarity 91.3%; Pred. No. 2,4e-115;
Matches 474; Conservative 11; Mismatches 31; Indels 3; Gaps 1;

```
QY 1 MGSNKSXPQASORRSLRLEPENVHAGGAFPAQSPSPKASADGRGSAAPAAAE 60
  |||:|||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 1 MGSNKSXPQPSQRHSLRLEPPDSTH--HGFPASQTPDERTAPDAHNPERSGTYATE 57
QY 61 PKLFGFNSSDVTYSPPRAGPLAGVTTFFVALYDESRTETDLSFKKGERLQIVNTEGD 120
  |||:|||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 58 PKLFGFNSTSDVTYSPPRAGPLAGVTTFFVALYDESRTETDLSFKKGERLQIVNTEGD 117
QY 121 WMLASHLSTGQTGYIPSNYYAPSDSIQAEEMYPFKITRRSEERLLNAENRGTFLYRES 180
  |||:|||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 118 WMLASHLTTGQTGYIPSNYYAPSDSIQAEEMYPFKITRRSEERLLNPENRGTFLYRKS 177
QY 181 ETTKGAATCLSVSDPDNKGKLVNKHKTKRKLDGSGFYITSTRQFMSLQQLVAYYSKADGL 240
  |||:|||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 178 ETTKGAATCLSVSDPDNKGKLVNKHKTKRKLDGSGFYITSTRQFMSLQQLVAYYSKADGL 237
QY 241 CHRLTTCPTSPKPTQGLADAMEIPRESLRLEVKLGQGCFGFVWGMGTWNGTTRVALIKTL 300
  |||:|||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 238 CHRLANVCPTSPKPTQGLADAMEIPRESLRLEVKLGQGCFGFVWGMGTWNGTTRVALIKTL 297
QY 301 KPGTMSPEAFLOEAQVWKRLRHEKLVOLYAVVSEEPYIYTEYWSKSLDPLKGETGKY 360
  |||:|||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 298 KPGTMSPEAFLOEAQVWKRLRHEKLVOLYAVVSEEPYIYTEYWSKSLDPLKGETGKY 357
QY 361 LRLPOLVDMAAQIASGAAVYERMYVHRDLRAANILVGENLVCAVADFGRLLEDNEYT 420
  |||:|||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 358 LRLPOLVDMAAQIASGAAVYERMYVHRDLRAANILVGENLVCAVADFGRLLEDNEYT 417
QY 421 ARQAKPPIKMTAPEALYGRFTIKSDVMSFGILLTETTKGRVPYPMVNRREVLDQVER 480
  |||:|||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 418 ARQAKPPIKMTAPEALYGRFTIKSDVMSFGILLTETTKGRVPYPMVNRREVLDQVER 477
QY 481 GYRMPCEPCEPSLHDMCCQWRKEPERPTEYLQAF 519
  |||:|||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 478 GYRMPCEPCEPSLHDMCCQWRKEPERPTEYLQAF 516
```

RESULT 11

TVFVR

protein-tyrosine kinase (EC 2.7.1.112) src - Rous sarcoma virus (strain Prague C)

C:Species: Rous sarcoma virus

C>Date: 01-Sep-1981 #sequence_revision 17-Dec-1982 #text_change 05-Oct-2004

C:Accession: A00632

R:Schwartz, D.; Tizard, R.; Gilbert, W.

submitted to the Nucleic Acid Sequence Database, September 1982

A:Reference number: A00632

A:Accession: A00632

A:Molecule type: genomic RNA

A:Residues: 1-526 <SCH>

A:Cross-references: UNIPROT:P00526; UNIPROT:O92806; UNIPARC:UPI000002BA63

A:Note: as a result of base variations, residues 242 and 288 may be replaced by Thr and

Nature 291, 675-677, 1981

A:Title: Homologous tyrosine phosphorylation sites in transformation-specific gene prod

A:Reference number: A38019; MUID:81220979; PMID:6264320

A:Contents: annotation; phosphorylation site

C:Genetics:

A:Gene: src

C:Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology

C:Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; onc

F:88-137/Domain: SH3 homology <SH3>

F:148-245/Domain: SH2 homology <SH2>

F:265-523/Domain: protein kinase homology <KIN>

F:273-281/Region: protein kinase ATP-binding motif

F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted

F:285/Active site: lys #status predicted

F:416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status experime

Query Match 87.6%; Score 2481.5; DB 1; Length 526;
Best Local Similarity 91.1%; Pred. No. 3,4e-115;
Matches 473; Conservative 11; Mismatches 32; Indels 3; Gaps 1;

```
QY 1 MGSNKSXPQASORRSLRLEPENVHAGGAFPAQSPSPKASADGRGSAAPAAAE 60
  |||:|||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 1 MGSNKSXPQPSQRHSLRLEPPDSTH--HGFPASQTPDERTAPDAHNPERSGTYATE 57
QY 61 PKLFGFNSSDVTYSPPRAGPLAGVTTFFVALYDESRTETDLSFKKGERLQIVNTEGD 120
  |||:|||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 58 PKLFGFNSTSDVTYSPPRAGPLAGVTTFFVALYDESRTETDLSFKKGERLQIVNTEGD 117
QY 121 WMLASHLSTGQTGYIPSNYYAPSDSIQAEEMYPFKITRRSEERLLNAENRGTFLYRES 180
  |||:|||||:|||||:|:|:~|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 118 WMLASHLTTGQTGYIPSNYYAPSDSIQAEEMYPFKITRRSEERLLNPENRGTFLYRKS 177
QY 181 ETTKGAATCLSVSDPDNKGKLVNKHKTKRKLDGSGFYITSTRQFMSLQQLVAYYSKADGL 240
  |||:|||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 178 ETTKGAATCLSVSDPDNKGKLVNKHKTKRKLDGSGFYITSTRQFMSLQQLVAYYSKADGL 237
QY 241 CHRLTTCPTSPKPTQGLADAMEIPRESLRLEVKLGQGCFGFVWGMGTWNGTTRVALIKTL 300
  |||:|||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 238 CHRLANVCPTSPKPTQGLADAMEIPRESLRLEVKLGQGCFGFVWGMGTWNGTTRVALIKTL 297
QY 301 KPGTMSPEAFLOEAQVWKRLRHEKLVOLYAVVSEEPYIYTEYWSKSLDPLKGETGKY 360
  |||:|||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 298 KPGTMSPEAFLOEAQVWKRLRHEKLVOLYAVVSEEPYIYTEYWSKSLDPLKGETGKY 357
QY 361 LRLPOLVDMAAQIASGAAVYERMYVHRDLRAANILVGENLVCAVADFGRLLEDNEYT 420
  |||:|||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 358 LRLPOLVDMAAQIASGAAVYERMYVHRDLRAANILVGENLVCAVADFGRLLEDNEYT 417
QY 421 ARQAKPPIKMTAPEALYGRFTIKSDVMSFGILLTETTKGRVPYPMVNRREVLDQVER 480
  |||:|||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 418 ARQAKPPIKMTAPEALYGRFTIKSDVMSFGILLTETTKGRVPYPMVNRREVLDQVER 477
QY 481 GYRMPCEPCEPSLHDMCCQWRKEPERPTEYLQAF 519
  |||:|||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 478 GYRMPCEPCEPSLHDMCCQWRKEPERPTEYLQAF 516
```

RESULT 12

S26420 protein-tyrosine kinase (EC 2.7.1.112) src - Rous sarcoma virus

C:Species: Rous sarcoma virus

C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Oct-2004

C:Accession: S26420; S20676

R:Kashuba, V.I.; Ryndlich, A.V.; Dostelova, V.; Hlozaneek, I.; Zubak, S.V.; Kavanan, V.M.

submitted to the EMBL Data Library, September 1992

A:Description: Molecular cloning and DNA sequence analysis of duck-adapted variant of Ro

A:Reference number: S26417

A:Accession: S26420

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-526 <KAS>

A:Cross-references: UNIPROT:Q07461; UNIPARC:UPI000010512B; EMBL:X68524; NID:961903; PIDN

R:Kashuba, V.I.; Serge, Z.V.; Ryndlich, A.V.; Kavanan, V.M.; Hlozaneek, I.

submitted to the EMBL Data Library, March 1990

A:Reference number: S20676

A:Accession: S20676

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-526 <KX2>

A:Cross-references: UNIPARC:UPI000010512B; EMBL:X51861; NID:961896; PIDN:CAA36154.1; PID

C:Genetics:

A:Gene: src

C:Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology,

C:Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; phos

F:88-137/Domain: SH3 homology <SH3>

F:148-245/Domain: SH2 homology <SH2>

F:265-523/Domain: protein kinase homology <KIN>

F:273-281/Region: protein kinase ATP-binding motif

F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:295/Active site: Lys #status predicted
F:416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match	87.0%	Score 2465.5	DB 2	Length 526
Similarity	90.6%	Pred. No. 1.9e-114		
Best Local				
Matches 470	Conservative 13	Mismatches 33	Indels 3	Gaps 1

Qy	1	MGSKSKRPKDASQRRRSLEPEANVHGAGGGAFPSAQTSKPASADGHRGPAALAPAAAE	60
Db	1	MGSSKSKRPRDSQGRHSLEPDSH---HGFPASQTPDETHAARDAHNRPSRSQVATE	57
Qy	61	PKLFGGNSSDTTSPOQAGPLAGCVTTVALYDYESRTETDLSFKKGERLQIYNNTEGD	120
Db	58	PKLFGGNTSTQTVASPOQAGLAGVTTFVALYDYESWTEETDLSFKKGERLQIYNNTEGY	117
Qy	121	WMLHSLSTGTGTGIIPSNYVAPSDSIQAEEMYFGKITRSESERLILNAENPRGTFVARS	180
Db	118	WMLHSLTGTGTGIIPSNYVAPSDSIQAEEMYFGKITRSEERILLNAPENRGTFVLRKS	177
Qy	181	ETTKGAYCLAVSDFDNAGKLVNKKYIKIKLDSGGFYITSRTOFNSLQQLVAYYSKADGL	240
Db	178	ETAGAACVLSDDDNAGPVMKKYIKLYKLSGGFYITLRFQFGLSLOQLVAYHYEKHADGL	237
Qy	241	CHRLTTCQPSKSPOTOGIAXDAWEIPRESLLEVKLGQCGEYVMGTMMNTSTVAIKTL	300
Db	238	CHRLTTCQPSKSPOTOGIAXDAWEIPRESLLEAKLGQCGEYVMGTMMNTSTVAIKTL	297
Qy	301	KPGTMSBEAPLQEAQVNMKQLRHEKLVOLYAVVSEPIYIVTEYMSKSLDLFLKGETGY	360
Db	298	KPGTMSBEAPLQEAQVNMKFRHEKLVOLYAVVSEPIYIVTEYMSKSLDLFLKGEMGY	357
Qy	361	LRLPOLVDMAQIISGMAVYERNNYVHRDLAAAILVGENIVCYVADPGLARLLEDNEYT	420
Db	358	LRLPOLVDMAQIISGMAVYERNNYVHRDLAAAILVGENIVCYVADPGLARLLEDNEYT	417
Qy	421	ARQAKAPPIKWTAEALYGRFTIKSDVMSFGILLTELTTRGAVYPGMVNRVLDQYER	480
Db	418	ARQAKAPPIKWTAEALYGRFTIKSDVMSFGILLTELTTRGAVYPCGMVNRVLDQYER	477
Qy	481	GYRMPCEPCEGESLHDLACOCMKRKEPERPRFEYLQAFLL 519	
Db	478	GYRMPCEPCEGESLHDLACOCMKRKEPERPRFKYLQAFLL 516	

RESULT 13
 B34104
 protein-tyrosine kinase (EC 2.7.1.112) src 2 [similarity] - African clawed frog
 N:Alternate names: kinase-related transforming protein (src); kinase-related transforming
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 05-Oct-2004
 C:Accession: B34104; 151563
 R:Steele, R.E.; Unger, T.F.; Mardis, M.J.; Ferro, J.B.
 J:J Biol. Chem. 264, 10649-10653, 1989
 A:Title: The two Xenopus laevis SRC genes are co-expressed and each produces functional
 A:Reference number: A34104; MUID:89276134; PMID:249582
 A:Accession: B34104
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-532 <STB>
 A:Cross-references: UNIPROT:P13116; UNIPARC:UPI000017159F; GB:M23422; GB:J04822; NID:g22
 R:Steele, R.E.
 Nucleic Acids Res. 13, 1747-1761, 1985
 A:Title: Two divergent cellular src genes are expressed in Xenopus laevis.
 A:Reference number: 151563; MUID:85215578; PMID:2987836
 A:Accession: 151563
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 439-492 <ST2>
 A:Cross-references: UNIPARC:UPI00001715A0; GB:M30858; NID:g214799; PIDN:AA51644.1; PID:
 C:Genetics:
 A:Gene: src
 A:Introns: 464/1

C:Superfamily Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C:Keywords: ATP; autophosphorylation; blocked amino end; lipidprotein; myristylation; phospho-
F:187-136/Domain: SH3 homology <SH3>
F:147-244/Domain: SH2 homology <SH2>
F:264-532/Domain: protein kinase homology <KIN>
F:327-280/Region: protein kinase ATP-binding motif
F:2/Modified site: myristylated amino end (Gly) (1n mature form) #status predicted
F:129/Active site: Lys #status predicted
F:415,526/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match	86.94%	Score 2463	DB 1	Length 532
Best Local Similarity	87.94%	Pred. No. 2,86	114	
Matches 471	Conservative	24	Mismatches 37	Indels 4
			Gaps	3

[illegible]

RESULT 14
A34104
protein-tyrosine kinase (BC 2.7.1.112) src 1 [similarity] - African clawed frog
N/Alternate names: kinase-related transforming protein (src); kinase-related transforming
C/Species: Xenopus laevis (African clawed frog)
C/Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 31-Dec-2004
C/Accession: A34104; 151564
J.Steele, R.E.; Unger, T.F.; Mardis, M.J.; Fero, J.B.
J. Biol. Chem. 264, 10649-10653, 1989
A/Title: The two Xenopus laevis SRC genes are co-expressed and each produces functional P
A/Reference number: A34104; PMID:89278134; PMID:2493582
A/Accession: A34104
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-532 <STR>
A/Cross-references: UNIPROT:091851; UNIPARC:UPI0000172581; GB:M24704; GB:J04822; NID:g214
J.Steele, R.E.; Choyn, R.; Ral, B.B.A.; Winokur, S.T.; Unger, T.F.
Oncogene 7, 2345-2350, 1992
A/Title: Structural organization of a src gene from xenopus laevis.
A/Reference number: 151564; MUID:93064714; PMID:1337158
A/Accession: 151564
A/Status: translated from GB/EMBL/DBD

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 5, 2006, 17:01:48 ; Search time 153.616 Seconds
(without alignments)
3227.587 Million cell updates/sec

Title: US-10-691-079-2

Perfect score: 2834
Sequence: 1 MGSNKSXPKKASQRRSLRP.....AFLEDYFTSTPEYQPGENL 536

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2829	99.8	535	1 SRC_HUMAN	P12931 homo sapien
2	2821	99.5	542	2 Q76P87_HUMAN	Q76P87 homo sapien
3	2799.5	98.8	535	2 Q80XU2_MOUSE	Q80XU2 mus musculu
4	2786.5	98.3	541	2 Q2M414_MOUSE	Q2M414 mus musculu
5	2782.5	98.2	535	2 Q3UKD6_MOUSE	Q3UKD6 mus musculu
6	2781	98.1	542	2 Q9JUI0_RAT	Q9JUI0 rattus norv
7	2773.5	97.9	540	1 SRC_MOUSE	P05480 mus musculu
8	2771	97.8	535	1 SRC_RAT	Q9WUD9 rattus norv
9	2706	95.5	523	2 Q45Q02_RAT	Q45Q02 rattus norv
10	2661.5	93.9	532	1 SRC_CHICK	P00523 gallus gall
11	2616.5	92.3	586	1 SRC_AVIS2	P15054 avian sarco
12	2609.5	92.1	567	1 SRC_AVIS5	P14084 avian sarco
13	2608.5	92.0	587	2 Q64817_GRETR	Q64817 avian sarco
14	2594.5	91.5	556	1 SRC_AVIS1	P14085 avian sarco
15	2528.5	89.2	525	1 SRC_AVISR	P00524 avian sarco
16	2528.5	89.2	525	1 SRC_RSVA	P00524 avian sarco
17	2497.5	88.1	526	2 Q60567_GRETR	Q60567 rous sarcom
18	2486.5	87.7	525	1 SRC_RSVH1	P25020 rous sarcom
19	2486	87.7	532	2 Q5MA59_XENTR	Q5MA59 xenopus tro
20	2485.5	87.7	526	2 Q64994_GRETR	Q64994 rous sarcom
21	2483.5	87.6	523	2 Q93080_GRETR	Q93080 rous sarcom
22	2482	87.6	523	2 Q85477_GRETR	Q85477 rous sarcom
23	2481.5	87.6	535	2 Q92957_RSVSB	Q92957 rous sarcom
24	2481.5	87.6	526	2 Q92806_GRETR	Q92806 rous sarcom
25	2480.5	87.5	525	1 SRC_RSVSE	P63185 rous sarcom
26	2476.5	87.4	525	1 SRC_RSVS	P00526 rous sarcom
27	2470.5	87.2	526	2 Q64993_RSVSR	Q64993 rous sarcom
28	2466.5	87.0	526	2 Q07461_GRETR	Q07461 rous sarcom
29	2463	86.9	532	2 Q2TA71_XENLA	Q2TA71 xenopus lae
30	2458	86.7	531	1 SRC2_XENLA	P13116 xenopus lae
31	2457.5	86.7	537	2 Q7ZX73_XENLA	Q7ZX73 xenopus lae

32	2454	86.6	531	1 SRC1_XENLA	P13115 xenopus lae
33	2453.5	86.6	545	2 Q86352_GRETR	Q86352 rous sarcom
34	2446.5	86.3	546	2 Q86363_GRETR	Q86363 rous sarcom
35	2413	85.1	522	1 SRC_RSVPA	P13163 rous sarcom
36	2318	81.8	534	2 Q6EMH0_BRARE	Q6EMH0 brachydario
37	2193.5	77.4	527	2 Q91952_XIPXI	Q91952 xiphophorus
38	2137.5	75.4	537	2 Q64089_XENTR	Q64089 xenopus tro
39	2136.5	75.4	537	2 Q6PF70_XENTR	Q6PF70 xenopus lae
40	2129.5	75.1	537	2 Q49863_XENLA	Q49863 xenopus lae
41	2127.5	75.1	541	2 Q99PW1_RAT	Q99PW1 rattus norv
42	2125.5	75.0	536	1 YES_XENLA	P10936 xenopus lae
43	2123.5	74.9	541	2 Q8C762_MOUSE	Q8C762 mus musculu
44	2122	74.9	542	1 YES_HUMAN	P07947 homo sapien
45	2118.5	74.8	540	1 YES_MOUSE	Q04736 mus musculu

ALIGNMENTS

RESULT 1
ID SRC_HUMAN STANDARD; PRT; 535 AA.
AC P12931; Q86VB9; Q9H5A8;
DT 01-OCT-1989, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1995, sequence version 2.
DT 07-MAR-2006, entry version 79.
DE Proto-oncogene tyrosine-protein kinase Src (EC 2.7.1.112) (p60-Src)
DE (C-Src) (pp60c-src).
GN Name=SRC; Synonyms=SRC1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggaley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Codley V.B., Collier R.E., Connor R.E., Cordy N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Griffith D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.B.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Lelevaris M.H., Leverhna M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConachie L.J., McIay K., McMurtry A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsey H.,
RA Rice C.M., Rose M.T., Scott C.E., Sehra H.K., Showkhen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sultson J.E.,
RA Swann R.M., Symamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.,
RL "The DNA sequence and comparative analysis of human chromosome 20.",
RL Nature 414:865-871(2001).
[2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RC TISSUE=lung, and skin.
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.F., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.D., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,

RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uddin T.B., Toehlynyk S., Gennini P., Prange C.C.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richardson D.K., Muzny D.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.C., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Helton E., Kesteman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buttrifield Y.S.N., Krzywiński M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL [3]
 RN NUCLEOTIDE SEQUENCE OF 1-184 (ISOFORM 1).
 RP MEDLINE=87257903; PubMed=3299057;
 RX Tanaka A., Gibbs C.P., Arthur R.R., Anderson S.K., Kung H.-J.,
 RA Fujita D.J.,
 RT "DNA sequence encoding the amino-terminal region of the human c-src
 RT protein: implications of sequence divergence among src-type kinase
 RT oncogenes";
 RT Mol. Cell. Biol. 7:1978-1983(1987).
 RL [4]
 RN NUCLEOTIDE SEQUENCE OF 185-535 (ISOFORM 1).
 RP MEDLINE=85213463; PubMed=2582238;
 RX Anderson S.K., Gibbs C.P., Tanaka A., Kung H.-J., Fujita D.J.,
 RA "Human cellular src gene: nucleotide sequence and derived amino acid
 RT sequence of the region coding for the carboxy-terminal two-thirds of
 RT pp60c-src";
 RT Mol. Cell. Biol. 5:1122-1129(1985).
 RL [5]
 RN NUCLEOTIDE SEQUENCE OF 97-138 (ISOFORM 2).
 RP MEDLINE=90040822; PubMed=2681803;
 RX Pyper J.M., Bolen J.B.,
 RA "Neuron-specific splicing of C-SRC RNA in human brain";
 RT J. Neurosci. Res. 24:89-96(1989).
 RL [6]
 RN NUCLEOTIDE SEQUENCE OF 375-535 (ISOFORM 1).
 RP MEDLINE=85187961; PubMed=2581127;
 RX Parker R.C., Mardon G., Lebo R.V., Varnus H.E., Bishop J.M.,
 RA "Isolation of duplicated human c-src genes located on chromosomes 1
 RT and 20";
 RT Mol. Cell. Biol. 5:831-838(1985).
 RL [7]
 RN ALTERNATIVE SPLICING.
 RP PubMed=1691439;
 RX Pyper J.M., Bolen J.B.,
 RT "Identification of a novel neuronal C-SRC exon expressed in human
 RT brain";
 RT Mol. Cell. Biol. 10:2035-2040(1990).
 RL [8]
 RN X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 85-535.
 RP MEDLINE=97177105; PubMed=9024657; DOI=10.1038/38595a0;
 RX Xu W., Harrison S.C., Eck M.J.,
 RA "Three-dimensional structure of the tyrosine kinase c-Src";
 RT Nature 385:595-602(1997).
 RL [9]
 RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 144-248.
 RP MEDLINE=97317069; PubMed=9174343; DOI=10.1021/bj970019n;
 RX Charifson P.S., Shewchuk L.M., Rocque W., Hummel C.W., Jordan S.R.,
 RA Mohr C., Pecofsky G.J., Peel M.R., Rodriguez M., Sternbach D.D.,
 RA Conner T.G.,
 RT "Peptide ligands of pp60(c-src) SH2 domains: a thermodynamic and
 RT structural study";
 RT Biochemistry 36:6283-6293(1997).
 RL [10]
 RN STRUCTURE BY NMR OF 203-248.
 RP MEDLINE=95161382; PubMed=7532003;
 RX Xu R.X., Word J.M., Davis D.G., Rink M.J., Willard D.H. Jr.,
 RA Gampe R.T. Jr.,
 RT "Solution structure of the human pp60c-src SH2 domain complexed with a

RT phosphorylated tyrosine pentapeptide";
 RL Biochemistry 34:2107-2121(1995).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
 CC tyrosine phosphate.
 CC -1- INTERACTION:
 CC 06NVP1.Centod (xeno); NDBExp=3; InAct=EBI-621482, EBI-621463;
 CC 09Y6K9.IKBKG; NDBExp=1; InAct=EBI-621482, EBI-81279;
 CC 060749.Rhdbsal (xeno); NDBExp=1; InAct=EBI-621482, EBI-519077;
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=PI2931-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=PI2931-2; Sequence=VSP_012134;
 CC -1- PTM: Phosphorylated on Tyr-529 by c-Src kinase (CSK). The
 CC phosphorylated form is termed pp60c-src. The phosphorylated tail
 CC interacts with the SH2 domain thereby repressing kinase activity.
 CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
 CC subfamily.
 CC -1- SIMILARITY: Contains 1 SH2 domain.
 CC -1- SIMILARITY: Contains 1 SH3 domain.
 CC -----
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 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL, AI133293; CAC34523.1; -; Genomic_DNA.
 DR EMBL, BC011566; AAH11566.1; -; mRNA.
 DR EMBL, BC051270; AAH51270.2; -; mRNA.
 DR EMBL, K03218; AAA60584.1; -; Genomic_DNA.
 DR EMBL, M16237; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL, M16243; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL, M16244; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL, M16245; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL, K03212; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL, K03213; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL, K03215; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL, K03216; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL, K03217; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL, K02647; CAA26485.1; -; Genomic_DNA.
 DR EMBL, K03995; CAA26485.1; JOINED; Genomic_DNA.
 DR EMBL, K03996; CAA26485.1; JOINED; Genomic_DNA.
 DR EMBL, K03997; CAA26485.1; JOINED; Genomic_DNA.
 DR EMBL, K03998; CAA26485.1; JOINED; Genomic_DNA.
 DR EMBL, K03999; CAA26485.1; JOINED; Genomic_DNA.
 DR EMBL, X04000; CAA26485.1; JOINED; Genomic_DNA.
 DR PIR, A26891; TVHUSC.
 DR PDB, 1A07; X-ray; A/B=143-248.
 DR PDB, 1A08; X-ray; A/B=143-248.
 DR PDB, 1A09; X-ray; A/B=143-248.
 DR PDB, 1A1A; X-ray; A/B=143-248.
 DR PDB, 1A1B; X-ray; A/B=143-248.
 DR PDB, 1A1C; X-ray; A/B=143-248.
 DR PDB, 1A1E; X-ray; A/B=143-248.
 DR PDB, 1FKM; X-ray; @=85-535.
 DR PDB, 1HCS; NMR; B=143-248.
 DR PDB, 1HCT; NMR; B=143-248.
 DR PDB, 1KSW; X-ray; A=85-535.
 DR PDB, 1O41; X-ray; A=144-251.
 DR PDB, 1O42; X-ray; A=144-251.
 DR PDB, 1O43; X-ray; A=144-251.
 DR PDB, 1O47; X-ray; A=144-251.
 DR PDB, 1O46; X-ray; A=144-251.
 DR PDB, 1O45; X-ray; A=144-251.
 DR PDB, 1O44; X-ray; A=144-251.
 DR PDB, 1O4B; X-ray; A=144-251.
 DR PDB, 1O4C; X-ray; A=144-251.
 DR PDB, 1O4D; X-ray; A=144-251.
 DR PDB, 1O4E; X-ray; A=144-251.
 DR PDB, 1O4F; X-ray; A=144-251.

DR PDB; 1O4G; X-ray; A=144-251.
DR PDB; 1O4H; X-ray; A=144-251.

Query Match 99.8%; Score 2829; DB 1; Length 535;
Best Local Similarity 100.0%; Pred. No. 1.3e-177;
Matches 535; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GSNSKRPKDSQRRRSLEPENVHAGGGAFFPASOTPSKPSADGHRPSAFAFAAEP 61
DB 1 GSNSKRPKDSQRRRSLEPENVHAGGGAFFPASOTPSKPSADGHRPSAFAFAAEP 60

QY 62 KLFGGFNSSDTVSPORAGPLAGVTFVALYVESRTETDLSPFKGERLQIVNTEGDM 121
DB 61 KLFGGFNSSDTVSPORAGPLAGVTFVALYVESRTETDLSPFKGERLQIVNTEGDM 120

QY 122 WLAHSLSTGQTGYIPSNVAPSDSIQAEEMVFGKITRRESRLLINAEPRGTFLVRESE 181
DB 121 WLAHSLSTGQTGYIPSNVAPSDSIQAEEMVFGKITRRESRLLINAEPRGTFLVRESE 180

QY 182 TTYGAYCLSYSDPDMNAGLVKHYKIRKLDGSGFYITSRQPNLSIQQLVAYYSKADGLC 241
DB 181 TTYGAYCLSYSDPDMNAGLVKHYKIRKLDGSGFYITSRQPNLSIQQLVAYYSKADGLC 240

QY 242 HRLTTVCPTSKPOTQGLAKDAWEIPRESLRLEVKLGGCCFGEVMMGTNGTTRVAIKTLK 301
DB 241 HRLTTVCPTSKPOTQGLAKDAWEIPRESLRLEVKLGGCCFGEVMMGTNGTTRVAIKTLK 300

QY 302 PGTMSPEAFIQEAOVMKKLRHEKLVQLYAVVSEBPIYIVTEYMSKSLDPLKGETGKYL 361
DB 301 PGTMSPEAFIQEAOVMKKLRHEKLVQLYAVVSEBPIYIVTEYMSKSLDPLKGETGKYL 360

QY 362 RLPLVYMAAQIASGMAYVERMNVYHDLRAANILVGENLVCKYADFGALILBNETTA 421
DB 361 RLPLVYMAAQIASGMAYVERMNVYHDLRAANILVGENLVCKYADFGALILBNETTA 420

QY 422 ROGAKPPIKMTAPPAALYGRFTIKSDVMSFGILLTELTKGRVPPGVNREVLDQVERG 481
DB 421 ROGAKPPIKMTAPPAALYGRFTIKSDVMSFGILLTELTKGRVPPGVNREVLDQVERG 480

QY 482 YRMCPEPCESLHDLMOQCWRKEPERPFEYLQAFLEDYFTSTEPQYOGENU 536
DB 481 YRMCPEPCESLHDLMOQCWRKEPERPFEYLQAFLEDYFTSTEPQYOGENU 535

RESULT 2
Q76P87_HUMAN PRELIMINARY; PRT; 542 AA.
AC Q76P87;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DE 07-FEB-2006, entry version 12.
DT OTTHUMP0000030931.
GN Name=SRC; ORFNames=RP5-823N20.1-006;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Wallis J.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
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CC Distributed under the Creative Commons Attribution-NonDerivs license
CC -----
DR EMBL; AL333293; CAC10573.1; -; Genomic_DNA.
DR HSSP; P12931; 1A09.
DR SMK; Q76P87; 87-542.
DR Ensembl; ENSG00000197122; Homo sapiens.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.

DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001452; SH3.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR Pfam; PF07714; Kinase_Tyr; 1.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH3_1; 1.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRINTS; PR00452; SH3DOMAIN.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000003; Prot_kinase; 1.
DR ProDom; PD000093; SH2; 1.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 1.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS50001; SH2; 1.
DR PROSITE; PS50002; SH3; 1.
DR SEQUENCE 542 AA; 60589 MW; C12D30FB8CD5FF68 CRC64;

Query Match 99.5%; Score 2821; DB 2; Length 542;
Best Local Similarity 98.9%; Pred. No. 4.5e-177;
Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

QY 1 MGSNKSXPKDSQRRRSLEPENVHAGGGAFFPASOTPSKPSADGHRPSAFAFAAEP 60
DB 1 MGSNKSXPKDSQRRRSLEPENVHAGGGAFFPASOTPSKPSADGHRPSAFAFAAEP 60

QY 61 KLFGGFNSSDTVSPORAGPLAGVTFVALYVESRTETDLSPFKGERLQIVNTEGDM 117
DB 61 KLFGGFNSSDTVSPORAGPLAGVTFVALYVESRTETDLSPFKGERLQIVNTEGDM 120

QY 118 ---EGDWLAHSLSTGQTGYIPSNVAPSDSIQAEEMVFGKITRRESRLLINAEPRGT 174
DB 121 DVREGDWLAHSLSTGQTGYIPSNVAPSDSIQAEEMVFGKITRRESRLLINAEPRGT 180

QY 175 FLVRESSTTGAYCLSYSDPDMNAGLVKHYKIRKLDGSGFYITSRQPNLSIQQLVAYYS 234
DB 181 FLVRESSTTGAYCLSYSDPDMNAGLVKHYKIRKLDGSGFYITSRQPNLSIQQLVAYYS 240

QY 235 KHAAGLCHRLTTVCPTSKPOTQGLAKDAWEIPRESLRLEVKLGGCCFGEVMMGTNGTTR 294
DB 241 KHAAGLCHRLTTVCPTSKPOTQGLAKDAWEIPRESLRLEVKLGGCCFGEVMMGTNGTTR 300

QY 295 VAIITLKPGTMSPEAFIQEAOVMKKLRHEKLVQLYAVVSEBPIYIVTEYMSKSLDPLK 354
DB 301 VAIITLKPGTMSPEAFIQEAOVMKKLRHEKLVQLYAVVSEBPIYIVTEYMSKSLDPLK 360

QY 355 GETGKYRLPLVYMAAQIASGMAYVERMNVYHDLRAANILVGENLVCKYADFGALILI 414
DB 361 GETGKYRLPLVYMAAQIASGMAYVERMNVYHDLRAANILVGENLVCKYADFGALILI 420

QY 415 EDNEYTA ROGAKPPIKMTAPPAALYGRFTIKSDVMSFGILLTELTKGRVPPGVNREV 474
DB 421 EDNEYTA ROGAKPPIKMTAPPAALYGRFTIKSDVMSFGILLTELTKGRVPPGVNREV 480

QY 475 LDQVERGYRMCPEPCESLHDLMOQCWRKEPERPFEYLQAFLEDYFTSTEPQYOGGE 534
DB 481 LDQVERGYRMCPEPCESLHDLMOQCWRKEPERPFEYLQAFLEDYFTSTEPQYOGGE 540

QY 535 NL 536
DB 541 NL 542

RESULT 3
Q80XU2_MOUSE

ID Q80XU2 MOUSE PRELIMINARY; PRT; 535 AA.
AC Q80XU2;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE Rous sarcoma oncogene, isoform 2.
GN Name=Src;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PB/N; TISSUE=salivary gland;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marisina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boultard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grumet J., Schmutz J., Myers R.M.,
RA Butterfield Y.S., Krzywdinski M.I., Skalska U., Smallin D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PB/N; TISSUE=salivary gland;
RG NIH MGC Project;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
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EMBL: BC039953; AAH39953.1; -; mRNA.
HSSP: P12931; 1043.
DR SMR; Q80XU2; 86-535.
DR Ensembl; ENSMUSG00000027646; Mus musculus.
DR MGI; MGI:98397; Src.
DR GO; GO:0005515; P:protein binding; IPT.
DR GO; GO:0004674; P:protein serine/threonine kinase activity; RCA.
DR GO; GO:0004713; P:protein-tyrosine kinase activity; IMP.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IDA.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser Thr_kinase.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001452; SH3.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR Pfam; PF07714; Pkinase_Tyr; 1.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH3; 1.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRINTS; PR00452; SH3DOMAIN.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR ProDom; PD000093; SH2; 1.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00001; SH2; 1.
DR PROSITE; PS00002; SH3; 1.
SQ SEQUENCE 535 AA; 59891 MW; 22CB5CBBE7A061C0 CRC64;
Query Match 98.9%; Score 2799.5; DB 2; Length 535;
Best local similarity 98.9%; Pred. No. 1,2e-175;
Matches 530; Conservative 3; Mismatches 2; Indels 1; Gaps 1;
QY 1 MGSNKKPVDASQRRSLPEAENVHAGGAPASQPSKRPASADGHRGSAAPAAAE 60
DB 1 MGSNKKSPDASQRRSLPESENVHGA-GGAPASQPSKRPASADGHRGSAAFVPPAAE 59
QY 61 PKLFGFNSDPYTSQRRAGPLAGYTTVALYDYSRRTDLSFFKGRRLQVNNTEGD 120
DB 60 PKLFGFNSDPYTSQRRAGPLAGYTTVALYDYSRRTDLSFFKGRRLQVNNTEGD 119
QY 121 WMLAHLSTGQTYISNVAVPSDSIQAEEMWFGKITRRESERLLNAENPRTFLVRES 180
DB 120 WMLAHLSTGQTYISNVAVPSDSIQAEEMWFGKITRRESERLLNAENPRTFLVRES 179
QY 181 ETTGKAYCLSVSDFDNAKGLNVKHYKIRKLDGSGFYTSRTQFNSLQQLVAYYSKADGL 240
DB 180 ETTGKAYCLSVSDFDNAKGLNVKHYKIRKLDGSGFYTSRTQFNSLQQLVAYYSKADGL 239
QY 241 CHRLTVCTPSKQQTQGLAKDAEIPRESLRLEVLKGGCGFGEVWMTGNTTRVAIKTL 300
DB 240 CHRLTVCTPSKQQTQGLAKDAEIPRESLRLEVLKGGCGFGEVWMTGNTTRVAIKTL 299
QY 301 KPQTMSPEAFLOBAQVMKLRHEKLVQLYAVVSEBPIYVTEYMSKSLDPLKSGTGKY 360
DB 300 KPQTMSPEAFLOBAQVMKLRHEKLVQLYAVVSEBPIYVTEYMSKSLDPLKSGTGKY 359
QY 361 LRLPOLVDAQAQIASGMAVVERNVYHRDLRAANILVGENLVCKVADFGILARLIEDNEYT 420
DB 360 LRLPOLVDAQAQIASGMAVVERNVYHRDLRAANILVGENLVCKVADFGILARLIEDNEYT 419
QY 421 AAGGAKFPKMTAPKALYGRFTISDVMSFGILLTELTKKRVPPRGVNVREVLDOVER 480
DB 420 AAGGAKFPKMTAPKALYGRFTISDVMSFGILLTELTKKRVPPRGVNVREVLDOVER 479
QY 481 GYRMPCEPCPSLHLMCCWRKEPEERPFTEYLQAFLEDFYTSIEPQYQGENL 536
DB 480 GYRMPCEPCPSLHLMCCWRKEPEERPFTEYLQAFLEDFYTSIEPQYQGENL 535
RESULT 4
Q2M4I4 MOUSE PRELIMINARY; PRT; 541 AA.
AC Q2M4I4;
DT 21-FEB-2006, integrated into UniProtKB/TrEMBL.
DT 21-FEB-2006, sequence version 1.
DT 21-FEB-2006, entry version 1.
DE Src.
GN Name=Src;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CAST/EiJ; TISSUE=Brain;
RA Farber C.R., Corva P.M., Medrano J.F.,
RT "Characterization of quantitative trait loci influencing growth and
adiposity using congenic mouse strains.";
RT Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
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EMBL: AY902331; AAX90616.1; -; Genomic DNA.

SQ SEQUENCE 541 AA; 60645 MW; 0534AF027783BCFC CRC64;
 Query Match 98.3%; Score 2786.5; DB 2; Length 541;
 Best Local Similarity 97.8%; Pred. No. 8.5e-175;
 Matches 530; Conservative 3; Mismatches 2; Indels 7; Gaps 2;
 QY 1 MGSNKSXPKDASQRRSLPEAPENVHAGAGGAPASQTSKPSADGHRGSPAAPAPAAE 60
 DB 1 MGSNKSXPKDASQRRSLPEAPENVHAGAGGAPASQTSKPSADGHRGSPAAPAPAAE 59
 QY 61 PKLFGFNSDPTVTSPPRAGPLAGGVTTFVALVYESTETDLSFKKGERLQIVNNT--- 117
 DB 60 PKLFGFNSDPTVTSPPRAGPLAGGVTTFVALVYESTETDLSFKKGERLQIVNNTKV 119
 QY 118 ---BGDWMLAHSLSTGQTGYIPSNVAPSDSIQAEEMVFGKITRRESRLILNENPRGT 174
 DB 120 DVREGDWMLAHSLSTGQTGYIPSNVAPSDSIQAEEMVFGKITRRESRLILNENPRGT 179
 QY 175 FLVRESSTKAYCYCLSVDPFNAGLVNKHVKIRKLDGSGFYTSRTGFNSLQOLVAYYS 234
 DB 180 FLVRESSTKAYCYCLSVDPFNAGLVNKHVKIRKLDGSGFYTSRTGFNSLQOLVAYYS 239
 QY 235 KHAAGLCHRLTTVCPPTSQPTQGLAKDAMEIPRESLRLEVKLGGCGFGEVMWGTVNGTTR 294
 DB 240 KHAAGLCHRLTTVCPPTSQPTQGLAKDAMEIPRESLRLEVKLGGCGFGEVMWGTVNGTTR 299
 QY 295 VAITLKRGTVSPFAFLQEAQVMKKLRHEKLVQVAVVSEBPIYIVTEYMSKSLDPLK 354
 DB 300 VAITLKRGTVSPFAFLQEAQVMKKLRHEKLVQVAVVSEBPIYIVTEYMSKSLDPLK 359
 QY 355 GGTGKTYRLPOLVMAAQIASGMAVYEMNVYHDLRAANILNGNLYCKVADRLAALI 414
 DB 360 GGTGKTYRLPOLVMAAQIASGMAVYEMNVYHDLRAANILNGNLYCKVADRLAALI 419
 QY 415 EDNEYTAQAGKFPKMTAPPAALYGRFTIKSDVMSFGILLTELTTKGRVVPYGVNREV 474
 DB 420 EDNEYTAQAGKFPKMTAPPAALYGRFTIKSDVMSFGILLTELTTKGRVVPYGVNREV 479
 QY 475 LDQYRGYRMPCEPCPSLHDLMCQCRKKEPEERPFTEYLQAFLEDYFTSTEPYQGE 534
 DB 480 LDQYRGYRMPCEPCPSLHDLMCQCRKKEPEERPFTEYLQAFLEDYFTSTEPYQGE 539
 QY 535 NT 536
 DB 540 NT 541
 RESULT 5
 Q3UKD6_MOUSE PRELIMINARY; PRT; 535 AA.
 ID Q3UKD6_MOUSE
 AC Q3UKD6;
 DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
 DT 11-OCT-2005, sequence version 1.
 DT 07-FEB-2006, entry version 5.
 DE 12 days pregnant adult female placenta cDNA, RIKEN full-length
 DE enriched library, clone:153027F01 product:Kous sarcoma oncogene, full
 DE insert sequence.
 GN Name=SRC;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Muridae; Murinae; Mus.
 OC Mammalia; Eutheria; Muridae; Murinae; Mus.
 OC NCBI_Taxid=10090;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Methods Enzymol. 303:19-44(1999).
 RP NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Placenta;
 RP STRAIN=C57BL/6J; TISSUE=Placenta;

RX PubMed=16141072; DOI=10.1126/science.1112014;
 RA Carninci P., Kaasawa T., Katayama S., Gough J., Fritch M.C., Maeda N.,
 RA Oyama R., Kavaai T., Lenthart B., Wells C., Kodaira R., Shimokawa K.,
 RA Bajic V.B., Brenner S.B., Batalov S., Forrest A.R., Zavolan M.,
 RA Davis M.J., Wilming L.G., Aldred S., Allen J.E.,
 RA Amesni-Imbriato A., Apweiler R., Attalaya R.N., Bailey T.L.,
 RA Banerji M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
 RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
 RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
 RA di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
 RA Fletcher C.F., Fukushima T., Furumasa M., Fukui S., Gariboldi M.,
 RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
 RA Guetlich S., Harbers M., Hayashi Y., Henich T.K., Hirokawa N.,
 RA Hill D., Hummelbeck L., Iacono M., Ikeo K., Ijima A., Itoh K.,
 RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
 RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kumarfeld S.K.,
 RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
 RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
 RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
 RA Motaghi-Tabar S., Mulder N., Nakano N., Nakachi H., Ng P.,
 RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
 RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavoni G., Pesole G.,
 RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
 RA Roost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
 RA Schoenbach C., Setiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
 RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
 RA Sperling S., Stupka E., Sugita K., Sultana R., Takenaka Y., Taki K.,
 RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tejner J., Teichmann S.A.,
 RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yeai K.,
 RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide M., Bult C.,
 RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
 RA Walsted C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
 RA Fukuwa S., Kanamori-Katayama M., Suzuki M., Aoki J., Araiawa T.,
 RA Iida Y., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
 RA Kawaishima T., Kojima M., Kondo S., Kono H., Nakano K., Ninomiya N.,
 RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
 RA Tagami M., Waki K., Watanabe A., Okamura-Oho Y., Suzuki H., Kawai J.,
 RA Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563(2005).
 [3]
 RP NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Placenta;
 RX PubMed=16141073; DOI=10.1126/science.1112009;
 RG RIKEN Genome Exploration Research Group, and Genome Science Group
 RG (Genome Network Core Team) and the PANTOM Consortium;
 RT "Antisense Transcription in the Mammalian Transcriptome.";
 RL Science 309:1564-1566(2005).
 [4]
 RP NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Placenta;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kaasawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schirini L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Brad D., Brusic V., Chochia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragant T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Giesi C., Godzik A., Gough J.,
 RA Grimmond S., Guetlich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
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 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
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 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sadelain A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Walsted C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wysshaw-Boris A., Yanagisawa M., Yang L., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayashizaki Y.,
 RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,

RA Shitaki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imocani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yamanishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y. ;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
RN [5]
RP NCBI/ENCODE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Placenta;
RC MEDLINE=11085660; PubMed=11217851; DOI=10.1038/35055500;
RX Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gotohori T., Bono H., Kanakawa T., Saito R.,
RA Kadota K., Matsuda Y., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
RA Knehl P., Lewis S., Maternu Y., Nifield I., Peesle G., Quackenbush J.,
RA Schirral L.M., Staudt P., Suzuki R., Tomita M., Wagner L., Mashio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldaralli R., Barb G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bulc C., Fletcher C., Fujita M., Gariboldi M.,
RA Guelinich S., Hill D., Hofman M., Hume D.A., Kamita M., Lee N.H.,
RA Lyons P., Marchionni L., Maehina J., Mazzarelli J., Mommaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Haegawa Y., Kawaji H., Kontouki S.,
RA Hayashizaki Y. ;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [6]
RP NCBI/ENCODE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Placenta;
RC MEDLINE=20489374; PubMed=11042159; DOI=10.1101/gr.145100;
RX Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y. ;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:11617-1630(2000).
RN [7]
RP NCBI/ENCODE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Placenta;
RC MEDLINE=20530913; PubMed=11076661; DOI=10.1101/gr.152600;
RX Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki K., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kikunaga T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujisake S., Inoue K., Togawa Y., Izawa M., Ohara E., Matsubuchi M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsumura S., Kawai J.,
RA Okazaki Y., Muramatsu T., Inoue Y., Kira A., Hayashizaki Y. ;
RT "PIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multiplex capillary sequencer.";
RL Genome Res. 10:11757-1771(2000).
RN [8]
RP NCBI/ENCODE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Placenta;
RC STRAIN=C57BL/6J; TISSUE=Placenta;
RX Horii F., Iida J., Imamura K., Imocani K., Itoh M., Kanagawa S.,
RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Nimomiya N.,
RA Nishiyori H., Nomura K., Ono M., Sakazume N., Sano H., Sasaki D.,
RA Shibata K., Shitaki T., Tagami M., Tagami Y., Waki K., Watanabe A.,
RA Muramatsu M., Hayashizaki Y. ;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC
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CC Distributed under the Creative Commons Attribution-NonDerivs license
CC
CC
CC EMBL, AK146056, BA62865.1, -, mRNA.
CC
CC MGI, MGI:98397, Src.
CC
CC DR GO, GO:000515, F:protein binding, IPI.
CC
CC DR GO, GO:0004674, F:protein serine/threonine kinase activity, RCA.

ID	Q9J3J10_RAT	PREDIMINARY	PRT	542 AA
DR	GO: 00004713; F:protein-tyrosine kinase activity; IMP.			
DR	GO: 00006468; P:protein amino acid phosphorylation; IDA.			
DR	InterPro; IPR000719; Prot_Kinase.			
DR	InterPro; IPR002290; Ser_thr_kinase.			
DR	InterPro; IPR000980; SH2.			
DR	InterPro; IPR001452; SH3.			
DR	InterPro; IPR001245; Tyr_kinase.			
DR	InterPro; IPR008266; Tyr_kinase_AS.			
DR	Pfam; PF07714; Kinase_Tyr; 1.			
DR	Pfam; PF00017; SH2; 1.			
DR	Pfam; PF00018; SH3_1; 1.			
DR	PRINTS; PR00401; SH2DOMAIN.			
DR	PRINTS; PR00452; SH3DOMAIN.			
DR	PRINTS; PR00109; TYRKINASE.			
DR	ProDom; PD000001; Prot_kinase; 1.			
DR	ProDom; PD000093; SH2; 1.			
DR	ProDom; PD000066; SH3; 1.			
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DR	SMART; SM00326; SH3; 1.			
DR	SMART; SM00219; Tyrc; 1.			
DR	PROSITE; PS00107; PROTEIN KINASE ATP; 1.			
DR	PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.			
DR	PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.			
DR	PROSITE; PS50001; SH2; 1.			
DR	PROSITE; PS50002; SH3; 1.			
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Query Match	98.2%; Score 2782.5; DB 2; Length 535;			
Best Local Similarity	98.3%; Pred. No. 1.5e-174;			
Matches 527; Conservative	3; Mismatches 5; Indels 1; Gaps 1			
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DB	60 PKLFGGRFXKLDVTVSPQAPXLAGVTTFAVLYYESSTETFDLSPKKEERLIQVNNTEGD	119		
QY	121 WMLHSLSTGQGYIIPSNVYVAPSDSIQAEVYFGKITRSEERLLLNANPRGTFVRES	180		
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QY	181 ETTGAYCLVSPFDNAKGLNVKXIKIKLDSGFFYITSRTQFNSLQQLVAYYSKHADGL	240		
DB	180 ETTGAYCLVSPFDNAKGLNVKXIKIKLDSGFFYITSRTQFNSLQQLVAYYSKHADGL	239		
QY	241 CHRLTTVCPSKPTQGLAKDAWEIPRESLREVKLGCGCGEYVMGVMGNSTTRAIKTL	300		
DB	240 CHRLTTVCPSKPTQGLAKDAWEIPRESLREVKLGCGCGEYVMGVMGNSTTRAIKTL	299		
QY	301 KPGTMSPEAFLOEAQVKKLRHEKLVLYAVVSEEPYIVTEYNSKSLDPLKGETGKY	360		
DB	300 KPGTMSPEAFLOEAQVKKLRHEKLVLYAVVSEEPYIVTEYNSKSLDPLKGETGKY	359		
QY	361 LRLPOLYDMAAQLISGAAYYERNNYVYRDLRAANIIVGENIYCVADPGLARLIDENET	420		
DB	360 LRLPOLYDMAAQLISGAAYYERNNYVYRDLRAANIIVGENIYCVADPGLARLIDENET	419		
QY	421 ARQAKAPKIKMTAPAEALYGRFTTKSDVMSFGILLTETLTGKRVYDGMVREVLDOVER	480		
DB	420 ARQAKAPKIKMTAPAEALYGRFTTKSDVMSFGILLTETLTGKRVYDGMVREVLDOVER	479		
QY	481 GYRMPCEPCEPESLHIDMCQWRKEPERPTFEYLQFLBEDYFTSTEPQYQGENL	536		
DB	480 GYRMPCEPCEPESLHIDMCQWRKEPERPTFEYLQFLBEDYFTSTEPQYQGENL	535		
RESULT 6				
Q9J3J10_RAT	PREDIMINARY; PRT; 542 AA.			
AC 09J3J10;				
AT 01-OCT-2000, integrated into UniProtKB/TrEMBL.				

CC	-1 SIMILARITY: Contains 1 SH3 domain.
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC	Distributed under the Creative Commons Attribution-NonCommercial License
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DR	EMBL; M17031; AAAA0135.1; -, mRNA.
DR	PIR; A43610; A43610.
DR	HSSP; P12931; 1A09.
DR	SMR; P05480; 85-540.
DR	InAct; P05480; -.
DR	Ensembl; ENSMUSG00000027646; Mus musculus.
DR	MGI; MGI:98397; Src.
DR	GO; GO:0005515; F:protein binding; IPI.
DR	GO; GO:0004713; F:protein-tyrosine kinase activity; IMP.
DR	GO; GO:0006468; F:protein amino acid phosphorylation; IDA.
DR	InterPro; IPR00719; Prot_kinase.
DR	InterPro; IPR002290; Ser_thr_kinase.
DR	InterPro; IPR000980; SH2.
DR	InterPro; IPR001452; SH3.
DR	InterPro; IPR001245; Tyr_kinase.
DR	InterPro; IPR008266; Tyr_kinase_AS.
DR	Pfam; PF07714; Kinase_Tyr_1.
DR	Pfam; PF00017; SH2_1.
DR	Pfam; PF00018; SH3_1; 1.
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DR	PRINTS; PR00452; SH3DOMAIN.
DR	PRINTS; PR00109; TYRKINASE.
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DR	Produm; PD000066; SH3_1.
DR	SMART; SMO0252; SH2_1.
DR	SMART; SMO0326; SH3_1.
DR	SMART; SMO0219; TyKc_1.
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
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DR	PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR	PROSITE; PS50001; SH2_1.
DR	PROSITE; PS50002; SH3_1.
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KW	phosphorylation; proto-oncogene; SH2 domain; SH3 domain; Transferase;
KW	Tyrosine-protein kinase.
FT	CHAIN 1 540
FT	INIT MET 0
FT	By similarity.
FT	Neuronal proto-oncogene tyrosine-protein
FT	kinase Src.
FT	/FtId=PRO_0000088142.
FT	SH3.
FT	DOMAIN 82 149
FT	SH2.
FT	PROTEIN KINASE.
FT	ATP (By similarity).
FT	Proton acceptor (By similarity).
FT	ATP (By similarity).
FT	Phosphotyrosine (by autocatalysis) (By
FT	similarity).
FT	Phosphotyrosine (by CSK) (By similarity).
FT	N-myristoyl glycine (By similarity).
FT	MOD_RES 534 534
FT	LIPID 1 1
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Query Match	97.9%; Score 2773.5; DB 1; Length 540;
Best Local Similarity	97.6%; Pred. No. 6e-174;
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DB	1 GSNSKPPDAQRRRSLPEAEVNHAGGAAPPASQTPSPKPSADGHRGPSAAFAPAAEP 59
QY	62 KLFGGNSSDTVTSPORAGPLAGVTTTVALVDYSRTETDLSPFKKGRLQIVNNT---- 117
DB	60 KLFGGNSSDTVTSPORAGLAGGVTTTVALVDYSRTETDLSPFKKGRLQIVNNTTRAYD 119
QY	118 --EGDWMLAHLSLSTGCQTGYISNVVAPEDSIQAEWRYGKTKRRSERLLLAENPRGT 175
DB	120 VREDDWMVAHLSLSTGCQTGYISNVVAPEDSIQAEWRYGKTKRRSERLLLAENPRGT 179

Oy	176	LVARESETTGACVCLSYSDPDNAKGLNVHRYKRLKLDGCGFYTSRTQPNSLQQLVAYYSK	235
Db	180	LVARESETTGACVCLSYSDPDNAKGLNVHRYKRLKLDGCGFYTSRTQPNSLQQLVAYYSK	239
Oy	236	HADGLCHRLTYTCPTSPQTOGLADDAEIPRESIRLEVLKKGCGCFGBVMGWTNGTTRV	239
Db	240	HADGLCHRLTYTCPTSPQTOGLADDAEIPRESIRLEVLKKGCGCFGBVMGWTNGTTRV	299
Oy	296	AITKLKPTMSPEAFLOEAQVMKKLRHEKLVQLVAVNSEBPIYYVTEYMSKGLLDPLKG	355
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Oy	356	ETCKYLRPLQVLDMAAQIASGMAVYERNNVYHRDLRANILVGENIVCKVADPEGLALIE	415
Db	360	ETCKYLRPLQVLDMAAQIASGMAVYERNNVYHRDLRANILVGENIVCKVADPEGLALIE	419
Oy	416	DNEYTARQAGAKPFIKYTAPEALVGRFTIKSDVMSFGILLTELTKGRVPPYPGVNVREVL	475
Db	420	DNEYTARQAGAKPFIKYTAPEALVGRFTIKSDVMSFGILLTELTKGRVPPYPGVNVREVL	479
Oy	476	DOVERGYRMPCEPCESHLDMCCOMKKEPERPTEFYLAFLIEDYFTSTEPQYQGEN	535
Db	480	DOVERGYRMPCEPCESHLDMCCOMKKEPERPTEFYLAFLIEDYFTSTEPQYQGEN	539
Oy	536	L 536	
Db	540	L 540	
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ID	SRC_RAT	STANDARD;	PRT; 535 AA.
AC	O9WU9;		
DT	30-MAY-2000,	integrated into UniProtKB/Swiss-Prot.	
DT	30-MAY-2000,	sequence version 2.	
DT	07-MAR-2006,	entry version 46.	
DE	Protein- <i>oncogene tyrosine-protein kinase Src</i> (BC 2.7.1.112) (p60-Src)		
GN	(c-Src) (p60C-src).		
DN	Name=Src;		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;		
OC	Muridae; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE [mRNA].		
RC	STRAIN=Sprague-Dawley; TISSUE=Testis;		
RA	Stockend J.D., Al-Khalili O., Spier B.J., Batson D.C.;		
RT	"Rattus norvegicus proto-oncogene encoding tyrosine-protein kinase		
RT	p60C-src."		
RL	Submitted (PEB-1999) to the EMBL/Genbank/DBJ databases.		
CC	-1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein		
CC	tyrosine phosphate.		
CC	-1- P-TM: Phosphorylated on Tyr-529 by c-Src kinase (CSK). The		
CC	phosphorylated form is termed p60C-src. The phosphorylated tail		
CC	interacts with the SH2 domain thereby repressing kinase activity		
CC	(By similarity).		
CC	-1- SIMILARITY: Belongs to the Tyr protein kinase family. SRC		
CC	subfamily.		
CC	-1- SIMILARITY: Contains 1 SH2 domain.		
CC	-1- SIMILARITY: Contains 1 SH3 domain.		
CC	-----		
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms		
CC	Distributed under the Creative Commons Attribution-NoDerivs license		
CC	-----		
DR	EMBL; AF130457; AAD24180.1; -; mRNA.		
DR	HSSP; P12931; 1A09.		
DR	SMR; O9WU9; 86-535.		
DR	RGD; 620795; Src.		
DR	InterPro; IPR000719; Prot_kinase.		
DR	InterPro; IPR002290; Ser_thr_kinase.		
DR	InterPro; IPR000980; SH2.		

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DR InterPro: IPR001452; SH3.
DR InterPro: IPR001245; Tyr_kinase.
DR InterPro: IPR008266; Tyr_kinase_AS.
DR Pfam: PF07714; Pkinase_Tyr; 1.
DR Pfam: PF00017; SH2; 1.
DR Pfam: PF00018; SH3; 1.
DR PRINTS: PR00401; SH2DOMAIN.
DR PRINTS: PR00452; SH3DOMAIN.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Prot_kinase; 1.
DR ProDom: PD000093; SH2; 1.
DR ProDom: PD000066; SH3; 1.
DR SMART: SM00252; SH2; 1.
DR SMART: SM00326; SH3; 1.
DR SMART: SM00219; TyKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS50001; SH2; 1.
DR PROSITE: PS50002; SH3; 1.
KW ATP-binding; Kinase; Lipoprotein; Myristate; Nucleotide-binding;
KW Phosphorylation; Proto-oncogene; SH2 domain; SH3 domain; Transferase;
KW Tyrosine-protein kinase.
FT CHAIN 1 535
FT INIT MET 0
FT LIPID 1
FT MOD_RES 529
FT RES 1
FT SEQ 535 AA; 59947 MW; AD083DD2357890EC CRC64;
SQ
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Best Local Similarity 98.3%; Pred. No. 8.7e-174;
Matches 527; Conservative 4; Mismatches 3; Indels 2; Gaps 2;
QY 2 GSNKSRPKDASQRRRSLEPBNVHGAGCGAPASQTSKPSADGHRGPSAAR-PAAE 60
DB 1 GSNKSRPKDASQRRRSLEPBNVHGAGCGAPASQTSKPSADGHRGPSAAR-PAAE 59
QY 61 PKLFGGNSSDVTSPPRAGPLAGGVTFVALVDYESTRTDLSFKKGERLQIVNTEGD 120
DB 60 PKLFGGNSSDVTSPPRAGPLAGGVTFVALVDYESTRTDLSFKKGERLQIVNTEGD 119
QY 121 WMLAHSISTGQTGYIPSNVYAPSDSIQAEEMVFGKIRRESERLLNAENPRGFLVRES 180
DB 120 WMLAHSISTGQTGYIPSNVYAPSDSIQAEEMVFGKIRRESERLLNAENPRGFLVRES 179
QY 181 ETTKGAACLSVSPDNAGKLVNKKYTKRKLDGSGFYITTSRTQNSLQQLVAYSKADGL 240
DB 180 ETTKGAACLSVSPDNAGKLVNKKYTKRKLDGSGFYITTSRTQNSLQQLVAYSKADGL 239
QY 241 CHRLTYVCPSTKPTQGLADAMEIPRESLRLEVKLGOGGCGEYMGTMGTTRVALTKL 300
DB 240 CHRLTYVCPSTKPTQGLADAMEIPRESLRLEVKLGOGGCGEYMGTMGTTRVALTKL 299
QY 301 KPGTMSBEAFLOEAQVWKKLRHEKLVQLYAVVSEEPYIYTEVNSKSLDPLKGETGKY 360
DB 300 KPGTMSBEAFLOEAQVWKKLRHEKLVQLYAVVSEEPYIYTEVNSKSLDPLKGETGKY 359
QY 361 LRLPOLVDMAAQIASGAAYVERMYVYRDLRAANIILVGENLVCKVADFGIARLIEDNEYT 420
DB 360 LRLPOLVDMAAQIASGAAYVERMYVYRDLRAANIILVGENLVCKVADFGIARLIEDNEYT 419
QY 421 ARQGAKEPIKMTAPEALYGRFTIKSDVWSPGILLTELTTRKGRPYDGMVNRVTLDOVER 480
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DB 420 ARQGAKEPIKMTAPEALYGRFTIKSDVWSPGILLTELTTRKGRPYDGMVNRVTLDOVER 479
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DB 480 GYRMPCEPCEPESGHLDMCCQWRKEPERPTEFLQAFLEDFYFSTEPQYQGNL 535
RESULT 9
ID Q450J2_RAT PRELIMINARY; PRT; 523 AA.
AC Q450J2;
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Tyrosine protein kinase c-src (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SHR, and WKY.
RA Jackson E.K., Zhu C.;
RT "Genetic Similarity Between Spontaneously Hypertensive Rats and
RT Wistar-Kyoto Rats in the Coding Regions of Signal Transduction
RT Proteins."
RT Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC tyrosine phosphate.
CC -1- SIMILARITY: Contains 1 SH3 domain.
CC -----
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CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
DR EMBL: DQ120510; AAC23849.1; -; mRNA.
DR EMBL: DQ120509; AAC23848.1; -; mRNA.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0000166; F:nucleotide binding; IEA.
DR GO: GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0007242; P:intracellular signaling cascade; IEA.
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR007019; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR InterPro: IPR000980; SH2.
DR InterPro: IPR001452; SH3.
DR InterPro: IPR001245; Tyr_kinase.
DR InterPro: IPR008266; Tyr_kinase_AS.
DR Pfam: PF07714; Pkinase_Tyr; 1.
DR Pfam: PF00017; SH2; 1.
DR Pfam: PF00018; SH3; 1.
DR PRINTS: PR00401; SH2DOMAIN.
DR PRINTS: PR00452; SH3DOMAIN.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Prot_kinase; 1.
DR ProDom: PD000093; SH2; 1.
DR ProDom: PD000066; SH3; 1.
DR SMART: SM00252; SH2; 1.
DR SMART: SM00326; SH3; 1.
DR SMART: SM00219; TyKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS50001; SH2; 1.
DR PROSITE: PS50002; SH3; 1.
KW ATP-binding; Kinase; Nucleotide-binding; SH3 domain; Transferase;
KW Tyrosine-protein kinase.
FT NON_TER 1
FT NON_TER 523
FT SEQ 523 AA; 58672 MW; 8D5DC2644FDF2FC CRC64;
SQ
Query Match 95.5%; Score 2706; DB 2; Length 523;
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Best Local Similarity 98.3%; Pred. No.1,6e-169;
Matches 515; Conservative 4; Mismatches 3; Indels 2; Gaps 2;

QY 7 KPRDASQRRRLSPLEPAENVHAGGAPASQTPSKPXSADCHRPASAFA-PAAAEPLRG 65
DB 1 KPRDASQRRRLSPLEPAENVHAGGAPASQTPSKPXSADCHRPASAFA-PAAAEPLRG 59
QY 66 GFFSSPTVTSPOBAGPLAGVTFVALDYESTRTEDLSFKKBERQIVNTGDMWLAH 125
DB 60 GFFSSPTVTSPOBAGPLAGVTFVALDYESTRTEDLSFKKBERQIVNTGDMWLAH 119
QY 126 SLSTGQGYIPSNVYAPSDSIQAEEMVFKITRRESERLLNANPRGTFLVRESSTKG 185
DB 120 SLSTGQGYIPSNVYAPSDSIQAEEMVFKITRRESERLLNANPRGTFLVRESSTKG 179
QY 186 AYCLASVSDPDNAGLVNKHKKIKLDSGCFYITSRQFNSLQOLVAYYSKADGLCHRLT 245
DB 180 AYCLASVSDPDNAGLVNKHKKIKLDSGCFYITSRQFNSLQOLVAYYSKADGLCHRLT 239
QY 246 TVCPSTKPTQGLAKDAMEIPRESRLLEVYLGQCGFGEVWMTNGTTRVAIKTLKPGTM 305
DB 240 TVCPSTKPTQGLAKDAMEIPRESRLLEVYLGQCGFGEVWMTNGTTRVAIKTLKPGTM 299
QY 306 SPEAFLOEAQVMKQLRHEKLVQLYAVVSEBPIYVTEYMSKSLDLFLKGETGKYLRLPQ 365
DB 300 SPEAFLOEAQVMKQLRHEKLVQLYAVVSEBPIYVTEYMSKSLDLFLKGETGKYLRLPQ 359
QY 366 LVDMAAQISGMAVYERNAVYHDLPAANLVGENLVCKADGLARLIEDNYTARQGA 425
DB 360 LVDMAAQISGMAVYERNAVYHDLPAANLVGENLVCKADGLARLIEDNYTARQGA 419
QY 426 KFPKMTABEALYGRFTYKSDVMSFGILLTELTTTGKRVYPPGMVREVLDOYERGRMP 485
DB 420 KFPKMTABEALYGRFTYKSDVMSFGILLTELTTTGKRVYPPGMVREVLDOYERGRMP 479
QY 486 CEPECESLHDLWCQCRKEPERPTEFYLAFLDYFTSTEPQ 529
DB 480 CEPECESLHDLWCQCRKEPERPTEFYLAFLDYFTSTEPQ 523

RESULT 10
SRC CHICK
ID _SRC CHICK STANDARD; PRT; 532 AA.
AC P00523; Q90992; Q90993; Q91343; Q91345; Q92013; Q98915;
AD 21-JUL-1986; Integrated into UniProtKB/Swiss-Prot.
DT 15-JUL-1999; sequence version 3.
DT 07-MAR-2006; entry version 78.
DE Proto-oncogene tyrosine-protein kinase Src (BC 2.7.1.112) (p60-Src)
DE (c-src) (pp60c-src).
GN Name=SRC;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORM 1).
RX MEDLINE=83155664; PubMed=6239580; DOI=10.1016/0092-8674(83)90073-9;
RA Takeya T., Hanafusa H.;
RT "Structure and sequence of the cellular gene homologous to the RSV src
RT gene and the mechanism for generating the transforming virus.",
RL Cell 32:881-890(1983).
RN [2]
RP ERRATUM, AND SEQUENCE REVISION TO 525.
RA Takeya T., Hanafusa H.;
RL Cell 34:319-319(1983).
RN [3]
RP NUCLEOTIDE SEQUENCE (ISOFORM 2).
RX TISSUE=pectoralis muscle; PubMed=2115117;
RA Doral T., Wang L.-H.;
RT "An alternative non-cytosine protein kinase product of the c-src gene
RT in chicken skeletal muscle.",

RL Mol. Cell. Biol. 10:4068-4079(1990).
RN [4]
RP NUCLEOTIDE SEQUENCE (ISOFORM 1), AND PHOSPHORYLATION SITES TYR-415 AND
RP TYR-435.
RX MEDLINE=97008971; PubMed=8856081;
RA Weiland A., Neubauer G., Courtneidge S.A., Mann M., Wierenga R.K.,
RA Superti-Furga G.;
RT "The purification and characterization of the catalytic domain of Src
RT expressed in Schistosoma chromocytes pombe. Comparison of unphosphorylated
RT and tyrosine phosphorylated species.",
RL Eur. J. Biochem. 240:756-764(1996).
RN [5]
RP NUCLEOTIDE SEQUENCE OF 1-6.
RX MEDLINE=83059861; PubMed=6292480;
RA Takeya T., Hanafusa H.;
RT "DNA sequence of the viral and cellular src gene of chickens. II.
RT Comparison of the src genes of two strains of Avian sarcoma virus and
RT of the cellular homolog.",
RL J. Virol. 44:12-18(1982).
RN [6]
RP NUCLEOTIDE SEQUENCE OF 1-18 AND 484-533 (ISOFORM 1).
RX MEDLINE=91304409; PubMed=1712905;
RA Doral T., Levy J.B., Kang L., Brugge J.S., Wang L.-H.;
RT "Analysis of cDNAs of the proto-oncogene c-src: heterogeneity in 5'
RT exon and possible mechanism for the genesis of the 3' end of v-src.",
RL Mol. Cell. Biol. 11:4165-4176(1991).
RN [7]
RP ATP-BINDING SITE.
RX MEDLINE=84270751; PubMed=6431300;
RA Kamp M.P., Taylor S.S., Setton B.M.;
RT "Direct evidence that oncogenic tyrosine kinases and cyclic AMP-
RT dependent protein kinase have homologous ATP-binding sites.",
RL Nature 310:589-592(1984).
RN [8]
RP PHOSPHORYLATION.
RX MEDLINE=86028181; PubMed=2996780; DOI=10.1016/0092-8674(85)90281-8;
RA Gould K.L., Woodgett J.R., Cooper J.A., Buss J.E., Shalloway D.,
RA Hunter T.;
RT "Protein kinase C phosphorylates pp60src at a novel site.",
RL Cell 42:849-857(1985).
RN [9]
RP PHOSPHORYLATION SITE TYR-415.
RX MEDLINE=82082387; PubMed=6273838;
RA Smart J.E., Oppermann H., Cernilofsky A.P., Purchio A.F.,
RA Erikson R.L., Bishop J.M.;
RT "Characterization of sites for tyrosine phosphorylation in the
RT transforming protein of Rous sarcoma virus (pp60v-src) and its normal
RT cellular homologue (pp60c-src).",
RL Proc. Natl. Acad. Sci. U.S.A. 78:6013-6017(1981).
RN [10]
RP PHOSPHORYLATION SITE TYR-526.
RX MEDLINE=86151652; PubMed=2420005;
RA Cooper J.A., Gould K.L., Cartwright C.A., Hunter T.;
RT "Tyrosine 526 is phosphorylated in pp60c-src: implications for regulation.",
RL Science 231:1431-1434(1986).
RN [11]
RP PHOSPHORYLATION SITES THR-33; THR-45 AND SER-71.
RX MEDLINE=89249341; PubMed=2470512; DOI=10.1016/0092-8674(89)90791-5;
RA Shenoy S., Choi J.K., Bagrodia S., Copeland T.D., Maller J.L.,
RA Shalloway D.;
RT "Purified maturation promoting factor phosphorylates pp60c-src at the
RT sites phosphorylated during fibroblast mitosis.",
RL Cell 57:763-774(1989).
RN [12]
RP X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 82-532.
RX MEDLINE=98070614; PubMed=9405157; DOI=10.1006/jmbi.1997.1426;
RA Williams J.C., Weiland A., Gonfloni S., Thompson A.,
RA Courtneidge S.A., Superti-Furga G., Wierenga R.K.;
RT "The 2.35 Å crystal structure of the inactivated form of chicken Src:
RT a dynamic molecule with multiple regulatory interactions.",
RL J. Mol. Biol. 274:757-775(1997).
RN [13]
RP STRUCTURE BY NMR OF 80-139.

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RX MEDLINE:93279385; PubMed:850463; DOI=10.1016/0014-5793(93)01538-B;
RA Yu H., Rosen M.K., Schreiber S.L.;
RT 1H and 15N assignments and secondary structure of the Src SH3
RT domain.";
RL FEBS Lett. 324:87-92(1993) .
CC
CC -1- FUNCTION: Unknown.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC tyrosine phosphate.
CC -1- ENZYME REGULATION: Becomes activated when its major tyrosine
CC phosphorylation site is not phosphorylated. It can also be
CC activated by point mutations as well as by truncations at the C-
CC terminal end or by other mutations.
CC -1- SUBUNIT: p60c-src forms a complex with polyoma virus middle T
CC antigen.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named Isoforms=2;
CC Name=1;
CC IsoId=P00523-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P00523-2; Sequence=VSP_011844, VSP_011845;
CC
CC Note=Membrane-bound;
CC -1- TISSUE SPECIFICITY: Expressed to high levels, and with a high
CC degree of kinase activity, in certain fully differentiated cells
CC such as neurons, platelets and macrophages. Isoform 1 is widely
CC expressed. Isoform 2 is expressed only in the muscle.
CC -1- PTM: Phosphorylated on Tyr-526 by c-Src kinase (CSK). The
CC phosphorylated form is termed p60c-src. The phosphorylated tail
CC interacts with the SH2 domain thereby repressing kinase activity
CC (by similarity).
CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
CC subfamily.
CC -1- SIMILARITY: Contains 1 SH2 domain.
CC -1- SIMILARITY: Contains 1 SH3 domain.
CC
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC EMBL; V00402; CAA23696.1; -; Genomic DNA.
DR EMBL; J00908; -; NOT ANNOTATED CDS; Genomic DNA.
DR EMBL; M57290; AAA49078.1; -; mRNA.
DR EMBL; S43604; AAD13831.1; -; mRNA.
DR EMBL; S43616; AAD13835.1; -; mRNA.
DR EMBL; S43587; AAD13830.1; -; mRNA.
DR EMBL; S43609; AAD13832.1; -; mRNA.
DR EMBL; S43614; AAD13834.1; -; mRNA.
DR EMBL; S43579; AAB19353.2; -; mRNA.
DR PIR; A00630; TVCHS.
DR PDB; 1F1W; X-ray; A=144-246.
DR PDB; 1F2F; X-ray; A=144-246.
DR PDB; 1N1Q; NMR; C=80-139.
DR PDB; 1NLP; NMR; C=80-139.
DR PDB; 1P13; X-ray; A/B=144-245.
DR PDB; 1PRL; NMR; C=76-139.
DR PDB; 1PRM; NMR; C=76-139.
DR PDB; 1RLQ; NMR; C=76-139.
DR PDB; 1SRL; NMR; @=76-139.
DR PDB; 1SRM; NMR; @=76-139.
DR PDB; 2PTK; X-ray; @=-.
DR Ensembl; ENSGALG00000003855; Gallus gallus.
DR LinkHub; P00523; -.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_fmr_kinase.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001452; SH3.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR Pfam; PF07714; Pkinase_Tyr; 1.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00019; SH3; 1.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRINTS; PR00452; SH3DOMAIN.
DR PRINTS; PR00109; TYRKINASE.

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DR	ProdDom: PD0000093	SH2; 1			
DR	ProdDom: PD0000066	SH3; 1			
DR	SMART; SMO0252	SH2; 1			
DR	SMART; SMO0326	SH3; 1			
DR	SMART; SMO0219	TyKc; 1			
DR	PROSITE; PS00107	PROTEIN KINASE ATP; 1			
DR	PROSITE; PS00101	PROTEIN KINASE DOM; 1			
DR	PROSITE; PS00109	PROTEIN_KINASE_TYR; 1			
DR	PROSITE; PS50001	SH2; 1			
DR	PROSITE; PS50002	SH3; 1			
KW	3D-structure; Alternative splicing; ATP-binding; Kinase; Lipoprotein;				
KW	Myristate; Nucleotide-binding; Phosphorylation; Proto-oncogene;				
KW	SH3 domain; SH3 domain; Transferase; Tyrosine-protein kinase.				
FT	INIT MET	0			
FT	CHAIN	1	532		
FT					
FT	DOMAIN	80	141		
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FT	NP BIND	272	280		
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DB	1 GSSSKSKRDEBQRKRSLEPPSTH---HGEPAPQTNKTKAAPTHHTIPRSFQVATPE	57			
QY	62 KLFQGFNSDVTVTSPOBAGPLAGGVTTVALVDYESTETDLSFKKGERLQIVNTEGDW	121			
DB	58 KLFQGFNTSDVTVTSPOBAGALAGGVTTVALVDYESTETDLSFKKGERLQIVNTEGDW	117			
QY	122 WLASLSLTGCGYIPSNVYAPSDSIQAEWYFGKITRRESRLLNMPNPGTFLVSE	181			
DB	118 WLASLTTGCGYIPSNVYAPSDSIQAEWYFGKITRRESRLLNMPNPGTFLVSE	177			
QY	182 TTGAAYCYSVDFPNAGLVNKHVKIRKLDGCGFYITSRTOFNSLQQLVAYYSKADGLC	241			
DB	178 TTGAAYCYSVDFPNAGLVNKHVKIRKLDGCGFYITSRTOFNSLQQLVAYYSKADGLC	237			
QY	242 HRLTTVGPSTKPTQGLAKDAWEIPRESLRLEVLGQCGFCFGEVVMGTNGTTRVAIKTLK	301			
DB	238 HRLTNVGPSTKPTQGLAKDAWEIPRESLRLEVLGQCGFCFGEVVMGTNGTTRVAIKTLK	297			
QY	302 PGTMSPPAFLQDAVMMKKLRHEKLVQLYAVYSEPIYIVTRYMKSGLDPLKKEGTGYL	361			
DB	298 PGTMSPPAFLQDAVMMKKLRHEKLVQLYAVYSEPIYIVTRYMKSGLDPLKKEMGXYL	357			
QY	362 RLPLQVMAAOIASGMAVYERMYVNHDLRAANLIVGENLVCKYADGFLARLIDNEXYA	421			
DB	358 RLPLQVMAAOIASGMAVYERMYVNHDLRAANLIVGENLVCKYADGFLARLIDNEXYA	417			
QY	422 RQGAKEPIKMTAPPAALYGRFTIKSDVMSFGILLTELTTKGRVYVPGVMNREVLDQYERG	481			
DB	418 RQGAKEPIKMTAPPAALYGRFTIKSDVMSFGILLTELTTKGRVYVPGVMNREVLDQYERG	477			
QY	482 YRMCPCEPCESLHDLMCQWRKKEPERPTEFYLQAFLEDYFTSTEPQYQGENU	536			
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DT	30-AUG-2005	sequence version 2.			
DT	07-MAR-2006	entry version 64.			
DE	Tyrosine-protein kinase transforming protein Src (EC 2.7.1.112) (p60-				

DE Src) (v-Src) (pp60v-src).
 GN Name=V-SRC;
 OS Avian sarcoma virus (strain PR257).
 OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
 OC Alpharetrovirus; unclassified Alpharetrovirus.
 OX NCBI_TaxId=11879;
 RN NUCLEOTIDE SEQUENCE (GENOMIC RNA).
 RP MEDLINE=89094972; PubMed=2463376;
 RX Geryk J., Dezelee P., Barnier J.V., Svoboda J., Nehyba J., Karakoz I.,
 RA Rynditch A.V., Yatsula B.A., Calothy G.;
 RT "Transduction of the cellular src gene and 3' adjacent sequences in
 avian sarcoma virus PR257.";
 RL J. Virol. 63:481-492(1989).
 CC [2]
 CC NUCLEOTIDE SEQUENCE (GENOMIC RNA).
 RA Yatsula B.A., Geryk J., Svoboda J., Rynditch A.V., Calothy G.,
 RA Dezelee P.;
 RL Submitted (APR-1992) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: This phosphoprotein, required for both the initiation
 and the maintenance of neoplastic transformation, is a protein
 kinase that catalyzes the phosphorylation of tyrosine residues in
 vitro.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
 tyrosine phosphate.
 CC -1- PTM: The phosphorylated form is termed pp60v-src.
 CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
 subfamily.
 CC -1- SIMILARITY: Contains 1 SH2 domain.
 CC -1- SIMILARITY: Contains 1 SH3 domain.
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NonDerivs License
 CC -----
 CC EMBL; M21526; AAA42583.1; -; Genomic RNA.
 DR EMBL; X51863; CAA36156.1; -; Genomic RNA.
 DR PIR; A30174; TVFVPR.
 DR HSSP; P00523; 2PTK.
 DR SMR; P15054; 83-524.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR008266; Tyr_kinase_AS.
 DR Pfam; PF00017; SH2_1; 1.
 DR Pfam; PF00018; SH3_1; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00453; SH3DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR ProDom; PD000093; SH2_1.
 DR ProDom; PD000066; SH3_1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00219; Tyrc; 1.
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 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS500109; PROTEIN_KINASE_TYR; 1.
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 DR PROSITE; PS50002; SH3; 1.
 DR ATP-binding; Kinase; Lipoprotein; Myristate; Nucleotide-binding;
 KM Oncogene; Phosphorylation; SH2 domain; SH3 domain; Transferase;
 KW Tyrosine-protein kinase.
 FT INIT MET 0
 FT CHAIN 1 586
 FT By similarity.
 FT Tyrosine-protein kinase transforming
 FT protein Src.
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 FT DOMAIN 80 141
 FT DOMAIN 147 244
 FT DOMAIN 266 519
 FT NP_BIND 272 280
 FT ATP (By similarity).

FT ACT SITE 385 385 Proton acceptor (By similarity).
 FT BINDING 294 294 ATP (By similarity).
 FT MOD_RES 415 415 Phosphotyrosine (By autocatalysis) (By
 FT similarity).
 FT LIPID 1 1 N-myristoyl glycine (by host) (By
 FT similarity).
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 DB 118 WLAHSLTTGQGYIRSNVYAPSDSIQAEWYFGKTTRESERLLNPNPRGTFVRESB 177
 QY 182 TTKGAYCLVSDPDNAKGLNVKRYKRLKDGSGFYITSTQFNSLQQLVAYYSKADGIC 241
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 QY 242 HRLTVCPSTKPTQGLADAMEIPRESLRLEVKLGQCGFGEVMGNTGNTRVAIKTLK 301
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 QY 362 RLPLQVDMAAQASGAVYERNNVYHRDRAANILVGENLVCKVDFGLARLIEDNEYTA 421
 DB 358 RLPLQVDMAAQASGAVYERNNVYHRDRAANILVGENLVCKVDFGLARLIEDNEYTA 417
 QY 422 RQGAKEPIKTAPEALYGRFTIKSDVSGILLTELTTKGRVPPYGVNREVLDQVERG 481
 DB 418 RQGAKEPIKTAPEALYGRFTIKSDVSGILLTELTTKGRVPPYGVNREVLDQVERG 477
 QY 482 YMPCPPECPESLHDMCCMKRPEPERTEYLAQFLDYFTSTSP 528
 DB 478 YMPCPPECPESLHDMCCMKRPEPERTEYLAQFLDYFTSTSP 524
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 ID SRC_AVIS5
 AC P14084;
 DT 01-JAN-1990, integrated into UniProtKB/Swiss-Prot.
 DT 30-AUG-2005, sequence version 2.
 DT 07-MAR-2006, entry version 60.
 DE Tyrosine-protein kinase transforming protein Src (BC 2.7.1.112) (p60-
 DE Src) (v-Src) (pp60v-src).
 GN Name=V-SRC;
 OS Avian sarcoma virus (strain S1).
 OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
 OC Alpharetrovirus; unclassified Alpharetrovirus.
 OX NCBI_TaxId=11881;
 RN NUCLEOTIDE SEQUENCE.
 RP MEDLINE=87064539; PubMed=3097513;
 RX Ikawa S., Hagino-Yamagishi K., Kawai S., Yamamoto T., Toyoshima K.;
 RA "Activation of the cellular src gene by transducing retrovirus.";
 RL Mol. Cell. Biol. 6:2420-2428(1986).
 CC -1- FUNCTION: This phosphoprotein, required for both the initiation
 and the maintenance of neoplastic transformation, is a protein
 kinase that catalyzes the phosphorylation of tyrosine residues in
 vitro.

CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
 CC tyrosine phosphate.
 CC -1- PTM: The phosphorylated form is termed ppcov-src.
 CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
 CC subfamily.
 CC -1- SIMILARITY: Contains 1 SH2 domain.
 CC -1- SIMILARITY: Contains 1 SH3 domain.
 CC -----
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 CC -----
 DR PIR: A25375; TVFVS1.
 DR HSP: P00523; 2PTK.
 DR SMR: P14084; 83-524.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR008265; Tyr_kinase.
 DR InterPro: IPR008266; Tyr_kinase_AS.
 DR Pfam: PF07714; Kinase_Tyr; 1.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00018; SH3; 1; 1.
 DR PRINTS: PR00401; SH2DOMAIN.
 DR PRINTS: PR00452; SH3DOMAIN.
 DR PRINTS: PR00109; TYRKINASE.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR ProDom: PD000093; SH2; 1.
 DR ProDom: PD000066; SH3; 1.
 DR SMART: SM00252; SH2; 1.
 DR SMART: SM00326; SH3; 1.
 DR SMART: SM00219; Tyrc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS50001; SH2; 1.
 DR PROSITE: PS50002; SH3; 1.
 DR ATP-binding; Kinase; Lipoprotein; Myristate; Nucleotide-binding;
 KW Oncogene; Phosphorylation; SH2 domain; SH3 domain; Transferase;
 KM Tyrosine-protein kinase.
 FT CHAIN 0 0
 FT INIT MET 1 567
 FT -----
 FT By similarity.
 FT Tyrosine-protein kinase transforming
 FT protein Src.
 FT /FTid=PRO_0000088150.
 FT -----
 FT DOMAIN 80 141
 FT DOMAIN 147 244
 FT DOMAIN 266 519
 FT NP_BIND 272 280
 FT ACT_SITE 385 385
 FT BINDING 294 294
 FT MOD_RES 415 415
 FT -----
 FT LIPID 1 1
 FT SEQUENCE 567 AA; 63501 MW; EA4FC38195A099D CRC64;
 N-myristoyl glycine (by hsc).
 Query Match 92.1%; Score 2609.5; DB 1; Length 567;
 Best Local Similarity 93.7%; Pred. No. 4e-163;
 Matches 494; Conservative 12; Mismatches 18; Indels 3; Gaps 1;
 QY 2 GSNKSRPKDASQRRRLSEPNVHAGAGGAPASQTSKSPASADGHGSPSAAPAAAP 61
 DB 1 GSSKSRPKDQSORRSLSEPDSTH--HGGRPASQTNKKAAPTHRTPSRSGVTATEP 57
 QY 62 KLFGGFNSDPTVSPORAGPPLAGVTFVALYDVESTETDLSFKGGERLQIVNTGDM 121
 DB 58 KLFGGFNTSTVSPQRAAGALAGVTFVALYDVESTETDLSFKGERLQIVNTGDM 117
 QY 122 WLHSLSTGQGYIPSNVYVAPSDSIQAEWYFGKITRRESERLLILNENPRGTFVASE 181
 DB 118 WLHSLTGTQGYIPSNVYVAPSDSIQAEWYFGKITRRESERLLILNENPRGTFVASE 177
 QY 182 TTYGAYCLSYSDPDNAGLVKHKIKKLDGSGFYITSRQFNLSQOLVAYYKHAQGLC 241

DB 178 TTYGAYCLSYSDPDNAGLVKHKIKKLDGSGFYITSRQFNLSQOLVAYYKHAQGLC 237
 QY 242 HRLTTCPTSKPQTQGIKAKAMEIPRESLRLVYLGGCGCEGVMMGTWNGTTTVAITLK 301
 DB 238 HRLTNCPSTSKPQTQGIKAKAMEIPRESLRLVYLGGCGCEGVMMGTWNGTTTVAITLK 297
 QY 302 PGTMSPAPFOEAQVMKLRHEKLVOLYAVVSEPIYIVTEVYNSKSLDPLKGETGKYL 361
 DB 298 PGTMSPAPFOEAQVMKLRHEKLVRLYAVVSEPIYIVTEVYNSKSLDPLKGETGKYL 357
 QY 362 RLPLVDMAQIISGNAVYERMYVHRDLRAANILVGENIVCKYADPGLARLIDNEYTA 421
 DB 358 RLPLVDMAQIISGNAVYERMYVHRDLRAANILVGENIVCKYADPGLARLIDNEYTA 417
 QY 422 RQGAKEPIKWTAPBALYGFITKSDVMSGILITELTTTGRVYPCGVNREVLDOVERG 481
 DB 418 RQGAKEPIKWTAPBALYGFITKSDVMSGILITELTTTGRVYPCGVNREVLDOVERG 477
 QY 482 YRMPCEPECSLHDLMOGCMRKEPERPTFEYLQAFLEDFYFSTEP 528
 DB 478 YRMPCEPECSLHDLMOGCMRKEPERPTFEYLQAFLEDFYFSTEP 524
 RESULT 13
 ID 064817_9RETR PRELIMINARY; PRT; 567 AA.
 AC 064817;
 DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
 DT 01-NOV-1996, sequence version 1.
 DT 07-FEB-2006, entry version 28.
 DE Protein-tyrosine kinase.
 DE Name=src;
 OS Avian sarcoma virus.
 OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
 OC Alpharetrovirus; unclassified Alpharetrovirus.
 OX NCBI_Taxid=11876;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PR2257/16;
 RX MEDLINE=95016532; PubMed=7931166;
 RA Yatsula B.A., Geryk J., Svoboda J., Rynditch A.V., Calochy G.,
 RA Desjeux P.;
 RT "Evolution and origin of virus PR2257, a recent c-src transducing
 RT virus.";
 RL J. Gen. Virol. 75:2777-2781 (1994).
 CC -----
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 CC -----
 CC EMBL: L21974; AAC37877.1; -; Genomic_DNA.
 CC -----
 DR HSP: P00523; 2PTK.
 DR SMR: 064817; 84-525.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO: GO:0007242; P:intracellular signaling cascade; IEA.
 DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR001245; Tyr_kinase.
 DR InterPro: IPR008266; Tyr_kinase_AS.
 DR Pfam: PF07714; Kinase_Tyr; 1.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00018; SH3; 1; 1.
 DR PRINTS: PR00401; SH2DOMAIN.
 DR PRINTS: PR00452; SH3DOMAIN.
 DR PRINTS: PR00109; TYRKINASE.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR ProDom: PD000093; SH2; 1.
 DR ProDom: PD000066; SH3; 1.
 DR SMART: SM00252; SH2; 1.
 DR SMART: SM00326; SH3; 1.

DR SMART; SM00219; TYKc; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 KW Kinase; Tyrosine-protein kinase.
 SQ SEQUENCE 587 AA; 65779 MW; BAAC3F5A44234F02 CRC64;

Query Match 92.0%; Score 2608.5; DB 2; Length 587;
 Best Local Similarity 93.8%; Pred. No. 4.3e-163; Indels 3; Gaps 1;
 Matches 495; Conservative 10; Mismatches 20;

QY 1 MSNKSXPDAASQRRSLSEPAENVHAGGAGAPPASQTPSKPASADGHRGSAFAPAAAE 60
 1 MSSSKSKPDPSPQRRSLSEPPDSTH---HGFPAQTPNKTAAPDTHRTSRBFGVATE 57
 DB 61 PKLFGFNSSDVYTSQRAAGPLAGVTTFAALYDYSRTEYDLSFKKGERLQIVNTEGD 120
 58 PKLFGFNTSDVYTSQRAAGLAGVTTFAALYDYSRTEYDLSFKKGERLQIVNTEGD 117
 QY 121 WMLAHSLTGQGYIISNVVAPSDSIQAEHWYFGKTRRSERLINPENRGTFIVRES 180
 118 WMLAHSLTGQGYIISNVVAPSDSIQAEHWYFGKTRRSERLINPENRGTFIVRES 177
 QY 181 ETTKGAYCISVSPDPAKGLNVGHYKIRKLDSCGFYITSRTQNSIQQLVAYYSKADGL 240
 178 ETTKGAYCISVSPDPAKGLNVGHYKIRKLDSCGFYITSRTQNSIQQLVAYYSKADGL 237
 DB 241 CHRLTVCTSKRQIQGLADAMEIPRESIRLEVKLGQCGFGEVWMTNGTTRVAIKTL 300
 238 CHRLTVCTSKRQIQGLADAMEIPRESIRLEVKLGQCGFGEVWMTNGTTRVAIKTL 297
 QY 301 KRGTSPEAFLEAOVKKLRHEKLVQVAVVSEEPYIVTEYMSGSLDPLKGETGY 360
 298 KRGTSPEAFLEAOVKKLRHEKLVQVAVVSEEPYIVTEYMSGSLDPLKGETGY 357
 DB 361 LRLPOLVDMAAOIASGMAYVERMYHRLDRAANILVGENLVCKVADFGLARLIENEXT 420
 358 LRLPOLVDMAAOIASGMAYVERMYHRLDRAANILVGENLVCKVADFGLARLIENEXT 417
 QY 421 AEOGAKFPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVPYGVNREVLDOVER 480
 418 AEOGAKFPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVPYGVNREVLDOVER 477
 DB 481 GYRMPCPECPESLHLMQCWRKEBERPTPEYLQAFLEDYFTSTEP 528
 478 GYRMPCPECPESLHLMQCWRKEBERPTPEYLQAFLEDYFTSTEP 525

RESULT 14
 SRC_AVIST STANDARD; PRT; 556 AA.
 ID SRC_AVIST
 AC P14085;
 DT 01-JAN-1990, integrated into UniProtKB/Swiss-Prot.
 DT 30-AUG-2005, sequence version 2.
 DT 07-MAR-2006, entry version 60.
 DE Tyrosine-protein kinase transforming protein Src (EC 2.7.1.112) (p60-Src) (v-Src) (pp60v-src).
 GN Name=v-Src;
 OS Avian sarcoma virus (strain S2).
 OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
 CC Alpharetrovirus; unclassified Alpharetrovirus.
 CC NCBITaxid=11882;
 RN NUCLEOTIDE SEQUENCE.
 RP MEDLINE=87064539; PubMed=3097513;
 RA Ikawa S., Hagiino-Yamagishi K., Kawai S., Yamamoto T., Toyoshima K.;
 RT "Activation of the cellular src gene by transducing retrovirus.";
 RL Mol. Cell. Biol. 6:2420-2428(1986).
 CC -!- FUNCTION: This phosphoprotein, required for both the initiation and the maintenance of neoplastic transformation, is a protein kinase that catalyzes the phosphorylation of tyrosine residues in

CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
 CC tyrosine phosphate.
 CC -!- PTM: The phosphorylated form is termed p60v-src.
 CC -!- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
 CC subfamily.
 CC -!- SIMILARITY: Contains 1 SH2 domain.
 CC -!- SIMILARITY: Contains 1 SH3 domain.
 CC
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 CC
 CC PIR; B25375; TVFV82.
 DR HSSP; P00523; 2PTR.
 DR SWR; P14085; 83-532.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002230; Ser_Thr_kinase.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR008266; Tyr_kinase_AS.
 DR Pfam; PF07714; Pkinase_Tyr; 1.
 DR Pfam; PF00017; SH2_1; 1.
 DR Pfam; PF00018; SH3_1; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR ProDom; PD000063; SH2; 1.
 DR ProDom; PD000066; SH3; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00219; TYKc; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 KW ATP-binding; kinase; Lipoprotein; Myristate; Nucleotide-binding;
 KW Oncogene; Phosphorylation; SH2 domain; SH3 domain; Transferase;
 KW Tyrosine-protein kinase.
 FT INIT MET 0 0
 FT CHAIN 1 556
 FT
 FT DOMAIN 80 141
 FT DOMAIN 147 244
 FT DOMAIN 266 519
 FT NP_BIND 272 280
 FT ACT_SITE 385 385
 FT BINDING 294 294
 FT MOD_RES 415 415
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 FT LIPID 1 1
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 SQ SEQUENCE 556 AA; 62452 MW; 0F7A904CA3FEA9CC CRC64;

Query Match 91.5%; Score 2594.5; DB 1; Length 556;
 Best Local Similarity 89.7%; Pred. No. 3.8e-162;
 Matches 495; Conservative 14; Mismatches 22; Indels 21; Gaps 2;

QY 2 GSNKSXPDAASQRRSLSEPAENVHAGGAGAPPASQTPSKPASADGHRGSAFAPAAAE 61
 1 GSSSKSKPDPSPQRRSLSEPPDSTH---HGFPAQTPNKTAAPDTHRTSRBFGVATEP 57
 DB 62 KLFGEFNSSDVYTSQRAAGPLAGVTTFAALYDYSRTEYDLSFKKGERLQIVNTEGD 121
 58 KLFGEFNTSDVYTSQRAAGLAGVTTFAALYDYSRTEYDLSFKKGERLQIVNTEGD 117
 QY 122 WMLAHSLTGQGYIISNVVAPSDSIQAEHWYFGKTRRSERLINPENRGTFIVRES 181
 118 WMLAHSLTGQGYIISNVVAPSDSIQAEHWYFGKTRRSERLINPENRGTFIVRES 177

QY 182 TTGAYCLSYSDFDNAGLNKHYKIRKLDSGFGYITSRTQFNLSQOLVAAYSKHADGLC 241
 DB 178 TTGAYCLSYSDFDNAGLNKHYKIRKLDSGFGYITSRTQFNLSQOLVAAYSKHADGLC 237
 QY 242 HRLTTCPTSKPQTQGLAKDAMEIPRESLRLEVLKGGCCFGEVWMTGTTTRVAIKTLK 301
 DB 238 HRLTTCPTSKPQTQGLAKDAMEIPRESLRLEVLKGGCCFGEVWMTGTTTRVAIKTLK 297
 QY 302 PGTMSPPAFIOEAQVWKKLRHEKLVOLYAVVSEEPYIVTETMKSGSLDPLKGETGKYL 361
 DB 298 PGTMSPPAFIOEAQVWKKLRHEKLVOLYAVVSEEPYIVTETMKSGSLDPLKGETGKYL 357
 QY 362 RLPLVMAAIOISGMAVVERMYVHRDLRAANILVGENLVCKYADFGALRLIDNEXYA 421
 DB 358 RLPLVMAAIOISGMAVVERMYVHRDLRAANILVGENLVCKYADFGALRLIDNEXYA 417
 QY 422 ROGAKPFIKWTAPBAALYGRFTIKSDVWSPGILLTELTTKGRVVPYPGWVNEVLDOYERG 481
 DB 418 ROGAKPFIKWTAPBAALYGRFTIKSDVWSPGILLTELTTKGRVVPYPGWVNEVLDOYERG 477
 QY 482 YRNPCEPCEPSLHDMCCCKRKEPERPTEFYIQAFLDYGLIATWPMEDKQEGPGE 537
 DB 478 YRNPCEPCEPSLHDMCCCKRKEPERPTEFYIQAFLDYGLIATWPMEDKQEGPGE 537
 QY 524 TSTEPQYQPGEN 535
 DB 538 TSNVKQERPGED 549

RESULT 15
 SRC_AVISR STANDARD; PRT: 525 AA.
 AC P00525; 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
 DT 30-AUG-2005, sequence version 2.
 DT 07-MAR-2006, entry version 72.
 DE Tyrosine-protein kinase transforming protein Src (EC 2.7.1.112) (p60-Src) (v-Src) (pp60v-src).
 GN Name=v-Src;
 OS Avian sarcoma virus (strain RASV1441).
 OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
 OC Alpharetrovirus; unclassified Alpharetrovirus.
 OX NCBI_TaxID=11894;
 RN NUCLEOTIDE SEQUENCE (GENOMIC RNA).
 RP MEDLINE=83059858; PubMed=6292477;
 RA Takeya T., Feldman R.A., Hanafusa H.;
 RT "DNA sequence of the viral and cellular src gene of chickens. 1.
 RT Complete nucleotide sequence of an EcoRI fragment of recovered avian
 RT sarcoma virus which codes for gp37 and pp60src.";
 RT J. Virol. 44:1-11(1982).
 RN [2]
 RP PHOSPHORYLATION SITE TYR-415.
 RX MEDLINE=81220979; PubMed=6264320;
 RA Neil J.C., Ghysdael J., Vogt P.K., Smart J.E.;
 RT "Homologous tyrosine phosphorylation sites in transformation-specific
 RT gene products of distinct avian sarcoma viruses.";
 RT Nature 291:675-677(1981).
 RN [3]
 RP STRUCTURE BY NMR OF 84-139.
 RX MEDLINE=95063997; PubMed=7526465;
 RA Peng S., Chen J.K., Yu H., Simon J.A., Scheibler S.L.;
 RT "Two binding orientations for peptides to the Src SH3 domain:
 RT development of a general model for SH3-ligand interactions.";
 RT Science 266:1241-1247(1994).
 RL -1- FUNCTION: This phosphoprotein, required for both the initiation
 CC and the maintenance of neoplastic transformation, is a protein
 CC kinase that catalyzes the phosphorylation of tyrosine residues in
 CC vitro.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
 CC tyrosine phosphate.
 CC -1- PTM: The phosphorylated form is termed pp60v-src.
 CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. SRC

CC subfamily.
 CC -1- SIMILARITY: Contains 1 SH2 domain.
 CC -1- SIMILARITY: Contains 1 SH3 domain.
 CC -----
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 DR EMBL: K00928; AAA42565.1; -; Genomic_RNA.
 DR PDB: 1QWE; NMR; A=80-139.
 DR PDB: 1QWF; NMR; A=80-139.
 DR SMR: P00525; 83-515.
 DR LinkHub; P00525; -
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_Thr_kinase.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR008266; Tyr_kinase_AS.
 DR Pfam; PF07714; Pkinase_Tyr; 1.
 DR Pfam; PF00017; SH2_1.
 DR Pfam; PF00018; SH3_1; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR ProDom; PD000093; SH2_1.
 DR ProDom; PD000066; SH3; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00219; TYRKC; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 KM 3D-structure: ATP-binding; Kinase; Lipoprotein; Myristate;
 KM Nucleotide-binding; Oncogene; Phosphorylation; SH2 domain; SH3 domain;
 KM Transferase; Tyrosine-protein kinase.
 FT INIT_MET 0
 FT CHAIN 1 525
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 FT DOMAIN 80 141
 FT DOMAIN 147 244
 FT NP_BIND 266 516
 FT ACT_SITE 272 280
 FT BINDING 385 385
 FT BINDING 294 294
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 FT LIPID 1 1
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 FT STRAND 91 91
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 FT STRAND 98 98
 FT STRAND 101 101
 FT TURN 103 104
 FT STRAND 105 109
 FT STRAND 117 122
 FT TURN 123 126
 FT STRAND 127 132
 FT HELIX 133 135
 FT STRAND 136 138
 FT SEQUENCE 525 AA; 58747 MW; 0683903F8038E04C CRC64;
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Query Match 89.2%; Score 2528.5; DB 1; Length 525;
 Best Local Similarity 92.9%; Pred. No. 7.7e-158;
 Matches 481; Conservative 12; Mismatches 22; Indels 3; Gaps 1;

QY 2 GSNKSKPKDASQRRSLPEAENVHAGGAFPAASQTPSPASADGHRGPAAPAPAAAP 61
 DB 1 GSSKSKPKDPSQRRSGRSLPEPDSH---HGGFPAASQTPNKTAADVTRTPSRSGVATRP 57

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OM protein - protein search, using sw model

Run on: June 5, 2006, 17:15:49 ; Search time 30.7894 Seconds

(Without alignments)
1523.786 Million cell updates/sec

Title: US-10-691-079-2

Perfect score: 2834
Sequence: 1 MSGNKSXPKDASQRRSLRP.....AFLEDYRTSTPEYQGENL 536Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: /EMC_Celerra_SID3/prodata/2/iaa/5.COMB.pep:*
2: /EMC_Celerra_SID3/prodata/2/iaa/6.COMB.pep:*
3: /EMC_Celerra_SID3/prodata/2/iaa/7.COMB.pep:*
4: /EMC_Celerra_SID3/prodata/2/iaa/H.COMB.pep:*
5: /EMC_Celerra_SID3/prodata/2/iaa/PCTUS.COMB.pep:*
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7: /EMC_Celerra_SID3/prodata/2/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2834	100.0	536	1 US-07-820-011A-4	Sequence 4, Appli
2	2834	100.0	536	2 US-08-426-509A-13	Sequence 13, Appli
3	2834	100.0	536	2 US-08-232-545-13	Sequence 13, Appli
4	2834	100.0	536	2 US-09-444-711A-2	Sequence 2, Appli
5	2834	100.0	536	2 US-09-929-266-10	Sequence 10, Appli
6	2834	100.0	536	2 US-09-977-261-13	Sequence 13, Appli
7	2834	100.0	536	5 PCT-US93-00445-4	Sequence 4, Appli
8	2834	100.0	536	5 PCT-US95-05008-13	Sequence 13, Appli
9	2834	100.0	537	2 US-09-949-016-10282	Sequence 10282, A
10	2801	98.8	530	2 US-09-444-711A-4	Sequence 4, Appli
11	2663.5	94.0	533	2 US-07-820-011A-2	Sequence 2, Appli
12	2660.5	93.9	533	1 US-07-820-011A-2	Sequence 3, Appli
13	2660.5	93.9	533	5 PCT-US93-00445-2	Sequence 2, Appli
14	2123.5	74.9	543	2 US-08-426-509A-14	Sequence 14, Appli
15	2123.5	74.9	543	2 US-08-232-545-14	Sequence 14, Appli
16	2123.5	74.9	543	2 US-09-470-881-8	Sequence 8, Appli
17	2123.5	74.9	543	2 US-09-538-092-870	Sequence 870, Appli
18	2123.5	74.9	543	2 US-09-977-261-14	Sequence 14, Appli
19	2123.5	74.9	543	5 PCT-US95-05008-14	Sequence 14, Appli
20	2121.5	74.9	541	2 US-08-864-281-20	Sequence 20, Appli
21	1949	68.8	536	2 US-08-426-509A-12	Sequence 12, Appli
22	1949	68.8	536	2 US-08-232-545-12	Sequence 12, Appli
23	1949	68.8	536	2 US-09-977-261-12	Sequence 12, Appli
24	1949	68.8	536	5 PCT-US95-05008-12	Sequence 12, Appli
25	1944	68.6	532	1 US-08-594-447-1	Sequence 1, Appli
26	1944	68.6	532	1 US-08-665-647-1	Sequence 1, Appli

27	1932.5	68.2	537	2 US-08-426-509A-11	Sequence 11, Appli
28	1932.5	68.2	537	2 US-08-232-545-11	Sequence 11, Appli
29	1932.5	68.2	537	2 US-09-977-261-11	Sequence 11, Appli
30	1932.5	68.2	537	5 PCT-US95-05008-11	Sequence 11, Appli
31	1932	68.2	536	2 US-09-538-092-859	Sequence 859, App
32	1924.5	67.9	537	2 US-09-771-161A-212	Sequence 212, App
33	1924.5	67.9	537	2 US-09-771-161A-213	Sequence 213, App
34	1856	65.5	529	2 US-08-426-509A-15	Sequence 15, Appli
35	1856	65.5	529	2 US-08-232-545-15	Sequence 15, Appli
36	1856	65.5	529	2 US-09-538-092-885	Sequence 885, App
37	1856	65.5	529	2 US-09-977-261-15	Sequence 15, Appli
38	1856	65.5	529	5 PCT-US95-05008-15	Sequence 15, Appli
39	1738.5	61.3	485	2 US-10-094-749-2726	Sequence 2726, Ap
40	1532	54.1	573	2 US-09-949-016-10415	Sequence 10415, A
41	1528.5	53.9	505	2 US-08-426-509A-17	Sequence 17, Appli
42	1528.5	53.9	505	2 US-08-232-545-17	Sequence 17, Appli
43	1528.5	53.9	505	2 US-09-977-261-17	Sequence 17, Appli
44	1528.5	53.9	505	5 PCT-US95-05008-17	Sequence 17, Appli
45	1464	51.7	508	2 US-09-862-154-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-07-820-011A-4
Sequence 4, Application US/07820011A
Patent No. 5336615
GENERAL INFORMATION:
APPLICANT: Bell, Leonard
APPLICANT: Madri, Joseph A.
APPLICANT: Warren, Stephen L.
APPLICANT: Luthringer, Daniel J.
TITLE OF INVENTION: Genetically Engineered
TITLE OF INVENTION: Endothelial Cells Exhibiting Enhanced
TITLE OF INVENTION: Migration
TITLE OF INVENTION: and Plasminogen Activator Activity
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maurice M. Klee
STREET: 1951 Burr Street
CITY: Fairfield
STATE: Connecticut
COUNTRY: USA
ZIP: 06430
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 KB storage
COMPUTER: IBM PC XT
OPERATING SYSTEM: PC-DOS/MS-DOS 2.10
SOFTWARE: Displaywrite 3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/820, 011A
FILING DATE: 19920106
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399
REFERENCE/DOCKET NUMBER: LB-101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255 1400
TELEFAX: (203) 254 1101
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 536 amino acids
TYPE: AMINO ACID
TOPOLOGY: Linear
MOLECULE TYPE: Protein
HYPOTHETICAL: No
FRAGMENT TYPE: Complete Sequence
ORIGINAL SOURCE:
ORGANISM: Homo sapien
PUBLICATION INFORMATION:
AUTHORS: Anderson, Stephen K.

AUTHORS: Gibbs, Carol P.
AUTHORS: Tanaka, Akio
AUTHORS: Kung, Hsing-Jien
AUTHORS: Fujita, Donald J.
TITLE: Human Cellular src Gene:
TITLE: Nucleotide Sequence and Derived Amino
TITLE: Acid Sequence of the Region Coding for
TITLE: the Carboxy-Terminal Two-Thirds of
TITLE: pp60c-src
JOURNAL: Molecular and Cellular Biology
VOLUME: 5
ISSUE: 5
PAGES: 1122-1129
DATE: May, 1985
PUBLICATION INFORMATION:
AUTHORS: Tanaka, Akio
AUTHORS: Gibbs, Carol P.
AUTHORS: Arthur, Richard R.
AUTHORS: Anderson, Stephen K.
AUTHORS: Kung, Hsing-Jien
AUTHORS: Fujita, Donald J.
TITLE: DNA Sequence Encoding the
TITLE: Amino-Terminal Region of the Human c-src
TITLE: Protein: Implications of Sequence
TITLE: Divergence among src-Type Kinase
TITLE: Oncogenes
JOURNAL: Molecular and Cellular Biology
VOLUME: 7
ISSUE: 5
PAGES: 1978-1983
DATE: May, 1987
US-07-820-011A-4

Query Match 100.0%; Score 2834; DB 1; Length 536;
Best Local Similarity 100.0%; Pred. No. 2.6e-215;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MGSNKSXPDAASQRRSLSPAEVNHGAGGAPASQTPSKPASADGHRPSAFAFAAAE 60
1 MGSNKSXPDAASQRRSLSPAEVNHGAGGAPASQTPSKPASADGHRPSAFAFAAAE 60
61 PKLFGFNSSDVTYSPQRAGPLAGVTTFVALYDSESRTEITLSFKKGERLQIVNTEGD 120
61 PKLFGFNSSDVTYSPQRAGPLAGVTTFVALYDSESRTEITLSFKKGERLQIVNTEGD 120
121 WMLAHSLSGTQGYIPSNVYAPSDSIQAEEMWFGKITRRESERLLINAEPRGTFLVRES 180
121 WMLAHSLSGTQGYIPSNVYAPSDSIQAEEMWFGKITRRESERLLINAEPRGTFLVRES 180
181 ETTKGAICYLSVDFDNAGKLVNHYKIRKLDGSGFYITSTRQFNSIQQLVAAYYSKADGL 240
181 ETTKGAICYLSVDFDNAGKLVNHYKIRKLDGSGFYITSTRQFNSIQQLVAAYYSKADGL 240
241 CHRLLTVCTSPKQTOGLAKDAWEIPRESLRLEVKLGQCGFGEVWNGTTRVAIKTL 300
241 CHRLLTVCTSPKQTOGLAKDAWEIPRESLRLEVKLGQCGFGEVWNGTTRVAIKTL 300
301 KEGTMSPEAFLOEAQVMKLRHEKLVQLYAVVSEBPIYIVTEYMSKGSLLDFLKGETGKY 360
301 KEGTMSPEAFLOEAQVMKLRHEKLVQLYAVVSEBPIYIVTEYMSKGSLLDFLKGETGKY 360
361 LRLPOLVDMAAOASGMAVYERNNYVHRDLRAANILVGENLVCKVADFGLARLIBENEY 420
361 LRLPOLVDMAAOASGMAVYERNNYVHRDLRAANILVGENLVCKVADFGLARLIBENEY 420
421 ABOGAKFPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVPYPGWVREVLDOVER 480
421 ABOGAKFPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVPYPGWVREVLDOVER 480
481 GYRMPCPEPCPSLHLMCCQWKEPEBEPTEFYLOAFLEDYTSSTBPQYQPEENTL 536
481 GYRMPCPEPCPSLHLMCCQWKEPEBEPTEFYLOAFLEDYTSSTBPQYQPEENTL 536

RESULT 2
US-08-426-509A-13
Sequence 13, Application US/08426509A
Patent No. 6326469

GENERAL INFORMATION:
APPLICANT: Ulrich, Axel
APPLICANT: Glabirsky, Mikhail
APPLICANT: Sures, Irman G.
TITLE OF INVENTION: NOVEL MEKAKARYOCYTIC PROTEIN
TITLE OF INVENTION: TYROSINE KINASES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Penile & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York,
STATE: NY
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/426, 509A
FILING DATE: 21-APR-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/232,545

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Cornuzzi, Laura A

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7683-0074-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-790-9090

TELEFAX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 536 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: No. 6326469e

Query Match 100.0%; Score 2834; DB 2; Length 536;
Best Local Similarity 100.0%; Pred. No. 2.6e-215;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MGSNKSXPDAASQRRSLSPAEVNHGAGGAPASQTPSKPASADGHRPSAFAFAAAE 60
1 MGSNKSXPDAASQRRSLSPAEVNHGAGGAPASQTPSKPASADGHRPSAFAFAAAE 60
61 PKLFGFNSSDVTYSPQRAGPLAGVTTFVALYDSESRTEITLSFKKGERLQIVNTEGD 120
61 PKLFGFNSSDVTYSPQRAGPLAGVTTFVALYDSESRTEITLSFKKGERLQIVNTEGD 120
121 WMLAHSLSGTQGYIPSNVYAPSDSIQAEEMWFGKITRRESERLLINAEPRGTFLVRES 180
121 WMLAHSLSGTQGYIPSNVYAPSDSIQAEEMWFGKITRRESERLLINAEPRGTFLVRES 180
181 ETTKGAICYLSVDFDNAGKLVNHYKIRKLDGSGFYITSTRQFNSIQQLVAAYYSKADGL 240
181 ETTKGAICYLSVDFDNAGKLVNHYKIRKLDGSGFYITSTRQFNSIQQLVAAYYSKADGL 240
241 CHRLLTVCTSPKQTOGLAKDAWEIPRESLRLEVKLGQCGFGEVWNGTTRVAIKTL 300
241 CHRLLTVCTSPKQTOGLAKDAWEIPRESLRLEVKLGQCGFGEVWNGTTRVAIKTL 300
301 KEGTMSPEAFLOEAQVMKLRHEKLVQLYAVVSEBPIYIVTEYMSKGSLLDFLKGETGKY 360
301 KEGTMSPEAFLOEAQVMKLRHEKLVQLYAVVSEBPIYIVTEYMSKGSLLDFLKGETGKY 360

Db 301 KPRTMSBEALFQEQVWKLRHEKLVOLYAVVSEEPITYIVTEVMSKSLDPLGEGTGY 360
Qy 361 LRLPOLVMAAQIASGMAVYERNYVARDLPAANILVGENLVCKVADFGRLIEDNEYT 420
Db 361 LRLPOLVMAAQIASGMAVYERNYVARDLPAANILVGENLVCKVADFGRLIEDNEYT 420
Qy 421 ARQAKRPPIKWTAEALYGRFTIKSDVWSFGILLTTLTKGRVPYFGMVNREVLDOVER 480
Db 421 ARQAKRPPIKWTAEALYGRFTIKSDVWSFGILLTTLTKGRVPYFGMVNREVLDOVER 480
Qy 481 GYRMPCEPCEPSLHDMCCMRKPEBERPFEYLQAFLEDFYFSTEROYQGENL 536
Db 481 GYRMPCEPCEPSLHDMCCMRKPEBERPFEYLQAFLEDFYFSTEROYQGENL 536

RESULT 3

US-08-232-545-13
; Sequence 13, Application US/08232545
; Patent No. 6506578
; GENERAL INFORMATION:
; APPLICANT: Ullrich, Axel
; APPLICANT: Gishizky, Mikhail
; APPLICANT: Sures, Irmun G.
; TITLE OF INVENTION: No. 6506578el Megakaryocytic Protein Tyrosine
; TITLE OF INVENTION: Kinases
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,545
; FILING DATE: 22-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Cornuzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7683-050
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)790-9090
; TELEFAX: (212)869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 536 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-232-545-13

Query Match 100.0%; Score 2834; DB 2; Length 536;
Best Local Similarity 100.0%; Pred. No. 2,6e-215;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGSNKSXPXKASORRSLEPAENVHAGGAFPAASQTPSKPASADGHRGSPAAAPAAAE 60
Db 1 MGSNKSXPXKASORRSLEPAENVHAGGAFPAASQTPSKPASADGHRGSPAAAPAAAE 60
Qy 61 PKLFGFNSSDVTYVSPORAGPLAGGVTTFVALYDYESRTEITDLSFKKGERLQIVNTEGD 120
Db 61 PKLFGFNSSDVTYVSPORAGPLAGGVTTFVALYDYESRTEITDLSFKKGERLQIVNTEGD 120
Qy 121 WMLAHSISTGQTGITPSNYVAPSDSIQAEEMYPFKITRRSEERLLNAENRGTFLVRES 180
Db 121 WMLAHSISTGQTGITPSNYVAPSDSIQAEEMYPFKITRRSEERLLNAENRGTFLVRES 180

Db 121 WMLAHSISTGQTGITPSNYVAPSDSIQAEEMYPFKITRRSEERLLNAENRGTFLVRES 180
Qy 181 ETTKGAYCLSVSDPDNAKGLNVKHYKIRKLDGSGFYITTSRTQFNSLOQLVAYYSKADGL 240
Db 181 ETTKGAYCLSVSDPDNAKGLNVKHYKIRKLDGSGFYITTSRTQFNSLOQLVAYYSKADGL 240
Qy 241 CHRLTYVCPSPKPTQGLADAMEIPRESLRLEVKLQCGCGEVMGMNQTTRVALIKTL 300
Db 241 CHRLTYVCPSPKPTQGLADAMEIPRESLRLEVKLQCGCGEVMGMNQTTRVALIKTL 300
Qy 301 KPRTMSBEALFQEQVWKLRHEKLVOLYAVVSEEPITYIVTEVMSKSLDPLGEGTGY 360
Db 301 KPRTMSBEALFQEQVWKLRHEKLVOLYAVVSEEPITYIVTEVMSKSLDPLGEGTGY 360
Qy 361 LRLPOLVMAAQIASGMAVYERNYVARDLPAANILVGENLVCKVADFGRLIEDNEYT 420
Db 361 LRLPOLVMAAQIASGMAVYERNYVARDLPAANILVGENLVCKVADFGRLIEDNEYT 420
Qy 421 ARQAKRPPIKWTAEALYGRFTIKSDVWSFGILLTTLTKGRVPYFGMVNREVLDOVER 480
Db 421 ARQAKRPPIKWTAEALYGRFTIKSDVWSFGILLTTLTKGRVPYFGMVNREVLDOVER 480
Qy 481 GYRMPCEPCEPSLHDMCCMRKPEBERPFEYLQAFLEDFYFSTEROYQGENL 536
Db 481 GYRMPCEPCEPSLHDMCCMRKPEBERPFEYLQAFLEDFYFSTEROYQGENL 536

RESULT 4

US-09-444-711A-2
; Sequence 2, Application US/09444711A
; Patent No. 6764833
; GENERAL INFORMATION:
; APPLICANT: Yeatman, Timothy J.
; APPLICANT: Irdy, Rosalyn B.
; TITLE OF INVENTION: Mutated SRC Oncogene Composition and Methods
; FILE REFERENCE: USF-1136
; CURRENT APPLICATION NUMBER: US/09/444,711A
; CURRENT FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(536)
; OTHER INFORMATION: amino acid sequence of non-receptor tyrosine kinase encoded
; OTHER INFORMATION: by the normal c-Src coding region
US-09-444-711A-2

Query Match 100.0%; Score 2834; DB 2; Length 536;
Best Local Similarity 100.0%; Pred. No. 2,6e-215;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGSNKSXPXKASORRSLEPAENVHAGGAFPAASQTPSKPASADGHRGSPAAAPAAAE 60
Db 1 MGSNKSXPXKASORRSLEPAENVHAGGAFPAASQTPSKPASADGHRGSPAAAPAAAE 60
Qy 61 PKLFGFNSSDVTYVSPORAGPLAGGVTTFVALYDYESRTEITDLSFKKGERLQIVNTEGD 120
Db 61 PKLFGFNSSDVTYVSPORAGPLAGGVTTFVALYDYESRTEITDLSFKKGERLQIVNTEGD 120
Qy 121 WMLAHSISTGQTGITPSNYVAPSDSIQAEEMYPFKITRRSEERLLNAENRGTFLVRES 180
Db 121 WMLAHSISTGQTGITPSNYVAPSDSIQAEEMYPFKITRRSEERLLNAENRGTFLVRES 180
Qy 181 ETTKGAYCLSVSDPDNAKGLNVKHYKIRKLDGSGFYITTSRTQFNSLOQLVAYYSKADGL 240
Db 181 ETTKGAYCLSVSDPDNAKGLNVKHYKIRKLDGSGFYITTSRTQFNSLOQLVAYYSKADGL 240
Qy 241 CHRLTYVCPSPKPTQGLADAMEIPRESLRLEVKLQCGCGEVMGMNQTTRVALIKTL 300
Db 241 CHRLTYVCPSPKPTQGLADAMEIPRESLRLEVKLQCGCGEVMGMNQTTRVALIKTL 300

[illegible]

RESULT 5

```

US-09-929-266-10
Sequence 10, Application US/09929266
Patent No. 6824861
GENERAL INFORMATION:
APPLICANT: Brian T. Chait
APPLICANT: Darin R. Latimer
APPLICANT: Paul M. Iizardi
APPLICANT: Eric R. Keremnar
APPLICANT: Jon S. Morrow
APPLICANT: Matthew E. Roth
APPLICANT: Martin J. Matcseisch
APPLICANT: Kevin J. McConnell
TITLE OF INVENTION: ULTRA-SENSITIVE DETECTION SYSTEMS
FILE REFERENCE: 01173.00030U
CURRENT APPLICATION NUMBER: US/09/929.266
CURRENT FILING DATE: 2001-08-13
PRIOR APPLICATION NUMBER: 60/1224,939
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/283,498
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 536
TYPE: PRF
ORGANISM: Homo sapiens
US-09-929-266-10

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Query match 100.0%; Score 2834; DB 2; Length 536;

Best Local Similarity 100.0%; Pred. No. 2.6e-215;

Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MGSNKSRKMDASORRRSLLEPAENYHAGAGGAPASOTPEKPPASADHRGSAFAFAAAAE	60
Db	1	MGSNKSRKMDASORRRSLLEPAENYHAGAGGAPASOTPEKPPASADHRGSAFAFAAAAE	60
QY	61	PXLFGGNSDVTYSPPORAGPLAGGVTTFVALYDYSRTETDLSFKKGRLOIVNNTGED	120
Db	61	PXLFGGNSDVTYSPPORAGPLAGGVTTFVALYDYSRTETDLSFKKGRLOIVNNTGED	120
QY	121	WMLHSLSTGQTGYPSNYVVAAPSDSIQAEEMFGKTRRESRLILNAENPQTFIVRES	180
Db	121	WMLHSLSTGQTGYPSNYVVAAPSDSIQAEEMFGKTRRESRLILNAENPQTFIVRES	180
QY	181	ETTGGAYCCLVSDPFDNAGLNVKHKIRKLDGSGFYITSRTQFNSIQQLVAYYSKADGL	240
Db	181	ETTGGAYCCLVSDPFDNAGLNVKHKIRKLDGSGFYITSRTQFNSIQQLVAYYSKADGL	240
QY	241	CHRLITVCPSTKPCQYGLAKDAAMEIPRESRLREVLQGGCCFGEVWMTGNTGTRVAIKTL	300
Db	241	CHRLITVCPSTKPCQYGLAKDAAMEIPRESRLREVLQGGCCFGEVWMTGNTGTRVAIKTL	300

QY 301 KPGTMSPEAPFLOEAOVMKKLHREKLVOLYAVVSEBPIYVTEYMSKGLDLDFKSGTGXK 360

Db 301 KPGTMSPEAPFLOEAOVMKKLHREKLVOLYAVVSEBPIYVTEYMSKGLDLDFKSGTGXK 360

QY 361 LRLPOLYMAAQIASGMAVVERMNTVHRDLRAANTLVGENLVCKVADFGIARLIEDNEYT 420

Db 361 LRLPOLYMAAQIASGMAVVERMNTVHRDLRAANTLVGENLVCKVADFGIARLIEDNEYT 420

QY 421 ARQGAKEPIKNTAPPAALYGRFTISKDWSFGILLTELTKKRVPPGMVNRBVLDOVER 480

Db 421 ARQGAKEPIKNTAPPAALYGRFTISKDWSFGILLTELTKKRVPPGMVNRBVLDOVER 480

QY 481 GYRMPCEPECCESLHDLMOCCMRKREPERPTEYLAQFLIEDFTSTBPQYOGENL 536

Db 481 GYRMPCEPECCESLHDLMOCCMRKREPERPTEYLAQFLIEDFTSTBPQYOGENL 536

RESULT 6

US-09-977-261-13
 : Sequence 13, Application US/09977261
 : Patent No. 6908984
 : GENERAL INFORMATION:
 :
 : APPLICANT: URSACH, AXEL
 : APPLICANT: GISHITZKY, MICHAEL
 : APPLICANT: SORES, IRMINGARD
 : TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES
 : FILE REFERENCE: 038602/1259
 : CURRENT APPLICATION NUMBER: US/09/977,261
 : CURRENT FILING DATE: 2001-10-16
 : PRIOR APPLICATION NUMBER: 08/232,545
 : PRIOR FILING DATE: 1994-04-22
 : NUMBER OF SEQ ID NOS: 24
 : SOFTWARE: PatentIn Ver. 2.1
 : SEQ ID NO 13
 :
 : LENGTH: 536
 :
 : TYPE: PRT
 : ORGANISM: Homo sapiens
 : US-09-977-261-13

Query Match	100.0%;	Score 2834;	DB 2;	Length 536;
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Best Local Similarity 100.0%; Pred. No. 2.6e-215;

Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGSNKSRKQDASQRRRSLEPEANVHAGGGGAFPSAQTSKPSASADGHGSPSAFPAALAE	60
Dd	1	MGSNKSRKQDASQRRRSLEPEANVHAGGGGAFPSAQTSKPSASADGHGSPSAFPAALAE	60
Qy	61	PKLFGFNSSDVTIVSPQAGPLAGVTTFVALYDIESRTEITDLSFKGGERLOIVNNTGED	120
Dd	61	PKLFGFNSSDVTIVSPQAGPLAGVTTFVALYDIESRTEITDLSFKGGERLOIVNNTGED	120
Qy	121	WMLAHSLSGTQGYIPSNVYVAPSDSIQAEWYFGKITRRESERLLLNENPRGTFLVRES	180
Dd	121	WMLAHSLSGTQGYIPSNVYVAPSDSIQAEWYFGKITRRESERLLLNENPRGTFLVRES	180
Qy	181	ETTQGAICYLSVSDPDNAKGLNVKHKIRKLDGSGGYITSRTOFNSLOOLVAYYSKHADGL	240
Dd	181	ETTQGAICYLSVSDPDNAKGLNVKHKIRKLDGSGGYITSRTOFNSLOOLVAYYSKHADGL	240
Qy	241	CHRLTTYCPTSPKQTOGLAKDAWEIPRESLBLEVTLGGCGCGEYVMGTMNGTTRVAIKTL	300
Dd	241	CHRLTTYCPTSPKQTOGLAKDAWEIPRESLBLEVTLGGCGEYVMGTMNGTTRVAIKTL	300
Qy	301	KPGMSPEALFOEAQVWKKLHBEKLYOOLYAVVSEEPITYLMEVMSKGSLLDPLKSBETGX	360
Dd	301	KPGMSPEALFOEAQVWKKLHBEKLYOOLYAVVSEEPITYLMEVMSKGSLLDPLKSBETGX	360
Qy	361	LRLPOLVMAAQISAGMAVYERMMYVHBDLPAANILVEENLVCKADFGIARLIDENEXT	420
Dd	361	LRLPOLVMAAQISAGMAVYERMMYVHBDLPAANILVEENLVCKADFGIARLIDENEXT	420
Qy	421	ARQAKAPPIKWTAPAEALYGRFTIKSDWMSFGILLTELITGRVAPYPCGVNREVLDOVER	480

Db 421 ARGAKPPIKWTAPBALYGRFTIKSDVWSFGILLTELTGKRVYPYGMVNRVLDQVER 480
QY 481 GYRMPCEPCEBSLHDMCCQMKRKEPBERPFEYLQAFLEDFYFSTEPQYQGENL 536
Db 481 GYRMPCEPCEBSLHDMCCQMKRKEPBERPFEYLQAFLEDFYFSTEPQYQGENL 536

RESULT 7
PCT-US93-00445-4
; Sequence 4, Application PC/TUS9300445
; GENERAL INFORMATION:
; APPLICANT: Bell, Leonard
; APPLICANT: Madri, Joseph A.
; APPLICANT: Warren, Stephen L.
; APPLICANT: Luchinger, Daniel J.
; TITLE OF INVENTION: Genetically Engineered
; TITLE OF INVENTION: Endothelial Cells
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maurice M. Klee
; STREET: 1951 Burr Street
; CITY: Fairfield
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06430

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 760 Kb storage
; COMPUTER: DELL 486/50
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: Displaywrite 3
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/00445
; FILING DATE: 19930105
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/820, 011
; FILING DATE: 06-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Klee, Maurice M.
; REGISTRATION NUMBER: 30,399
; REFERENCE/DOCKET NUMBER: ALX-101PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203) 255 1400
; TELEFAX: (203) 254 1101
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 536 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: Linear
; MOLECULE TYPE: Protein
; HYPOTHEetical: No
; FRAGMENT TYPE: Complete Sequence
; ORIGINAL SOURCE:
; ORGANISM: Homo sapien
; PUBLICATION INFORMATION:
; AUTHORS: Anderson, Stephen K.
; AUTHORS: Gibbs, Carol P.
; AUTHORS: Tanaka, Akio
; AUTHORS: Kung, Hsing-Jien
; AUTHORS: Fujita, Donald J.
; TITLE: Human Cellular src Gene:
; TITLE: Nucleotide Sequence and Derived Amino
; TITLE: Acid Sequence of the Region Coding for
; TITLE: the Carboxy-Terminal Two-Thirds of
; TITLE: pp60-c-src
; JOURNAL: Molecular and Cellular Biology
; VOLUME: 5
; ISSUES: 5
; PAGES: 1122-1129
; DATE: May, 1985
; PUBLICATION INFORMATION:
; AUTHORS: Tanaka, Akio
; AUTHORS: Gibbs, Carol P.

; AUTHORS: Arthur, Richard R.
; AUTHORS: Anderson, Stephen K.
; AUTHORS: Kung, Hsing-Jien
; AUTHORS: Fujita, Donald J.
; TITLE: DNA Sequence Encoding the
; TITLE: Amino-Terminal Region of the Human c-src
; TITLE: Protein: Implications of Sequence
; TITLE: Divergence among src-Type Kinase
; TITLE: Oncogenes
; JOURNAL: Molecular and Cellular Biology
; VOLUME: 7
; ISSUES: 5
; PAGES: 1978-1983
; DATE: May, 1987
; PCT-US93-00445-4

Query Match 100.0%; Score 2834; DB 5; Length 536;
Best Local Similarity 100.0%; Pred. No. 2,6e-215;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSNKSYPKQASQRRRLSEPAENVHAGGAFPPASQTPSKPASADGHRGSAAPAPAAE 60
Db 1 MGSNKSYPKQASQRRRLSEPAENVHAGGAFPPASQTPSKPASADGHRGSAAPAPAAE 60
QY 61 PKLFGFNSSDVTYSPQAGAGVTFVALYDRESRTEDLSFKKGERLQIVNTEGD 120
Db 61 PKLFGFNSSDVTYSPQAGAGVTFVALYDRESRTEDLSFKKGERLQIVNTEGD 120
QY 121 WMLNHSLSGTGTGYPNNYVAPSDSIQAEWYFQKTRRESERLLNENRGTFLVRES 180
Db 121 WMLNHSLSGTGTGYPNNYVAPSDSIQAEWYFQKTRRESERLLNENRGTFLVRES 180
QY 181 ETTKGAYCLSVSDPDKAGLVNKKYKIRKLDGSGFYTSRTQFNSLQQLVAYYSKADGL 240
Db 181 ETTKGAYCLSVSDPDKAGLVNKKYKIRKLDGSGFYTSRTQFNSLQQLVAYYSKADGL 240
QY 241 CHRLTYVCPNPKPTQGLADAWKIPRESLPLFKLQGCCEGVNMGVNTTVAIKTL 300
Db 241 CHRLTYVCPNPKPTQGLADAWKIPRESLPLFKLQGCCEGVNMGVNTTVAIKTL 300
QY 301 KPGTMSPEAFLOEAQVWKKLRHEKLVLYAVVSEPIYIVTEVYSKSLDPLKGETSKY 360
Db 301 KPGTMSPEAFLOEAQVWKKLRHEKLVLYAVVSEPIYIVTEVYSKSLDPLKGETSKY 360
QY 361 LRPLQVDMAAQIASGNAVYERNYVARDLRAANILVGENLVCKVADFGRLLEDNEYT 420
Db 361 LRPLQVDMAAQIASGNAVYERNYVARDLRAANILVGENLVCKVADFGRLLEDNEYT 420
QY 421 ARGAKPPIKWTAPBALYGRFTIKSDVWSFGILLTELTGKRVYPYGMVNRVLDQVER 480
Db 421 ARGAKPPIKWTAPBALYGRFTIKSDVWSFGILLTELTGKRVYPYGMVNRVLDQVER 480
QY 481 GYRMPCEPCEBSLHDMCCQMKRKEPBERPFEYLQAFLEDFYFSTEPQYQGENL 536
Db 481 GYRMPCEPCEBSLHDMCCQMKRKEPBERPFEYLQAFLEDFYFSTEPQYQGENL 536

RESULT 8
PCT-US93-05008-13
; Sequence 13, Application PC/TUS9505008
; GENERAL INFORMATION:
; APPLICANT: Sugen, Inc.
; APPLICANT: 515 Galveston Drive
; APPLICANT: Redwood City, California 94063-4720
; APPLICANT: United States of America
; APPLICANT: Miesgenchafen E.V.
; APPLICANT: Horgarten Str. 2
; APPLICANT: Munchen 80539
; APPLICANT: Germany
; TITLE OF INVENTION: Novel Megakaryocytic Protein Tyrosine
; TITLE OF INVENTION: Kinases
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:

```

ADDRESS: Penile & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05008
FILING DATE: 24-Apr-1995
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/232,545
FILING DATE: 22-Apr-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-074
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
TELEFAX: (212)669-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 536 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
PCT-US95-05008-13

Query Match      100.0%; Score 2834; DB 5; Length 536;
Best Local Similarity 100.0%; Pred. No. 2.6e-215;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSNKKPXDASGRRSLBPAENVHAGGAFPASQTPSKPASADGHRGSAAPAPAAE 60
DB 1 MGSNKKPXDASGRRSLBPAENVHAGGAFPASQTPSKPASADGHRGSAAPAPAAE 60
QY 61 PKLFGFNSSDVTTSQORAGPLAGVTTFVALVDYESTRTDLSFKKGERLQIVNTEGD 120
DB 61 PKLFGFNSSDVTTSQORAGPLAGVTTFVALVDYESTRTDLSFKKGERLQIVNTEGD 120
QY 121 WMLAHSLSGTQTCYIPSNVYAPSDSIQAEEMVFGKITRRESERLLNAENPRGTFLVRES 180
DB 121 WMLAHSLSGTQTCYIPSNVYAPSDSIQAEEMVFGKITRRESERLLNAENPRGTFLVRES 180
QY 181 ETTKGAIVCLSVDPDNAGKLVNHYKIRKLDGSGFYITSTRTOFNSLQOLVAAYYSKADGL 240
DB 181 ETTKGAIVCLSVDPDNAGKLVNHYKIRKLDGSGFYITSTRTOFNSLQOLVAAYYSKADGL 240
QY 241 CHRLTVCPYTSKQOTGLAKDAWEIPRESLRLEVKLGQCGFGEVWMTGNVTTRVAIKTL 300
DB 241 CHRLTVCPYTSKQOTGLAKDAWEIPRESLRLEVKLGQCGFGEVWMTGNVTTRVAIKTL 300
QY 301 KPGTMSPEAFLOAQVMKLRHEKLVQLYAVVSEBPIYIVTEYMSKGSLLDFLKGETGKY 360
DB 301 KPGTMSPEAFLOAQVMKLRHEKLVQLYAVVSEBPIYIVTEYMSKGSLLDFLKGETGKY 360
QY 361 LRLPQLVDMAAQIAGSMAYVERMYVHRDLRAANIIVGENLVCKVADFGIARLIIDNEYT 420
DB 361 LRLPQLVDMAAQIAGSMAYVERMYVHRDLRAANIIVGENLVCKVADFGIARLIIDNEYT 420
QY 421 ARQGAAPFKMTAPBALYGRFTIKSDVMSFGILLTELTKGVPYPGMNNREVLDOVER 480
DB 421 ARQGAAPFKMTAPBALYGRFTIKSDVMSFGILLTELTKGVPYPGMNNREVLDOVER 480
QY 481 GYRMPCEPCEBSLHDLMCQWKRKEPERPTFEYLQAFLEDYFTSTPEPOQPGENL 536
DB 481 GYRMPCEPCEBSLHDLMCQWKRKEPERPTFEYLQAFLEDYFTSTPEPOQPGENL 536

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DB 481 GYRMPCEPCEBSLHDLMCQWKRKEPERPTFEYLQAFLEDYFTSTPEPOQPGENL 536

RESULT 9
US-09-949-016-10282
Sequence 10282, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10282
LENGTH: 537
TYPE: PRT
ORGANISM: Human
US-09-949-016-10282

Query Match      100.0%; Score 2834; DB 2; Length 537;
Best Local Similarity 100.0%; Pred. No. 2.6e-215;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSNKKPXDASGRRSLBPAENVHAGGAFPASQTPSKPASADGHRGSAAPAPAAE 60
DB 2 MGSNKKPXDASGRRSLBPAENVHAGGAFPASQTPSKPASADGHRGSAAPAPAAE 61
QY 61 PKLFGFNSSDVTTSQORAGPLAGVTTFVALVDYESTRTDLSFKKGERLQIVNTEGD 120
DB 62 PKLFGFNSSDVTTSQORAGPLAGVTTFVALVDYESTRTDLSFKKGERLQIVNTEGD 121
QY 121 WMLAHSLSGTQTCYIPSNVYAPSDSIQAEEMVFGKITRRESERLLNAENPRGTFLVRES 180
DB 122 WMLAHSLSGTQTCYIPSNVYAPSDSIQAEEMVFGKITRRESERLLNAENPRGTFLVRES 181
QY 181 ETTKGAIVCLSVDPDNAGKLVNHYKIRKLDGSGFYITSTRTOFNSLQOLVAAYYSKADGL 240
DB 182 ETTKGAIVCLSVDPDNAGKLVNHYKIRKLDGSGFYITSTRTOFNSLQOLVAAYYSKADGL 241
QY 241 CHRLTVCPYTSKQOTGLAKDAWEIPRESLRLEVKLGQCGFGEVWMTGNVTTRVAIKTL 300
DB 242 CHRLTVCPYTSKQOTGLAKDAWEIPRESLRLEVKLGQCGFGEVWMTGNVTTRVAIKTL 301
QY 301 KPGTMSPEAFLOAQVMKLRHEKLVQLYAVVSEBPIYIVTEYMSKGSLLDFLKGETGKY 360
DB 302 KPGTMSPEAFLOAQVMKLRHEKLVQLYAVVSEBPIYIVTEYMSKGSLLDFLKGETGKY 361
QY 361 LRLPQLVDMAAQIAGSMAYVERMYVHRDLRAANIIVGENLVCKVADFGIARLIIDNEYT 420
DB 362 LRLPQLVDMAAQIAGSMAYVERMYVHRDLRAANIIVGENLVCKVADFGIARLIIDNEYT 421
QY 421 ARQGAAPFKMTAPBALYGRFTIKSDVMSFGILLTELTKGVPYPGMNNREVLDOVER 480
DB 422 ARQGAAPFKMTAPBALYGRFTIKSDVMSFGILLTELTKGVPYPGMNNREVLDOVER 481
QY 481 GYRMPCEPCEBSLHDLMCQWKRKEPERPTFEYLQAFLEDYFTSTPEPOQPGENL 536
DB 482 GYRMPCEPCEBSLHDLMCQWKRKEPERPTFEYLQAFLEDYFTSTPEPOQPGENL 537

RESULT 10
US-09-444-711A-4
Sequence 4, Application US/09444711A

```

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; Patent No. 6764833
; GENERAL INFORMATION:
; APPLICANT: Yeatman, Timothy J.
; APPLICANT: Iddy, Rosalyn B.
; TITLE OF INVENTION: Mutated SRC Oncogene Composition and Methods
; FILE REFERENCE: USF-T136
; CURRENT APPLICATION NUMBER: US/09/444,711A
; CURRENT FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 530
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(530)
; OTHER INFORMATION: amino acid sequence of the mutant c-src polypeptide encoded
; OTHER INFORMATION: by the mutant c-src coding region
; US-09-444-711A-4

Query Match          98.8%; Score 2801; DB 2; Length 530;
Best Local Similarity 100.0%; Pred. No. 1e-212;
Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSNKSXPDKASQRRSLRLEPAENVHAGGAFPASQTPSPKASADGHRGSAAPAPAAE 60
DB 1 MGSNKSXPDKASQRRSLRLEPAENVHAGGAFPASQTPSPKASADGHRGSAAPAPAAE 60
QY 61 PKLFGFNSSDPTVTSPPRAGLAGVTTFFVALYDESRTEITDLSFKKGERLQIVNTEGD 120
DB 61 PKLFGFNSSDPTVTSPPRAGLAGVTTFFVALYDESRTEITDLSFKKGERLQIVNTEGD 120
QY 121 WMLAHSLSLTGQTYIPSNVYAPSDSIQAEWYFGKITRRESERLLNENRGTFVRES 180
DB 121 WMLAHSLSLTGQTYIPSNVYAPSDSIQAEWYFGKITRRESERLLNENRGTFVRES 180
QY 181 ETTGAYCLSVSDPDNAKGLNVKHYKIRKLDGSGFYITSRTOFNSLQQLVAYYSKADGL 240
DB 181 ETTGAYCLSVSDPDNAKGLNVKHYKIRKLDGSGFYITSRTOFNSLQQLVAYYSKADGL 240
QY 241 CHRLTYVCPTSPKPTQGLADAMEIPRESLRLRYKLGQCGCGEYMGTMGTTTVAIKTL 300
DB 241 CHRLTYVCPTSPKPTQGLADAMEIPRESLRLRYKLGQCGCGEYMGTMGTTTVAIKTL 300
QY 241 CHRLTYVCPTSPKPTQGLADAMEIPRESLRLRYKLGQCGCGEYMGTMGTTTVAIKTL 300
DB 241 CHRLTYVCPTSPKPTQGLADAMEIPRESLRLRYKLGQCGCGEYMGTMGTTTVAIKTL 300
QY 301 KPGTMSPEAFLOEAQVWKKLRHEKLVOLYAVVSEPIYIVTEYMSKSLDFLKGEGKY 360
DB 301 KPGTMSPEAFLOEAQVWKKLRHEKLVOLYAVVSEPIYIVTEYMSKSLDFLKGEGKY 360
QY 361 LRLPOLVDMAAQIASGNAVYERNYVHRDLRAANILVGENLVCKVADFGRLIEDNEYT 420
DB 361 LRLPOLVDMAAQIASGNAVYERNYVHRDLRAANILVGENLVCKVADFGRLIEDNEYT 420
QY 421 ARQAKRPPIKMTAPBALYGRFTIKSDVMSFGILLTELTTGKRPVPGMVNREVLDOVER 480
DB 421 ARQAKRPPIKMTAPBALYGRFTIKSDVMSFGILLTELTTGKRPVPGMVNREVLDOVER 480
QY 481 GYRMPCEPCEPSLHDLMCQMRKEPERPTEYLQAFLEDPYFSTSEQY 530
DB 481 GYRMPCEPCEPSLHDLMCQMRKEPERPTEYLQAFLEDPYFSTSEQY 530

RESULT 11
US-09-470-881-3
; Sequence 3, Application US/09470881
; Patent No. 6685938
; GENERAL INFORMATION:
; APPLICANT: CHERESH, David A.
; APPLICANT: ELICERI, Brian
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR MODULATION OF
; TITLE OF INVENTION: ANGIOGENESIS AND VASCULAR PERMEABILITY USING SRC OR
; TITLE OF INVENTION: YES TYROSINE KINASES
; FILE REFERENCE: TSRI 651.2
```

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; CURRENT APPLICATION NUMBER: US/09/470, 881
; CURRENT FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: PCT/US99/11780
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087, 220
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 533
; TYPE: PRT
; ORGANISM: Chicken
; US-09-470-881-3

Query Match          94.0%; Score 2663.5; DB 2; Length 533;
Best Local Similarity 94.0%; Pred. No. 7.4e-202;
Matches 504; Conservative 11; Mismatches 18; Indels 3; Gaps 1;

QY 1 MGSNKSXPDKASQRRSLRLEPAENVHAGGAFPASQTPSPKASADGHRGSAAPAPAAE 60
DB 1 MGSNKSXPDKASQRRSLRLEPDSTH--HGCFPASQTPNKTAADPTKTPSRSGTVAATB 57
QY 61 PKLFGFNSSDPTVTSPPRAGLAGVTTFFVALYDESRTEITDLSFKKGERLQIVNTEGD 120
DB 58 PKLFGFNSSDPTVTSPPRAGLAGVTTFFVALYDESRTEITDLSFKKGERLQIVNTEGD 117
QY 121 WMLAHSLSLTGQTYIPSNVYAPSDSIQAEWYFGKITRRESERLLNENRGTFVRES 180
DB 118 WMLAHSLSLTGQTYIPSNVYAPSDSIQAEWYFGKITRRESERLLNENRGTFVRES 177
QY 181 ETTGAYCLSVSDPDNAKGLNVKHYKIRKLDGSGFYITSRTOFNSLQQLVAYYSKADGL 240
DB 178 ETTGAYCLSVSDPDNAKGLNVKHYKIRKLDGSGFYITSRTOFNSLQQLVAYYSKADGL 237
QY 241 CHRLTYVCPTSPKPTQGLADAMEIPRESLRLRYKLGQCGCGEYMGTMGTTTVAIKTL 300
DB 238 CHRLTYVCPTSPKPTQGLADAMEIPRESLRLRYKLGQCGCGEYMGTMGTTTVAIKTL 297
QY 301 KPGTMSPEAFLOEAQVWKKLRHEKLVOLYAVVSEPIYIVTEYMSKSLDFLKGEGKY 360
DB 298 KPGTMSPEAFLOEAQVWKKLRHEKLVOLYAVVSEPIYIVTEYMSKSLDFLKGEGKY 357
QY 361 LRLPOLVDMAAQIASGNAVYERNYVHRDLRAANILVGENLVCKVADFGRLIEDNEYT 420
DB 358 LRLPOLVDMAAQIASGNAVYERNYVHRDLRAANILVGENLVCKVADFGRLIEDNEYT 417
QY 421 ARQAKRPPIKMTAPBALYGRFTIKSDVMSFGILLTELTTGKRPVPGMVNREVLDOVER 480
DB 418 ARQAKRPPIKMTAPBALYGRFTIKSDVMSFGILLTELTTGKRPVPGMVNREVLDOVER 477
QY 481 GYRMPCEPCEPSLHDLMCQMRKEPERPTEYLQAFLEDPYFSTSEQY 536
DB 478 GYRMPCEPCEPSLHDLMCQMRDPERPTEYLQAFLEDPYFSTSEQY 533

RESULT 12
US-07-820-011A-2
; Sequence 2, Application US/07820011A
; Patent No. 533615
; GENERAL INFORMATION:
; APPLICANT: Bell, Leonard
; APPLICANT: Madri, Joseph A.
; APPLICANT: Warren, Stephen L.
; APPLICANT: Luthinger, Daniel J.
; TITLE OF INVENTION: Genetically Engineered
; TITLE OF INVENTION: Endothelial Cells Exhibiting Enhanced
; TITLE OF INVENTION: Migration
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESS: Maurice M. Klee
; STREET: 1951 Burr Street
; CITY: Fairfield
```

STATE: Connecticut
COUNTRY: USA
ZIP: 06430
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb storage
COMPUTER: IBM PC XT
OPERATING SYSTEM: PC-DOS/MS-DOS 2.10
SOFTWARE: Displaywrite 3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/820.011A
FILING DATE: 19920106
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399
REFERENCE/DOCKET NUMBER: LB-101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 254 1101
TELEFAX: (203) 254 1400
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 513 amino acids
TYPE: AMINO ACID
TOPOLOGY: Linear
MOLECULE TYPE: Protein
HYPOTHETICAL: No
FRAGMENT TYPE: Complete Sequence
ORIGINAL SOURCE:
ORGANISM: Gallus, gallus
PUBLICATION INFORMATION:
AUTHORS: Takeya, Tatsuo
AUTHORS: Hanafusa, Hidesaburo
TITLE: Structure and Sequence of the
TITLE: Cellular Gene Homologous to the RSV SRC
TITLE: Gene and the Mechanism for Generating the
JOURNAL: Cell
VOLUME: 32
PAGES: 881-890
DATE: March, 1983
US-07-820-011A-2

Query Match	93.9%	Score 2660.5	DB 1	length 533
Best Local Similarity	93.8%	Pred. No. 1.3e-201		
Matches 503	Conservative 12	Mismatches 16	Indels 3	Gaps 1
QY	1	MGSNKSKPKDASQRRSLLEPAENVHAGAGAFPA\$QTP\$KPA\$ADGHR\$P\$AFA\$PAA\$	60	
Db	1	MGSSKSKPKD\$QRRSLLEPPD\$T\$--HG\$P\$ASQTPNKTAA\$P\$TH\$TP\$RS\$F\$VATE	57	
QY	61	PKLPGGNS\$PT\$M\$SPQ\$AGPLAGVTT\$FV\$LYD\$EST\$END\$LSK\$K\$ERLOI\$VNNTEGD	120	
Db	58	PKLFGGNT\$PT\$V\$PSQ\$AGL\$AGVTT\$FV\$LYD\$EST\$END\$LSK\$K\$ERLOI\$VNNTEGD	117	
QY	121	WMLA\$LSL\$TG\$TG\$YIP\$SNYV\$AP\$DSIO\$AEWY\$FGKITR\$ESERLL\$N\$AENP\$GTE\$LV\$ES	180	
Db	118	WMLA\$LSL\$TG\$TG\$YIP\$SNYV\$AP\$DSIO\$AEWY\$FGKITR\$ESERLL\$N\$ENP\$GTE\$LV\$ES	177	
QY	181	ETT\$TG\$AVCL\$V\$SD\$PDNA\$KGL\$V\$K\$YIK\$RKL\$D\$SGCYIT\$SRQF\$N\$LOOL\$V\$AY\$S\$K\$ADGL	240	
Db	178	ETT\$TG\$AVCL\$V\$SD\$PDNA\$KGL\$V\$K\$YIK\$RKL\$D\$SGCYIT\$SRQF\$N\$LOOL\$V\$AY\$S\$K\$ADGL	237	
QY	241	CHRLITVCPT\$K\$P\$OT\$GL\$AD\$AMEI\$P\$RES\$L\$R\$EV\$L\$GGC\$G\$E\$V\$M\$G\$T\$NG\$TR\$V\$AI\$KTL	300	
Db	238	CHRLITVCPT\$K\$P\$OT\$GL\$AD\$AMEI\$P\$RES\$L\$R\$EV\$L\$GGC\$G\$E\$V\$M\$G\$T\$NG\$TR\$V\$AI\$KTL	297	
QY	301	KPGT\$S\$E\$AFLQ\$E\$AQV\$M\$K\$L\$R\$HEK\$L\$VOL\$Y\$AV\$S\$E\$P\$IY\$T\$EY\$M\$K\$S\$LLD\$FLK\$G\$ET\$K\$Y	360	
Db	298	KPGT\$S\$E\$AFLQ\$E\$AQV\$M\$K\$L\$R\$HEK\$L\$VOL\$Y\$AV\$S\$E\$P\$IY\$T\$EY\$M\$K\$S\$LLD\$FLK\$G\$EM\$K\$Y	357	
QY	361	LRL\$POLV\$DMAQI\$AS\$GA\$Y\$Y\$R\$M\$Y\$V\$H\$D\$L\$P\$A\$N\$L\$V\$E\$N\$LV\$CK\$AD\$G\$LA\$L\$ED\$N\$EY\$T	420	
Db	358	LRL\$POLV\$DMAQI\$AS\$GA\$Y\$Y\$R\$M\$Y\$V\$H\$D\$L\$P\$A\$N\$L\$V\$E\$N\$LV\$CK\$AD\$G\$LA\$L\$ED\$N\$EY\$T	417	

Oy ARQAGKFFI KMTAPAAALYGRFTISDWSFCILLTELTKRVPPGMVNEVLDOVR 480
 |||||
 Db ARQAGKFFI KMTAPAAALYGRFTISDWSFCILLTELTKRVPPGMVNEVLDOVR 477
 |||||
 Oy GYRNP CPPECESLHDMCCCKRKEPERPRFEYLAFLDXYFTSTPOYQGENL 536
 481 |||||
 Db GYRNP CPPECESLHDMCCCKRKEPERPRFEYLAFLDXYFTSTPOYQGENL 533
 478 |||||

RESULT 13
PCT-US93-00445-2

```

1 GENERAL INFORMATION:
2 APPLICANT: Bell, Leonard
3 APPLICANT: Madri, Joseph A.
4 APPLICANT: Warren, Stephen L.
5 APPLICANT: Luthringer, Daniel J.
6 TITLE OF INVENTION: Genetically Engineered
7 TITLE OF INVENTION: Endothelial Cells
8 NUMBER OF SEQUENCES: 4
9 CORRESPONDENCE ADDRESS:
10 ADDRESSEE: Maurice M. Klee
11 STREET: 1951 Burr Street
12 CITY: Fairfield
13 STATE: Connecticut
14 COUNTRY: USA
15 ZIP: 06430
16
17 COMPUTER READABLE FORM:
18 MEDIUM TYPE: 3.5 inch, 760 Kb storage
19 COMPUTER: DELL 486/50
20 OPERATING SYSTEM: DOS 5.0
21 SOFTWARE: Displaywrite 3
22 CURRENT APPLICATION DATA:
23 APPLICATION NUMBER: PCT/US93/00445
24 FILING DATE: 19930105
25 CLASSIFICATION:
26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER: 07/820,011
28 FILING DATE: 06-JAN-1992
29 ATTORNEY/AGENT INFORMATION:
30 NAME: Klee, Maurice M.
31 REGISTRATION NUMBER: 30,399
32 REFERENCE/DOCKET NUMBER: ALX-101PCT
33 TELECOMMUNICATION INFORMATION:
34 TELEPHONE: (203) 255 1400
35 TELEFAX: (203) 254 1101
36 INFORMATION FOR SEQ ID NO: 2:
37 SEQUENCE CHARACTERISTICS:
38 LENGTH: 533 amino acids
39 TYPE: AMINO ACID
40 TOPOLOGY: Linear
41 MOLECULE TYPE: Protein
42 HYPOTHEICAL: No
43 FRAGMENT TYPE: Complete Sequence
44 ORIGINAL SOURCE:
45 ORGANISM: Gallus, Gallus
46 PUBLICATION INFORMATION:
47 AUTHORS: Takeya, Tatsuo
48 TITLE: Structure and Sequence of the
49 TITLE: Cellular Gene Homologous to the RSV src
50 TITLE: Gene and the Mechanism for Generating the
51 TITLE: Transforming Virus
52 JOURNAL: Cell
53 VOLUME: 32
54 PAGES: 881-890
55 DATE: March, 1983
56
57 PCT-US93-00445-2
58
59 Query Match 93.9%; Score 2660.5; DB 5; Length 533;
60 Best Local Similarity 93.8%; Pred. No. 1.3e-201;
61 Matches 503; Conservative 12; Mismatches 18; Indels 3; Gaps 1;

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QY 1 MGSNKSXPXASORRSLPEAENVHAGGGAFPASQTPSKPASADGHRGSAAPAAAE 60
Db 1 MGSFKSPKQPSQRRSLPEPDSTH--HGSPASQTPNKTAADPTHTPERSFGVATE 57
QY 61 PKLFGFNSSDVTYSPQAPGLAGVTFVALYDESRTEETDLSFKKGERQIYVNTGEGD 120
Db 58 PKLFGFNSSDVTYSPQAPGLAGVTFVALYDESRTEETDLSFKKGERQIYVNTGEGD 117
QY 121 WMLAHSITGQGYIPSNVYAPSDSIQAEEMYPGKTRRESERLLNANRGTFLVRES 180
Db 118 WMLAHSITGQGYIPSNVYAPSDSIQAEEMYPGKTRRESERLLNANRGTFLVRES 177
QY 181 ETTKGAACLSVSDPDNAKGLNVKHKYIKLDSGGFYITSRTOFNSLOQLVAYYSKADGL 240
Db 178 ETTKGAACLSVSDPDNAKGLNVKHKYIKLDSGGFYITSRTOFNSLOQLVAYYSKADGL 237
QY 241 CHRLLTVCPYSPQTOGLADAMEIPRESLRLEVKLGCGCFGEVMMGTNGTTRVAIKTL 300
Db 238 CHRLLTVCPYSPQTOGLADAMEIPRESLRLEVKLGCGCFGEVMMGTNGTTRVAIKTL 297
QY 301 KPGTMSPEAFLOEAQVMKKLRHEKLVOLYAVVSEPIYIVTEYNSKSLDPLKGETGKY 360
Db 298 KPGTMSPEAFLOEAQVMKKLRHEKLVOLYAVVSEPIYIVTEYNSKSLDPLKGETGKY 357
QY 361 LRLLPOLVDMMAQIASGMAVYERMYVHRDLRAANILVGENLVCKVADPGLARLIEDNEYT 420
Db 358 LRLLPOLVDMMAQIASGMAVYERMYVHRDLRAANILVGENLVCKVADPGLARLIEDNEYT 417
QY 421 ARQAKPPIKMTAPEALYGRFTIKSDVMSFGILLTELTKGRVPYPMVREVLDOVER 480
Db 418 ARQAKPPIKMTAPEALYGRFTIKSDVMSFGILLTELTKGRVPYPMVREVLDOVER 477
QY 481 GYRMPCEPCEPSLHDMCCQWKEPBERPTFEYLQAFLEBDYFTSTEBPOYQGENL 536
Db 478 GYRMPCEPCEPSLHDMCCQWKEPBERPTFEYLQAFLEBDYFTSTEBPOYQGENL 533

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RESULT 14

US-08-426-509A-14

Sequence 14, Application US/08426509A

Patent No. 6326469

GENERAL INFORMATION:

APPLICANT: Ulrich, Axel

APPLICANT: Gishizky, Mikhail

APPLICANT: Sures, Iman G.

TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN

TITLE OF INVENTION: TYROSINE KINASES

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York,

STATE: NY

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/426,509A

FILING DATE: 21-APR-1995

CLASSIFICATION: 435

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 08/232,545

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7683-0074-999

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

```

; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIR
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 543 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: No. 6326469e
; US-08-426-509A-14

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Query Match 74.9%; Score 2123.5; DB 2; Length 543;
Best Local Similarity 74.5%; Pred. No. 3.3e-159;
Matches 407; Conservative 51; Mismatches 75; Indels 13; Gaps 4;

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QY 1 MGSNKSXPXASORRSLPEAENVHAGG--GAFPASQTPSKPASADGHRGSAAPAAAE 57
Db 1 MGSFKSPKQPSQRRSLPEPDSTH--HGSPASQTPNKTAADPTHTPERSFGVATE 57
QY 58 AAF-----KLFGRNSSDVTYSPQAPGLAGVTFVALYDESRTEETDLSFKKGER 110
Db 58 SMTPFGSSGVTPPGGASSFSVPSSYPAGLTGTGVTIIPVALYDEARTEETDLSFKKGER 117
QY 111 LOIVNTEGDMWMLAHSITGQGYIPSNVYAPSDSIQAEEMYPGKTRRESERLLNAN 170
Db 118 FOIVNTEGDMWMLAHSITGQGYIPSNVYAPSDSIQAEEMYPGKTRRESERLLNAN 177
QY 171 PRGTFVRESEETTKGAYCLSVSDPDNAKGLNVKHKYIKLDSGGFYITSRTOFNSLOQLV 230
Db 178 ORGTFVRESEETTKGAYCLSVSDPDNAKGLNVKHKYIKLDSGGFYITSRTOFNSLOQLV 237
QY 231 AYSKADGLCHRLLTVCPYSPQTOGLADAMEIPRESLRLEVKLGCGCFGEVMMGTNG 290
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QY 291 GTTFVATKTLKPGTMSPEAFLOEAQVMKKLRHEKLVOLYAVVSEPIYIVTEYNSKSL 350
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QY 351 DFLKGETGKYLRLLPOLVDMMAQIASGMAVYERMYVHRDLRAANILVGENLVCKVADPGL 410
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QY 411 ARLLIEDNEYTARQAKPPIKMTAPEALYGRFTIKSDVMSFGILLTELTKGRVPYPMV 470
Db 418 ARLLIEDNEYTARQAKPPIKMTAPEALYGRFTIKSDVMSFGILLTELTKGRVPYPMV 477
QY 471 NREVLDOVERGYRMPCEPCEPSLHDMCCQWKEPBERPTFEYLQAFLEBDYFTSTEB 530
Db 478 NREVLDOVERGYRMPCEPCEPSLHDMCCQWKEPBERPTFEYLQAFLEBDYFTSTEB 537
QY 531 QPGENL 536
Db 538 QPGENL 543

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RESULT 15

US-08-232-545-14

Sequence 14, Application US/08232545

Patent No. 6506578

GENERAL INFORMATION:

APPLICANT: Ulrich, Axel

APPLICANT: Gishizky, Mikhail

APPLICANT: Sures, Iman G.

TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE

TITLE OF INVENTION: KINASES

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

Search completed: June 5, 2006, 17:18:20
Job time : 31.7894 secs

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COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,545
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
TELEFAX: (212)869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ. ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 543 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-232-545-14

Query Match      74.9%; Score 2123.5; DB 2; Length 543;
Best Local Similarity 74.5%; Pred. No. 3.3e-159;
Matches 407; Conservative 51; Mismatches 75; Indels 13; Gaps 4;

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DB      1 MGCISKSKENKSPAIKRYRPENTPEPVSTSVSHYGAEPITVSPCPSSSA---KGTAVNPFSSL 57
QY      58 AAEF-----KLFEGFNSSDVTYSPQAGPLAGVTTFVALYDYSRTEETDLSFKKGER 110
DB      58 SMTPEGGSSGVTPFGGASSSFVSVPSSYPAGLTGGVTIFVALYDYERKTTEDLSFKKGER 117
QY      111 LOIVNNTBGDWMIAHSLSGTQGYIPSNVYAPSDSIQAEEMWYFGKITRRESERLLNAEN 170
DB      116 FQIINTBGDWMFARSIAATGKNGIYPSNVYAPADSIQAEEMWYFGKMGKDAERLLNPGN 177
QY      171 PRGTPLVRESEETKGAICYCLSVDPNAKGLNVKHYKIRKLDSCGFYITTSRTQNSLQOLY 230
DB      178 ORGIFLVRESEETKGAYSLSIRDMDEIRGDNVGHYKIRKLDNGGYITTRAQPDYLOKLV 237
QY      231 AVYSKADADGCHRLTTCVPTSKPQTQGLAKDAWEIPRESLRLEVKLGQCGFGEVMNGTWN 290
DB      238 KHTTEHADGICHKLITVCPTVKPQTQGLAKDAWEIPRESLRLEVKLGQCGFGEVMNGTWN 297
QY      291 GTTRVAIKTLKPGTMSPEAFLOEAQVMKLRHEKLVOLYAVVSEBPIYIVTEYMSKGSLL 350
DB      296 GTTKVAIKTLKPGTMMPEAFLOEAQIMKLRHDKLVPLVAVVSEBPIYIVTEFMSKGSLL 357
QY      351 DFLKSGTGYTLRPLQVLDMAAQASGMAYVERMNYVHRDLRAANILVGENLVCKVADFGI 410
DB      358 DFLKSGDGYTLRPLQVLDMAAQIADGMAYIERMNYIHRDLRAANILVGENLVCKIADFGI 417
QY      411 ARLIEDNETARQGAEPITKWTPEALVGRFTIKSDVMSFGILLTELTKGRVYPGMV 470
DB      418 ARLIEDNETARQGAEPITKWTPEALVGRFTIKSDVMSFGILLTELTKGRVYPGMV 477
QY      471 NREVLDOVERGYAMPPEPCRESLHDLIMCQMKRKEBERPTPEYLOAFLEDYFTSTEPQY 530
DB      478 NREVLQOVERGYAMPPEPCRESLHDLIMCQMKRKEBERPTPEYLOAFLEDYFTATEPQY 537
QY      531 QPGENL 536
DB      538 QPGENL 543
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OM protein - protein search, using sw model

Run on: June 5, 2006, 17:37:14 ; Search time 107.266 Seconds
(without alignments)
2314.645 Million cell updates/sec

Title: US-10-691-079-2

Perfect score: 2834

Sequence: 1 MGSNKSXPXKASQRRSLR.....AFLEDYFTSTPEYQDGENL 536

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.Main:

1: /EMC_Celerra_SIDS3/Products/2/pubppaa/US07_PUBCOMB.pep.*

2: /EMC_Celerra_SIDS3/Products/2/pubppaa/US08_PUBCOMB.pep.*

3: /EMC_Celerra_SIDS3/Products/2/pubppaa/US09_PUBCOMB.pep.*

4: /EMC_Celerra_SIDS3/Products/2/pubppaa/US10_PUBCOMB.pep.*

5: /EMC_Celerra_SIDS3/Products/2/pubppaa/US10_PUBCOMB.pep.*

6: /EMC_Celerra_SIDS3/Products/2/pubppaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2834	100.0	536	US-09-977-260-13	Sequence 13, Appl
2	2834	100.0	536	US-09-929-266-10	Sequence 10, Appl
3	2834	100.0	536	US-09-977-261-13	Sequence 13, Appl
4	2834	100.0	536	US-10-691-079-2	Sequence 2, Appl
5	2834	100.0	536	US-10-887-588-2	Sequence 2, Appl
6	2834	100.0	536	US-10-497-641-2	Sequence 2, Appl
7	2834	100.0	536	US-10-825-568-10	Sequence 10, Appl
8	2834	100.0	536	US-10-821-231C-1	Sequence 1, Appl
9	2834	100.0	536	US-10-469-469-273	Sequence 273, Appl
10	2834	100.0	536	US-11-233-510-24	Sequence 24, Appl
11	2829	99.8	535	US-10-394-322A-56	Sequence 56, Appl
12	2829	99.8	535	US-10-814-109-4	Sequence 4, Appl
13	2821	99.5	542	US-10-691-079-1	Sequence 1, Appl
14	2801	98.8	530	US-10-887-588-4	Sequence 4, Appl
15	2781	98.1	542	US-10-732-923-13447	Sequence 13447, A
16	2778.5	98.0	541	US-10-691-079-3	Sequence 3, Appl
17	2767	97.6	530	US-10-330-773-749	Sequence 749, Appl
18	2666.5	94.1	533	US-10-276-633-1	Sequence 1, Appl
19	2666.5	94.1	533	US-10-732-923-13652	Sequence 13652, A
20	2663.5	94.0	533	US-10-732-923-13654	Sequence 13654, A
21	2663.5	94.0	533	US-11-230-995-3	Sequence 3, Appl
22	2661.5	93.9	533	US-10-732-923-13650	Sequence 13650, A
23	2641.5	92.5	587	US-10-732-923-13472	Sequence 13472, A
24	2641.5	92.5	587	US-10-732-923-13474	Sequence 13474, A
25	2608.5	92.0	587	US-10-732-923-13469	Sequence 13469, A
26	2599.5	91.7	557	US-10-732-923-13475	Sequence 13475, A

28	2533.5	89.4	526	US-10-732-923-13499	Sequence 13499, A
29	2516.5	88.8	526	US-10-732-923-13484	Sequence 13484, A
30	2516.5	88.8	526	US-10-732-923-13485	Sequence 13485, A
31	2497.5	88.1	526	US-10-732-923-13483	Sequence 13483, A
32	2491.5	87.9	526	US-10-732-923-13497	Sequence 13497, A
33	2485.5	87.7	526	US-10-732-923-13493	Sequence 13493, A
34	2485.5	87.7	526	US-10-732-923-13489	Sequence 13489, A
35	2484.5	87.7	526	US-10-732-923-13489	Sequence 13489, A
36	2483.5	87.6	526	US-10-732-923-13486	Sequence 13486, A
37	2482	87.6	523	US-10-732-923-13488	Sequence 13488, A
38	2482	87.6	523	US-10-732-923-13495	Sequence 13495, A
39	2481.5	87.6	526	US-10-732-923-13491	Sequence 13491, A
40	2470.5	87.2	526	US-10-732-923-13492	Sequence 13492, A
41	2466.5	87.0	526	US-10-732-923-13487	Sequence 13487, A
42	2463	86.9	532	US-10-732-923-13633	Sequence 13633, A
43	2462	86.9	532	US-10-732-923-13635	Sequence 13635, A
44	2459	86.8	532	US-10-732-923-13637	Sequence 13637, A
45	2457.5	86.7	537	US-10-732-923-13636	Sequence 13636, A

ALIGNMENTS

RESULT 1
US-09-977-260-13

Sequence 13, Application US/09977260

Publication No. US20020192790A1

GENERAL INFORMATION:

APPLICANT: ULIRICH, AXEL

APPLICANT: GISHIZKY, MIKHAIL

APPLICANT: SIBRES, ILMINGARD

TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES

FILE REFERENCE: 038602/1260

CURRENT APPLICATION NUMBER: US/09/977, 260

CURRENT FILING DATE: 2001-10-16

PRIOR APPLICATION NUMBER: 08/232, 545

PRIOR FILING DATE: 1994-04-22

NUMBER OF SEQ ID NOS: 24

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 13

LENGTH: 536

TYPE: PRT

ORGANISM: Homo sapiens

US-09-977-260-13

Query Match

Best Local Similarity 100.0%; Score 2834; DB 3; Length 536;

Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 MGSNKSXPXKASQRRSLRPAENVHAGGAFPAASQTPSKPAPADGHRGSAAPAPAAE 60

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1 MGSNKSXPXKASQRRSLRPAENVHAGGAFPAASQTPSKPAPADGHRGSAAPAPAAE 60

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QY 361 LRLPOLVDMAAOIASGMAYYERNVYHRDLRAANILVGENLVCKVADFGIARLIEDNEYT 420
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Db 361 LRLPOLVDMAAOIASGMAYYERNVYHRDLRAANILVGENLVCKVADFGIARLIEDNEYT 420
QY 421 AROGAKFPIKMTAPBAALYGRFTIKSDVMSFGILLTELTTKGRVVPYPGMVNREVLDOVER 480
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Db 421 AROGAKFPIKMTAPBAALYGRFTIKSDVMSFGILLTELTTKGRVVPYPGMVNREVLDOVER 480
QY 481 GYRMPCEPPECPSLHDMCCQWKKEPERPTEFYLOAFLEDYFTSTPEYQOGENL 536
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Db 481 GYRMPCEPPECPSLHDMCCQWKKEPERPTEFYLOAFLEDYFTSTPEYQOGENL 536

RESULT 2
US-09-929-266-10
; Sequence 10, Application US/09929266
; Publication No. US20030045694A1
; GENERAL INFORMATION:
; APPLICANT: Brian T. Chait
; APPLICANT: Darin R. Latimer
; APPLICANT: Paul M. Lizardi
; APPLICANT: Eric R. Kezrenat
; APPLICANT: Jon S. Morrow
; APPLICANT: Matthew B. Roth
; APPLICANT: Martin J. Matthesich
; APPLICANT: Kevin J. McConnell
; TITLE OF INVENTION: ULTRA-SENSITIVE DETECTION SYSTEMS
; FILE REFERENCE: 01173.000302
; CURRENT APPLICATION NUMBER: US/09/929,266
; CURRENT FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/224,939
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/283,498
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 536
; TYPE: PRF
; ORGANISM: Homo sapiens
; US-09-929-266-10

Query Match 100.0%; Score 2834; DB 3; Length 536;
Best Local Similarity 100.0%; Pred. No. 1,1e-174;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 PKLFGFNSSDVTYSPQRAPIPLAGVTTFVALYDYESRTETDLSFKKGERLOIVNNTGEGD 120
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Db 121 WMLAHLSTGQCYTISNTVVAAPSDSIQAEEMWFGKTRRESERLLNNAENPRTFLVRES 180
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Db 121 WMLAHLSTGQCYTISNTVVAAPSDSIQAEEMWFGKTRRESERLLNNAENPRTFLVRES 180
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Db 481 GYRMPCEPPECPSLHDMCCQWKKEPERPTEFYLOAFLEDYFTSTPEYQOGENL 536

RESULT 3
US-09-977-261-13
; Sequence 13, Application US/09977261
; Publication No. US20030004527A1
; GENERAL INFORMATION:
; APPLICANT: ULTRICH, AXEL
; APPLICANT: GISHIZKY, MIKHAIL
; APPLICANT: SURES, IRMINGARD
; TITLE OF INVENTION: NOVEL MEKAKARYOCYTIC PROTEIN TYROSINE KINASES
; FILE REFERENCE: 038602/1259
; CURRENT APPLICATION NUMBER: US/09/977,261
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 08/232,545
; PRIOR FILING DATE: 1994-04-22
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 13
; LENGTH: 536
; TYPE: PRF
; ORGANISM: Homo sapiens
; US-09-977-261-13

Query Match 100.0%; Score 2834; DB 3; Length 536;
Best Local Similarity 100.0%; Pred. No. 1,1e-174;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 421 AROGAKFPIKMTAPBAALYGRFTIKSDVMSFGILLTELTTKGRVVPYPGMVNREVLDOVER 480
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Db 481 GYRMPCEPPECPSLHDMCCQWKKEPERPTEFYLOAFLEDYFTSTPEYQOGENL 536
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RESULT 4
US-10-691-079-2
; Sequence 2, Application US/10691079
; Publication No. US2004017631A1
; GENERAL INFORMATION:
; APPLICANT: AVENTIS PHARMA S.A.
; TITLE OF INVENTION: Inhibitors of SRC kinase for use in Alzheimer's disease
; FILE REFERENCE: PAAV2002/0030
; CURRENT APPLICATION NUMBER: US/10/691,079
; CURRENT FILING DATE: 2003-10-22
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-691-079-2

Query Match      100.0%; Score 2834; DB 4; Length 536;
Best Local Similarity 100.0%; Pred. No. 1,1e-174;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSNKSXPDKASQRRSLRLEPAENVHAGGAFPASQTPSKPASADGHRGSAAPAAAE 60
DB 1 MGSNKSXPDKASQRRSLRLEPAENVHAGGAFPASQTPSKPASADGHRGSAAPAAAE 60
QY 61 PKLFGFNSSDVTTSPPRAGPLAGGVTTFVALYDSESTETDLSFKKGERLQIVNTEGD 120
DB 61 PKLFGFNSSDVTTSPPRAGPLAGGVTTFVALYDSESTETDLSFKKGERLQIVNTEGD 120
QY 121 WMLAHSISTGQTGYIPSNVYAPSDSIQAEWYFKKTRRSEERLLNAENRGTFVRES 180
DB 121 WMLAHSISTGQTGYIPSNVYAPSDSIQAEWYFKKTRRSEERLLNAENRGTFVRES 180
QY 181 ETTKGAAYCLASVSDPDNAKGLNVKHYKIRKLDGSGFYITSRQFNSLQOLVAVYSGHADGL 240
DB 181 ETTKGAAYCLASVSDPDNAKGLNVKHYKIRKLDGSGFYITSRQFNSLQOLVAVYSGHADGL 240
QY 241 CHRITTCPTSPKPTQGLADAMEIPRESLRLEVKLGCGCFGEVWMTGTTTVAIKTL 300
DB 241 CHRITTCPTSPKPTQGLADAMEIPRESLRLEVKLGCGCFGEVWMTGTTTVAIKTL 300
QY 301 KPGTMSBEAFLQEQVWKKLRHEKLVOLYAVVSEPIYIYEVMSKSLDLFLGEGTKY 360
DB 301 KPGTMSBEAFLQEQVWKKLRHEKLVOLYAVVSEPIYIYEVMSKSLDLFLGEGTKY 360
QY 361 LRLPOLVDMAQAQASGNAVYERMYVARDLRAANILVGENLVCKVADFGRLLEDNEYT 420
DB 361 LRLPOLVDMAQAQASGNAVYERMYVARDLRAANILVGENLVCKVADFGRLLEDNEYT 420
QY 421 ARQAKPEPIKWTABEALYGRFTIKSDVMSFGILLTELTTKGRVYPGQVNRREVLDQVER 480
DB 421 ARQAKPEPIKWTABEALYGRFTIKSDVMSFGILLTELTTKGRVYPGQVNRREVLDQVER 480
QY 481 GYRMPCEPCEPESLHDMCCQWKREPERPFEVLOAFLEBYFTSTEPQYQPGENTL 536
DB 481 GYRMPCEPCEPESLHDMCCQWKREPERPFEVLOAFLEBYFTSTEPQYQPGENTL 536

RESULT 5
US-10-887-588-2
; Sequence 2, Application US/10887588
; Publication No. US2004026114A2A1
; GENERAL INFORMATION:
; APPLICANT: Idby, Timothy J.
; APPLICANT: Yeatman, Timothy B.
; TITLE OF INVENTION: Mutated SRC Oncogene Composition and Methods
; FILE REFERENCE: USF-1136
; CURRENT APPLICATION NUMBER: US/10/887,588
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US/09/444,711
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 7
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SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(536)
; OTHER INFORMATION: amino acid sequence of non-receptor tyrosine kinase encoded
; OTHER INFORMATION: by the normal c-Src coding region
US-10-887-588-2

Query Match      100.0%; Score 2834; DB 5; Length 536;
Best Local Similarity 100.0%; Pred. No. 1,1e-174;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSNKSXPDKASQRRSLRLEPAENVHAGGAFPASQTPSKPASADGHRGSAAPAAAE 60
DB 1 MGSNKSXPDKASQRRSLRLEPAENVHAGGAFPASQTPSKPASADGHRGSAAPAAAE 60
QY 61 PKLFGFNSSDVTTSPPRAGPLAGGVTTFVALYDSESTETDLSFKKGERLQIVNTEGD 120
DB 61 PKLFGFNSSDVTTSPPRAGPLAGGVTTFVALYDSESTETDLSFKKGERLQIVNTEGD 120
QY 121 WMLAHSISTGQTGYIPSNVYAPSDSIQAEWYFKKTRRSEERLLNAENRGTFVRES 180
DB 121 WMLAHSISTGQTGYIPSNVYAPSDSIQAEWYFKKTRRSEERLLNAENRGTFVRES 180
QY 181 ETTKGAAYCLASVSDPDNAKGLNVKHYKIRKLDGSGFYITSRQFNSLQOLVAVYSGHADGL 240
DB 181 ETTKGAAYCLASVSDPDNAKGLNVKHYKIRKLDGSGFYITSRQFNSLQOLVAVYSGHADGL 240
QY 241 CHRITTCPTSPKPTQGLADAMEIPRESLRLEVKLGCGCFGEVWMTGTTTVAIKTL 300
DB 241 CHRITTCPTSPKPTQGLADAMEIPRESLRLEVKLGCGCFGEVWMTGTTTVAIKTL 300
QY 301 KPGTMSBEAFLQEQVWKKLRHEKLVOLYAVVSEPIYIYEVMSKSLDLFLGEGTKY 360
DB 301 KPGTMSBEAFLQEQVWKKLRHEKLVOLYAVVSEPIYIYEVMSKSLDLFLGEGTKY 360
QY 361 LRLPOLVDMAQAQASGNAVYERMYVARDLRAANILVGENLVCKVADFGRLLEDNEYT 420
DB 361 LRLPOLVDMAQAQASGNAVYERMYVARDLRAANILVGENLVCKVADFGRLLEDNEYT 420
QY 421 ARQAKPEPIKWTABEALYGRFTIKSDVMSFGILLTELTTKGRVYPGQVNRREVLDQVER 480
DB 421 ARQAKPEPIKWTABEALYGRFTIKSDVMSFGILLTELTTKGRVYPGQVNRREVLDQVER 480
QY 481 GYRMPCEPCEPESLHDMCCQWKREPERPFEVLOAFLEBYFTSTEPQYQPGENTL 536
DB 481 GYRMPCEPCEPESLHDMCCQWKREPERPFEVLOAFLEBYFTSTEPQYQPGENTL 536

RESULT 6
US-10-497-641-2
; Sequence 2, Application US/10497641
; Publication No. US20050037446A1
; GENERAL INFORMATION:
; APPLICANT: Schmitt and Stork
; TITLE OF INVENTION: AGENTS THAT RECOGNIZE SRC WHEN PHOSPHORYLATED AT SERINE 17
; FILE REFERENCE: 65064-02
; CURRENT APPLICATION NUMBER: US/10/497,641
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: PCT/US02/41564
; PRIOR FILING DATE: 2002-12-27
; PRIOR APPLICATION NUMBER: 60/345,888
; PRIOR FILING DATE: 2001-12-28
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-10-497-641-2

Query Match 100.0%; Score 2834; DB 5; Length 536;
Best Local Similarity 100.0%; Pred. No. 1,1e-174;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MGSNKSXPDAQORRRSLBPAENVHAGGAGFPASQTPSKPASADGHRGSAAPAPAAAE 60
DB 1 MGSNKSXPDAQORRRSLBPAENVHAGGAGFPASQTPSKPASADGHRGSAAPAPAAAE 60
QY 61 PKLFGFNSDPTVTSQQRAGPLAGGVTTFVALYDRESRTETDLSFKKGERLQIVNTEGD 120
DB 61 PKLFGFNSDPTVTSQQRAGPLAGGVTTFVALYDRESRTETDLSFKKGERLQIVNTEGD 120
QY 121 WMLAHSLSGTQGYIPSNVYAPSDSIQAEEMVFGKTRRESERLLNAENPGTFLYRES 180
DB 121 WMLAHSLSGTQGYIPSNVYAPSDSIQAEEMVFGKTRRESERLLNAENPGTFLYRES 180
QY 181 ETTKGA YCLSVSDFDNAGKLANVHYKIRKLDGSGFYITSRTQFNSLQQLVAAYSKHADGL 240
DB 181 ETTKGA YCLSVSDFDNAGKLANVHYKIRKLDGSGFYITSRTQFNSLQQLVAAYSKHADGL 240
QY 241 CHRLLTVCTSKPQTQGLAKDAWEIPRESLRLEVKLGQCGFGEVWMTNGTTRVAIKTL 300
DB 241 CHRLLTVCTSKPQTQGLAKDAWEIPRESLRLEVKLGQCGFGEVWMTNGTTRVAIKTL 300
QY 301 KPGTMSPEAFLOBAQVMKLRHEKLVOLYAVVSEBPIYIVTEYMSKSLDLDFLKGRTGY 360
DB 301 KPGTMSPEAFLOBAQVMKLRHEKLVOLYAVVSEBPIYIVTEYMSKSLDLDFLKGRTGY 360
QY 361 LRLPOLVDMAAQIASGMAVVERMNYVHRDLRAANILVGENLVCKVADFGIARLIEDNEYT 420
DB 361 LRLPOLVDMAAQIASGMAVVERMNYVHRDLRAANILVGENLVCKVADFGIARLIEDNEYT 420
QY 421 AROGAKFPITKWTAPBALYGRFTIKSDVWSFGILLTELTKGRVPPGVMNREVLDOVER 480
DB 421 AROGAKFPITKWTAPBALYGRFTIKSDVWSFGILLTELTKGRVPPGVMNREVLDOVER 480
QY 481 GYRMPCEPCPSLHDLMCQCRKEPERPTEYLOAFLEDYFTSTEPYOGENL 536
DB 481 GYRMPCEPCPSLHDLMCQCRKEPERPTEYLOAFLEDYFTSTEPYOGENL 536
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RESULT 7

```
US-10-825-568-10
; Sequence 10, Application US/10825568
; Publication No. US2005006916A1
; GENERAL INFORMATION:
; APPLICANT: Brian T. Chait
; APPLICANT: Darin R. Lattimer
; APPLICANT: Paul M. Lizardi
; APPLICANT: Eric R. Kershner
; APPLICANT: Jon S. Morrow
; APPLICANT: Matthew E. Roth
; APPLICANT: Martin J. Matlessich
; APPLICANT: Kevin J. McConnell
; TITLE OF INVENTION: ULTRA-SENSITIVE DETECTION SYSTEMS
; FILE REFERENCE: 01173.000302
; CURRENT APPLICATION NUMBER: US/10/825, 568
; PRIOR FILING DATE: 2004-04-14
; PRIOR APPLICATION NUMBER: US/09/929, 266
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/224, 939
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/283, 498
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-825-568-10
```

Query Match 100.0%; Score 2834; DB 5; Length 536;
Best Local Similarity 100.0%; Pred. No. 1,1e-174;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MGSNKSXPDAQORRRSLBPAENVHAGGAGFPASQTPSKPASADGHRGSAAPAPAAAE 60
DB 1 MGSNKSXPDAQORRRSLBPAENVHAGGAGFPASQTPSKPASADGHRGSAAPAPAAAE 60
QY 61 PKLFGFNSDPTVTSQQRAGPLAGGVTTFVALYDRESRTETDLSFKKGERLQIVNTEGD 120
DB 61 PKLFGFNSDPTVTSQQRAGPLAGGVTTFVALYDRESRTETDLSFKKGERLQIVNTEGD 120
QY 121 WMLAHSLSGTQGYIPSNVYAPSDSIQAEEMVFGKTRRESERLLNAENPGTFLYRES 180
DB 121 WMLAHSLSGTQGYIPSNVYAPSDSIQAEEMVFGKTRRESERLLNAENPGTFLYRES 180
QY 181 ETTKGA YCLSVSDFDNAGKLANVHYKIRKLDGSGFYITSRTQFNSLQQLVAAYSKHADGL 240
DB 181 ETTKGA YCLSVSDFDNAGKLANVHYKIRKLDGSGFYITSRTQFNSLQQLVAAYSKHADGL 240
QY 241 CHRLLTVCTSKPQTQGLAKDAWEIPRESLRLEVKLGQCGFGEVWMTNGTTRVAIKTL 300
DB 241 CHRLLTVCTSKPQTQGLAKDAWEIPRESLRLEVKLGQCGFGEVWMTNGTTRVAIKTL 300
QY 301 KPGTMSPEAFLOBAQVMKLRHEKLVOLYAVVSEBPIYIVTEYMSKSLDLDFLKGRTGY 360
DB 301 KPGTMSPEAFLOBAQVMKLRHEKLVOLYAVVSEBPIYIVTEYMSKSLDLDFLKGRTGY 360
QY 361 LRLPOLVDMAAQIASGMAVVERMNYVHRDLRAANILVGENLVCKVADFGIARLIEDNEYT 420
DB 361 LRLPOLVDMAAQIASGMAVVERMNYVHRDLRAANILVGENLVCKVADFGIARLIEDNEYT 420
QY 421 AROGAKFPITKWTAPBALYGRFTIKSDVWSFGILLTELTKGRVPPGVMNREVLDOVER 480
DB 421 AROGAKFPITKWTAPBALYGRFTIKSDVWSFGILLTELTKGRVPPGVMNREVLDOVER 480
QY 481 GYRMPCEPCPSLHDLMCQCRKEPERPTEYLOAFLEDYFTSTEPYOGENL 536
DB 481 GYRMPCEPCPSLHDLMCQCRKEPERPTEYLOAFLEDYFTSTEPYOGENL 536
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RESULT 8

```
US-10-821-231C-1
; Sequence 1, Application US/10821231C
; Publication No. US20050275837A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Dongman
; APPLICANT: Ben-Amotz, Dor
; APPLICANT: Xie, Yong
; APPLICANT: Davison, Vincent J.
; APPLICANT: Mrozek, Melissa
; TITLE OF INVENTION: PROCESS AND APPARATUS FOR SEGREGATION AND TESTING BY SPECTRAL
; FILE REFERENCE: 12264/17
; CURRENT APPLICATION NUMBER: US/10/821, 231C
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 60/462, 083
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: US 60/462, 472
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: US 60/490, 057
; PRIOR FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US 60/554, 701
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/551, 311
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 536
; TYPE: PRT
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ORGANISM: Homo sapiens
US-10-821-231C-1

Query Match 100.0%; Score 2834; DB 5; Length 536;
Best Local Similarity 100.0%; Pred. No. 1.1e-174;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSNKSXPKASQRRSLBPALVNHGAGGAFPASQTPSKPASADGHRGSAAPAPAAE 60
DB 1 MGSNKSXPKASQRRSLBPALVNHGAGGAFPASQTPSKPASADGHRGSAAPAPAAE 60
QY 61 PKLFGFNSSDVTSPORAGPLAGVTTFVALVDYESTRTDLSFKKGBERLOIVNNTG 120
DB 61 PKLFGFNSSDVTSPORAGPLAGVTTFVALVDYESTRTDLSFKKGBERLOIVNNTG 120
QY 121 WMLAHSISTGOTGYIPSNVYAPSDSIQAEEMWFGKTRRESERLLNAENPRGTFVRES 180
DB 121 WMLAHSISTGOTGYIPSNVYAPSDSIQAEEMWFGKTRRESERLLNAENPRGTFVRES 180
QY 181 ETTKGAYCLSVSPDNAGKLVNHYKIRKLDGSGFYITTSRTQFNSLQOLVAAYSKADGL 240
DB 181 ETTKGAYCLSVSPDNAGKLVNHYKIRKLDGSGFYITTSRTQFNSLQOLVAAYSKADGL 240
QY 241 CHRLLTVCPSTKQOTQGLADAMEIPRESIRLEVKLGQCGFGEVWMTGNTTRVAIKTL 300
DB 241 CHRLLTVCPSTKQOTQGLADAMEIPRESIRLEVKLGQCGFGEVWMTGNTTRVAIKTL 300
QY 301 KPGTMSPEAFLOBAQVWKKLRHEKLVQLYAVVSEBPIYIYTEYMSKSLDPLKGETGY 360
DB 301 KPGTMSPEAFLOBAQVWKKLRHEKLVQLYAVVSEBPIYIYTEYMSKSLDPLKGETGY 360
QY 361 LRLPOLVDMAAOJASGMAVYERMYVHRDLRAANILVGENLVCKVADFGIARLIEDNEYT 420
DB 361 LRLPOLVDMAAOJASGMAVYERMYVHRDLRAANILVGENLVCKVADFGIARLIEDNEYT 420
QY 421 AROGAKPPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVPYPGMVNREVLDOVER 480
DB 421 AROGAKPPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVPYPGMVNREVLDOVER 480
QY 481 GYRMPCEPCEPSLHDMCCMKRKEPERPTFEYLOAFLEBDYFSTEPYOQPGENTL 536
DB 481 GYRMPCEPCEPSLHDMCCMKRKEPERPTFEYLOAFLEBDYFSTEPYOQPGENTL 536

RESULT 9
US-10-469-469-273

; Sequence 273, Application US/10469469
; Publication No. US20060079493A1
; GENERAL INFORMATION:
; APPLICANT: FRITZ, LAWRENCE C.
; APPLICANT: BURROWS, FRANCIS J.
; TITLE OF INVENTION: METHODS FOR TREATING GENETICALLY-DEFINED PROLIFERATIVE
; TITLE OF INVENTION: DISORDERS WITH HSP90 INHIBITORS
; FILE REFERENCE: CON-0010-USN
; CURRENT APPLICATION NUMBER: US/10/469, 469
; CURRENT FILING DATE: 2003-08-27
; PRIOR APPLICATION NUMBER: PCT/US02/06518
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: 60/272,751
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 330
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 273
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-469-469-273

Query Match 100.0%; Score 2834; DB 5; Length 536;
Best Local Similarity 100.0%; Pred. No. 1.1e-174;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGSNKSXPKASQRRSLBPALVNHGAGGAFPASQTPSKPASADGHRGSAAPAPAAE 60

DB 1 MGSNKSXPKASQRRSLBPALVNHGAGGAFPASQTPSKPASADGHRGSAAPAPAAE 60

QY 61 PKLFGFNSSDVTSPORAGPLAGVTTFVALVDYESTRTDLSFKKGBERLOIVNNTG 120
DB 61 PKLFGFNSSDVTSPORAGPLAGVTTFVALVDYESTRTDLSFKKGBERLOIVNNTG 120
QY 121 WMLAHSISTGOTGYIPSNVYAPSDSIQAEEMWFGKTRRESERLLNAENPRGTFVRES 180
DB 121 WMLAHSISTGOTGYIPSNVYAPSDSIQAEEMWFGKTRRESERLLNAENPRGTFVRES 180
QY 181 ETTKGAYCLSVSPDNAGKLVNHYKIRKLDGSGFYITTSRTQFNSLQOLVAAYSKADGL 240
DB 181 ETTKGAYCLSVSPDNAGKLVNHYKIRKLDGSGFYITTSRTQFNSLQOLVAAYSKADGL 240
QY 241 CHRLLTVCPSTKQOTQGLADAMEIPRESIRLEVKLGQCGFGEVWMTGNTTRVAIKTL 300
DB 241 CHRLLTVCPSTKQOTQGLADAMEIPRESIRLEVKLGQCGFGEVWMTGNTTRVAIKTL 300
QY 301 KPGTMSPEAFLOBAQVWKKLRHEKLVQLYAVVSEBPIYIYTEYMSKSLDPLKGETGY 360
DB 301 KPGTMSPEAFLOBAQVWKKLRHEKLVQLYAVVSEBPIYIYTEYMSKSLDPLKGETGY 360
QY 361 LRLPOLVDMAAOJASGMAVYERMYVHRDLRAANILVGENLVCKVADFGIARLIEDNEYT 420
DB 361 LRLPOLVDMAAOJASGMAVYERMYVHRDLRAANILVGENLVCKVADFGIARLIEDNEYT 420
QY 421 AROGAKPPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVPYPGMVNREVLDOVER 480
DB 421 AROGAKPPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVPYPGMVNREVLDOVER 480
QY 481 GYRMPCEPCEPSLHDMCCMKRKEPERPTFEYLOAFLEBDYFSTEPYOQPGENTL 536
DB 481 GYRMPCEPCEPSLHDMCCMKRKEPERPTFEYLOAFLEBDYFSTEPYOQPGENTL 536

RESULT 10

US-11-233-510-24
; Sequence 24, Application US/11233510
; Publication No. US20060063190A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, Timothy J.
; APPLICANT: Whitehead, Clark M.
; APPLICANT: Malinowski, Douglas P.
; APPLICANT: Marcello, Raphael
; TITLE OF INVENTION: Methods and Compositions for Evaluating
; TITLE OF INVENTION: Breast Cancer Prognosis
; FILE REFERENCE: 46143/296738
; CURRENT APPLICATION NUMBER: US/11/233, 510
; CURRENT FILING DATE: 2005-09-22
; PRIOR APPLICATION NUMBER: 60/612,073
; PRIOR FILING DATE: 2004-09-22
; PRIOR APPLICATION NUMBER: 60/611,965
; PRIOR FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-233-510-24

Query Match 100.0%; Score 2834; DB 6; Length 536;
Best Local Similarity 100.0%; Pred. No. 1.1e-174;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSNKSXPKASQRRSLBPALVNHGAGGAFPASQTPSKPASADGHRGSAAPAPAAE 60
DB 1 MGSNKSXPKASQRRSLBPALVNHGAGGAFPASQTPSKPASADGHRGSAAPAPAAE 60
QY 61 PKLFGFNSSDVTSPORAGPLAGVTTFVALVDYESTRTDLSFKKGBERLOIVNNTG 120

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Db      61 PKLFGFNSSDVTYSPQRAGPLAGVTTFVALYDYESRTEITDLSFKKGERLQIVNTEGD 120
Qy      121 WMLAHLSTGQGTGYTISNYYAPSDSIQAEWYFGKTTTRRSERLLNAENPRGTFLVRES 180
Db      121 WMLAHLSTGQGTGYTISNYYAPSDSIQAEWYFGKTTTRRSERLLNAENPRGTFLVRES 180
Qy      181 ETTKGAACSVSPFDNAKGLNVKHYIKRKLDGSGFYITTSRTQFNSLQQLVAAYSKADGL 240
Db      181 ETTKGAACSVSPFDNAKGLNVKHYIKRKLDGSGFYITTSRTQFNSLQQLVAAYSKADGL 240
Qy      241 CHRLLTVCTPSKPTQGLAKDAWEIPRESLRLEVKLGQCGFGEVWMTNGTTRVAIKTL 300
Db      241 CHRLLTVCTPSKPTQGLAKDAWEIPRESLRLEVKLGQCGFGEVWMTNGTTRVAIKTL 300
Qy      301 KGTGMSPEAFLOAQWKKLRHEKLVQYAVVSEBPIYITEYMSKSLDPLKGETGKYL 360
Db      301 KGTGMSPEAFLOAQWKKLRHEKLVQYAVVSEBPIYITEYMSKSLDPLKGETGKYL 360
Qy      361 LRLPOLVDMAAQIASGMAVYERNNYVHRDLRAANILVGENLVCKVADFGLARLIEDNEYT 420
Db      361 LRLPOLVDMAAQIASGMAVYERNNYVHRDLRAANILVGENLVCKVADFGLARLIEDNEYT 420
Qy      421 ARQAKFPIMKTAPEALYGRFTIKSDVMSFGILLTELTTKGRVYPGVMNREVLDOVER 480
Db      421 ARQAKFPIMKTAPEALYGRFTIKSDVMSFGILLTELTTKGRVYPGVMNREVLDOVER 480
Qy      481 GRMPCPECPESLHDMCCMKRKEPERPTFEYLOAFLEDYFTSTSTEPQOPEBNTL 536
Db      481 GRMPCPECPESLHDMCCMKRKEPERPTFEYLOAFLEDYFTSTSTEPQOPEBNTL 536

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RESULT 11

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US-10-394-322A-56
; Sequence 56, Application US/10394322A
; Publication No. US20030232391A1
; GENERAL INFORMATION:
; APPLICANT: SUNESIS PHARMACEUTICALS, INC.
; APPLICANT: Prescott, John C.
; TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
; FILE REFERENCE: 39750-0006 US
; CURRENT APPLICATION NUMBER: US/10/394,322A
; PRIOR FILING DATE: 2003-03-30
; PRIOR APPLICATION NUMBER: US 60/366,892
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 535
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-394-322A-56

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Query Match      99.8%; Score 2829; DB 4; Length 535;
Best Local Similarity 100.0%; Pred. No. 2,3e-174;
Matches 535; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      2 GSNKSKPKDASQRRSLLEPAENVHAGGAFPASQTPSPKPSADGHRGSAAPAPAAAP 61
Db      1 GSNKSKPKDASQRRSLLEPAENVHAGGAFPASQTPSPKPSADGHRGSAAPAPAAAP 60
Qy      62 KLFGFNSSDVTYSPQRAGPLAGVTTFVALYDYESRTEITDLSFKKGERLQIVNTEGDM 121
Db      61 KLFGFNSSDVTYSPQRAGPLAGVTTFVALYDYESRTEITDLSFKKGERLQIVNTEGDM 120
Qy      122 WLAHLSTGQGTGYTISNYYAPSDSIQAEWYFGKTTTRRSERLLNAENPRGTFLVRES 181
Db      121 WLAHLSTGQGTGYTISNYYAPSDSIQAEWYFGKTTTRRSERLLNAENPRGTFLVRES 180
Qy      182 TTKGACSVSPFDNAKGLNVKHYIKRKLDGSGFYITTSRTQFNSLQQLVAAYSKADGL 241
Db      181 TTKGACSVSPFDNAKGLNVKHYIKRKLDGSGFYITTSRTQFNSLQQLVAAYSKADGL 240
Qy      242 HRLTVCTPSKPTQGLAKDAWEIPRESLRLEVKLGQCGFGEVWMTNGTTRVAIKTLK 301

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Db      241 HRLTVCTPSKPTQGLAKDAWEIPRESLRLEVKLGQCGFGEVWMTNGTTRVAIKTLK 300
Qy      302 PGTMSPEAFLOAQWKKLRHEKLVQYAVVSEBPIYITEYMSKSLDPLKGETGKYL 361
Db      301 PGTMSPEAFLOAQWKKLRHEKLVQYAVVSEBPIYITEYMSKSLDPLKGETGKYL 360
Qy      362 RLPOLVDMAAQIASGMAVYERNNYVHRDLRAANILVGENLVCKVADFGLARLIEDNEYT 421
Db      361 RLPOLVDMAAQIASGMAVYERNNYVHRDLRAANILVGENLVCKVADFGLARLIEDNEYT 420
Qy      422 ROGAKFPIMKTAPEALYGRFTIKSDVMSFGILLTELTTKGRVYPGVMNREVLDOVERG 481
Db      421 ROGAKFPIMKTAPEALYGRFTIKSDVMSFGILLTELTTKGRVYPGVMNREVLDOVERG 480
Qy      482 YRMPCPECPESLHDMCCMKRKEPERPTFEYLOAFLEDYFTSTSTEPQOPEBNTL 536
Db      481 YRMPCPECPESLHDMCCMKRKEPERPTFEYLOAFLEDYFTSTSTEPQOPEBNTL 535

```

RESULT 12

```

US-10-814-109-4
; Sequence 4, Application US/10814109
; Publication No. US20050222042A1
; GENERAL INFORMATION:
; APPLICANT: GlaxoSmithKline
; APPLICANT: Salter, Jeffrey
; TITLE OF INVENTION: Method for Modification of NMDA Receptors Through Inhibition of St
; FILE REFERENCE: 2560.004
; CURRENT APPLICATION NUMBER: US/10/814,109
; PRIOR FILING DATE: 2004-03-30
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 535
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-814-109-4

```

```

Query Match      99.8%; Score 2829; DB 5; Length 535;
Best Local Similarity 100.0%; Pred. No. 2,3e-174;
Matches 535; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      2 GSNKSKPKDASQRRSLLEPAENVHAGGAFPASQTPSPKPSADGHRGSAAPAPAAAP 61
Db      1 GSNKSKPKDASQRRSLLEPAENVHAGGAFPASQTPSPKPSADGHRGSAAPAPAAAP 60
Qy      62 KLFGFNSSDVTYSPQRAGPLAGVTTFVALYDYESRTEITDLSFKKGERLQIVNTEGDM 121
Db      61 KLFGFNSSDVTYSPQRAGPLAGVTTFVALYDYESRTEITDLSFKKGERLQIVNTEGDM 120
Qy      122 WLAHLSTGQGTGYTISNYYAPSDSIQAEWYFGKTTTRRSERLLNAENPRGTFLVRES 181
Db      121 WLAHLSTGQGTGYTISNYYAPSDSIQAEWYFGKTTTRRSERLLNAENPRGTFLVRES 180
Qy      182 TTKGACSVSPFDNAKGLNVKHYIKRKLDGSGFYITTSRTQFNSLQQLVAAYSKADGL 241
Db      181 TTKGACSVSPFDNAKGLNVKHYIKRKLDGSGFYITTSRTQFNSLQQLVAAYSKADGL 240
Qy      242 HRLTVCTPSKPTQGLAKDAWEIPRESLRLEVKLGQCGFGEVWMTNGTTRVAIKTLK 301
Db      241 HRLTVCTPSKPTQGLAKDAWEIPRESLRLEVKLGQCGFGEVWMTNGTTRVAIKTLK 300
Qy      302 PGTMSPEAFLOAQWKKLRHEKLVQYAVVSEBPIYITEYMSKSLDPLKGETGKYL 361
Db      301 PGTMSPEAFLOAQWKKLRHEKLVQYAVVSEBPIYITEYMSKSLDPLKGETGKYL 360
Qy      362 RLPOLVDMAAQIASGMAVYERNNYVHRDLRAANILVGENLVCKVADFGLARLIEDNEYT 421
Db      361 RLPOLVDMAAQIASGMAVYERNNYVHRDLRAANILVGENLVCKVADFGLARLIEDNEYT 420
Qy      422 ROGAKFPIMKTAPEALYGRFTIKSDVMSFGILLTELTTKGRVYPGVMNREVLDOVERG 481

```

Db 421 ROGAKFPIKWTAPAEALYGRFTIKSDVMSFGILLTELTKGRVYPGMVNRVLDQYERG 480
QY 482 YRMPCEPECESLHDLMOCCMRKEBERPTEFYLOAFLEDFYFSTEPQYQPGENL 536
Db 481 YRMPCEPECESLHDLMOCCMRKEBERPTEFYLOAFLEDFYFSTEPQYQPGENL 535

RESULT 13

US-10-691-079-1
; Sequence 1, Application US/10691079
; Publication No. US20040176313A1
; GENERAL INFORMATION:
; APPLICANT: AVENTIS PHARMA S.A.
; TITLE OF INVENTION: Inhibitors of SRC kinase for use in Alzheimer's disease
; FILE REFERENCE: PRAV2002/0030
; CURRENT APPLICATION NUMBER: US/10/691,079
; CURRENT FILING DATE: 2003-10-22
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 542
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-691-079-1

Query Match 99.5%; Score 2821; DB 4; Length 542;

Best Local Similarity 98.9%; Pred. No. 7.8e-174;

Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

QY 1 MGSNKSFKPKDASQRRSLBPAENVHAGGAFPASQTPSKPASADGHRGSAAPAPAAE 60
Db 1 MGSNKSFKPKDASQRRSLBPAENVHAGGAFPASQTPSKPASADGHRGSAAPAPAAE 60
QY 61 PKLFGFNSSDVTYSPQRAPILAGGVTTFVALYDYESRTETDLSFKKGERLQIYNNTEGD 117
Db 61 PKLFGFNSSDVTYSPQRAPILAGGVTTFVALYDYESRTETDLSFKKGERLQIYNNTRKY 120
QY 118 ---EGDWMALHSLSTQGTGYTPSNVYAPSDSIQAEEMYPFKITRRESERLLNAENPRGT 174
Db 121 DVBEGMMALHSLSTQGTGYTPSNVYAPSDSIQAEEMYPFKITRRESERLLNAENPRGT 180
QY 175 FLVRESSETKAGVCLASVDFDNAGKLVNKHVKIRKLDSSGFPYTSRTOFNSLQOLVAAYYS 234
Db 181 FLVRESSETKAGVCLASVDFDNAGKLVNKHVKIRKLDSSGFPYTSRTOFNSLQOLVAAYYS 240
QY 235 KHADGCHRLTYCPTSKPQTQGLADAMEIPRESRLLEVKGQCGFGEVWMTWNGTTR 294
Db 241 KHADGCHRLTYCPTSKPQTQGLADAMEIPRESRLLEVKGQCGFGEVWMTWNGTTR 300
QY 295 VAIKITLKPQMSPEAFLOEAQVMKLRHEKLVOLYAVVSEEPYITVEYMSKSLDLFLK 354
Db 301 VAIKITLKPQMSPEAFLOEAQVMKLRHEKLVOLYAVVSEEPYITVEYMSKSLDLFLK 360
QY 355 GENGKTLRLPOLVDMQAQIASGMAYVERMYVHRDLRAANILVGENLVCKVADFGARLRI 414
Db 361 GENGKTLRLPOLVDMQAQIASGMAYVERMYVHRDLRAANILVGENLVCKVADFGARLRI 420
QY 415 EDNEYTAQGAKEPIKWTAPAEALYGRFTIKSDVMSFGILLTELTKGRVYPGMVNRVLDQY 474
Db 421 EDNEYTAQGAKEPIKWTAPAEALYGRFTIKSDVMSFGILLTELTKGRVYPGMVNRVLDQY 480
QY 475 LDQVERGYRMPCEPECESLHDLMOCCMRKEBERPTEFYLOAFLEDFYFSTEPQYQPG 534
Db 481 LDQVERGYRMPCEPECESLHDLMOCCMRKEBERPTEFYLOAFLEDFYFSTEPQYQPG 540

QY 535 NL 536
Db 541 NL 542

RESULT 14

US-10-887-588-4
; Sequence 4, Application US/10887588

; Publication No. US20040261142A1
; GENERAL INFORMATION:
; APPLICANT: Yeaman, Timothy J.
; APPLICANT: Ildy, Rosalyn B.
; TITLE OF INVENTION: Mutated SRC Oncogene Composition and Methods
; FILE REFERENCE: USF-T136
; CURRENT APPLICATION NUMBER: US/10/887,588
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US/09/444,711
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 530
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(530)
; OTHER INFORMATION: amino acid sequence of the mutant c-Src polypeptide encoded
; OTHER INFORMATION: by the mutant c-Src coding region
US-10-887-588-4

Query Match 98.8%; Score 2801; DB 5; Length 530;

Best Local Similarity 100.0%; Pred. No. 1.5e-172;

Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSNKSFKPKDASQRRSLBPAENVHAGGAFPASQTPSKPASADGHRGSAAPAPAAE 60
Db 1 MGSNKSFKPKDASQRRSLBPAENVHAGGAFPASQTPSKPASADGHRGSAAPAPAAE 60
QY 61 PKLFGFNSSDVTYSPQRAPILAGGVTTFVALYDYESRTETDLSFKKGERLQIYNNTEGD 120
Db 61 PKLFGFNSSDVTYSPQRAPILAGGVTTFVALYDYESRTETDLSFKKGERLQIYNNTEGD 120
QY 121 WMLHSLSTQGTGYTPSNVYAPSDSIQAEEMYPFKITRRESERLLNAENPRGTFLVRES 180
Db 121 WMLHSLSTQGTGYTPSNVYAPSDSIQAEEMYPFKITRRESERLLNAENPRGTFLVRES 180
QY 181 ETTKGAIVCLASVDFDNAGKLVNKHVKIRKLDSSGFPYTSRTOFNSLQOLVAAYYSKHADGL 240
Db 181 ETTKGAIVCLASVDFDNAGKLVNKHVKIRKLDSSGFPYTSRTOFNSLQOLVAAYYSKHADGL 240
QY 241 CHRLTYCPTSKPQTQGLADAMEIPRESRLLEVKGQCGFGEVWMTWNGTTRVAIKTL 300
Db 241 CHRLTYCPTSKPQTQGLADAMEIPRESRLLEVKGQCGFGEVWMTWNGTTRVAIKTL 300
QY 301 KPQMSPEAFLOEAQVMKLRHEKLVOLYAVVSEEPYITVEYMSKSLDLFLKGETGKY 360
Db 301 KPQMSPEAFLOEAQVMKLRHEKLVOLYAVVSEEPYITVEYMSKSLDLFLKGETGKY 360
QY 361 LRLPOLVDMQAQIASGMAYVERMYVHRDLRAANILVGENLVCKVADFGARLRIEDNEYT 420
Db 361 LRLPOLVDMQAQIASGMAYVERMYVHRDLRAANILVGENLVCKVADFGARLRIEDNEYT 420
QY 421 AROGAKEPIKWTAPAEALYGRFTIKSDVMSFGILLTELTKGRVYPGMVNRVLDQY 480
Db 421 AROGAKEPIKWTAPAEALYGRFTIKSDVMSFGILLTELTKGRVYPGMVNRVLDQY 480
QY 481 GYRMPCEPECESLHDLMOCCMRKEBERPTEFYLOAFLEDFYFSTEPQY 530
Db 481 GYRMPCEPECESLHDLMOCCMRKEBERPTEFYLOAFLEDFYFSTEPQY 530

RESULT 15

US-10-732-923-13447
; Sequence 13447, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923

; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13447
; LENGTH: 542
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-732-923-13447

Query Match 98.1%; Score 2781; DB 5; Length 542;
Best Local Similarity 97.8%; Pred. No. 3e-171;
Matches 531; Conservative 3; Mismatches 1; Indels 8; Gaps 3;

QY 1 MGSNKSXPXASQRRSLPEAENVHAGGAFPASQTPSPKASADGHRGSAAPA--PAA 59
DB 1 MGSNKSXPXASQRRSLPEAENVHGA-CGAFPASQTPSPKASADGHRGSAAPA 59
QY 60 EPKLPFGFNSSDVTVPORAGPLAGGVTFVALYDYESRTETDLSFKKGERLQIVNNT-- 117
DB 60 EPKLPFGFNSSDVTVPORAGPLAGGVTFVALYDYESRTETDLSFKKGERLQIVNNT 119
QY 118 ---EGDWMLAHSLSGTQGYIPSNVAPSDSIQAEEMYPGKITRRESERLLNAENPRG 173
DB 120 VDVREGDWMLAHSLSGTQGYIPSNVAPSDSIQAEEMYPGKITRRESERLLNAENPRG 179
QY 174 TFLVRESETTKAYCISVSDPDNAKGLNVHYKIRKLDGCGFYITSTRQFNSLQOLVAY 233
DB 180 TFLVRESETTKAYCISVSDPDNAKGLNVHYKIRKLDGCGFYITSTRQFNSLQOLVAY 239
QY 234 SKRADGLCHRLTVCPTSKPQTQGLAKDAEIPRESLRLEVKLGQCGFGEVMNGTNGTT 293
DB 240 SKRADGLCHRLTVCPTSKPQTQGLAKDAEIPRESLRLEVKLGQCGFGEVMNGTNGTT 299
QY 294 RVAIKTLKPGTMSPEAFLOEAQVMKLRHEKLVQLVAVVSEEPYIYITEYMSKSLDFFL 353
DB 300 RVAIKTLKPGTMSPEAFLOEAQVMKLRHEKLVQLVAVVSEEPYIYITEYMSKSLDFFL 359
QY 354 KGETGYLRLPOLVDMAQIASGMAYVERNNYVHRDIPRANIIVGENLVCKVADFGIARL 413
DB 360 KGETGYLRLPOLVDMSAQIASGMAYVERNNYVHRDIPRANIIVGENLVCKVADFGIARL 419
QY 414 IEDNEYTAOGAKPPIKMTAPEAALYGRFTIKSDVMSFGILLTEITTKGRVPYPGMVNRE 473
DB 420 IEDNEYTAOGAKPPIKMTAPEAALYGRFTIKSDVMSFGILLTEITTKGRVPYPGMVNRE 479
QY 474 VLDQVERGYRMPCCPBCPSLHDLMOCCMRKEPEERPTFEYLQAFLEDYFTSTEPQYQPG 533
DB 480 VLDQVERGYRMPCCPBCPSLHDLMOCCMRKEPEERPTFEYLQAFLEDYFTSTEPQYQPG 539
QY 534 ENL 536
DB 540 ENL 542

Search completed: June 5, 2006, 17:43:04
Job time : 108.266 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 5, 2006, 17:37:49 ; Search time 6.95244 Seconds

(without alignments)

891.618 Million cell updates/sec

Title: US-10-691-079-2

Sequence: 1 MGSNKSXPKDASQRRSLRP.....AFLEDYTRTPQYQGENL 536

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 58871 seqs, 11565156 residues

Total number of hits satisfying chosen parameters: 58871

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA New:*
1: /EMC_Celerra_SIDS3/ptocdata/1/pubppa/US09_NEW_PUB pep:*
2: /EMC_Celerra_SIDS3/ptocdata/1/pubppa/US06_NEW_PUB pep:*
3: /EMC_Celerra_SIDS3/ptocdata/1/pubppa/US07_NEW_PUB pep:*
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8: /EMC_Celerra_SIDS3/ptocdata/1/pubppa/US60_NEW_PUB pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1528.5	53.9	505	US-10-511-937-2991	Sequence 2991, App
2	1464	51.7	512	US-10-505-928-353	Sequence 353, App
3	1464	51.7	512	US-10-511-937-2492	Sequence 2492, App
4	1461	51.6	509	US-10-511-937-2467	Sequence 2467, App
5	845	29.6	659	US-10-511-937-2593	Sequence 2593, App
6	838.5	29.6	631	US-11-312-958-60	Sequence 60, App
7	800.5	28.2	620	US-10-511-937-2859	Sequence 2959, App
8	586	20.7	983	US-11-302-678-2	Sequence 2, App
9	573	20.2	994	US-11-303-935-12	Sequence 12, App
10	571	20.1	998	US-11-303-935-2	Sequence 2, App
11	569.5	20.1	993	US-11-303-935-11	Sequence 11, App
12	558.5	19.7	1130	US-11-312-958-52	Sequence 52, App
13	492	17.4	894	US-11-251-465-21	Sequence 21, App
14	485.5	17.1	885	US-10-505-928-432	Sequence 432, App
15	485.5	17.1	885	US-11-251-465-20	Sequence 20, App
16	482	17.0	343	US-11-255-147-6	Sequence 6, App
17	481	17.0	806	US-11-251-465-22	Sequence 22, App
18	477.5	16.8	348	US-11-255-147-4	Sequence 2, App
19	477.5	16.8	348	US-11-255-147-2	Sequence 2, App
20	476.5	16.8	422	US-11-251-465-67	Sequence 67, App
21	476.5	16.8	422	US-11-251-465-70	Sequence 67, App
22	469	16.5	972	US-11-255-147-8	Sequence 8, App
23	459	16.2	1308	US-11-248-122-2	Sequence 2, App
24	448	15.8	999	US-10-196-749-434	Sequence 434, App
25	442	15.6	391	US-11-223-945-38	Sequence 38, App

26	442	15.6	1259	US-11-223-945-40	Sequence 40, App
27	441	15.6	550	US-10-538-066-757	Sequence 757, App
28	441	15.6	1255	US-10-538-066-364	Sequence 364, App
29	441	15.6	1255	US-11-223-945-43	Sequence 43, App
30	439	15.5	993	US-10-511-937-2463	Sequence 2463, App
31	436	15.4	976	US-10-511-937-2423	Sequence 2423, App
32	427	15.1	1006	US-10-511-937-2425	Sequence 2425, App
33	417.5	14.7	1338	US-10-505-928-634	Sequence 634, App
34	417.5	14.7	1338	US-10-505-928-857	Sequence 857, App
35	408.5	14.4	1298	US-11-312-958-56	Sequence 56, App
36	408	14.4	953	US-10-505-928-274	Sequence 274, App
37	403	14.2	374	US-10-953-349-3910	Sequence 3910, App
38	403	14.2	374	US-10-953-349-3909	Sequence 3909, App
39	403	14.2	412	US-10-953-349-3908	Sequence 3908, App
40	397	14.0	648	US-10-511-814-2	Sequence 2, App
41	397	14.0	648	US-10-511-814-14	Sequence 14, App
42	367.5	13.0	272	US-10-370-959-27	Sequence 27, App
43	367.5	13.0	278	US-10-370-959-17	Sequence 17, App
44	367.5	13.0	278	US-10-370-959-31	Sequence 31, App
45	367	12.9	247	US-11-251-465-75	Sequence 75, App

ALIGNMENTS

RESULT 1
US-10-511-937-2991
Sequence 2991, Application US/10511937
Publication No. US20060088836m1
GENERAL INFORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
APPLICANT: Prentice, James
APPLICANT: Morris, Macdonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
FILE REFERENCE: 506612000104
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR FILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 10/325,899
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2991
LENGTH: 505
TYPE: PRT
ORGANISM: Homo sapiens
US-10-511-937-2991

Query Match 53.9%, Score 1528.5; DB 6; Length 505;

Best Local Similarity 56.4%; Pred. No. 2.4e-76;

Matches 300; Conservative 84; Mismatches 117; Indels 31; Gaps 6;

QY 1 MGSNKSXPKDASQRRSLRPENYVAGAGAFPAQSPKPSKADGHRGSPAAPAAAE 60
DB 1 MGSNKSXPKDASQRRSLRPENYVAGAGAFPAQSPKPSKADGHRGSPAAPAAAE 60
QY 61 PKLGGFSPSTVTSFQAGPLAGVYTF-VALDYESRTTDTLSFKKGELOVNNTEG 119
DB 61 PKLGGFSPSTVTSFQAGPLAGVYTF-VALDYESRTTDTLSFKKGELOVNNTEG 119
QY 41 -----GPNSHNSNTPGIRE--AGSEDTIVVALDYERAIHHEDUSFQAGDM-VVLES 91
DB 41 -----GPNSHNSNTPGIRE--AGSEDTIVVALDYERAIHHEDUSFQAGDM-VVLES 91
QY 120 DWMLAHSLSQGYIPSNVYAPSDSIQAESEYFGKITRRESRLLLNAENPGTFVRE 179
DB 92 EWMFARSLATKKEGYIISNVYARVDSLETBEMFVKGISRKDAEQLLAPGMLSFMRD 151

QY 180 SETTKAGVCHSVSDFDNAKGLNVGHYKIRKLDGSGFYITSTRTORNSLOOLVAAYYSKADG 239
| | | | | : | : | | | | | : | | | | | : | : | | | : | : | |
DB 152 SETTKGSYSVADYDPRQGDYVGHYKIRLNDNGFIIISPRSTSTIQELVDHYKKANDG 211
| | | | | : | : | | | | | : | | | | | : | : | | | : | : | |
QY 240 LCHRLTVCPSTSKPQTQGLAKDAWEIPRESLRLEVKLGOCGFEVWNGTTRVAIKT 299
| | | | | : | : | | | | | : | | | | | : | : | | | : | : | |
DB 212 LCQKLSVPCWSSKPO-KPWEKDAWEIPRESLKEKKGAGQFGEVWMAATYKIKVAIKT 270
| | | | | : | : | | | | | : | | | | | : | : | | | : | : | |
QY 300 LKRGTSPEAFLOAQVMKKLRHEKLVOLFAVYSEETIYIVTEYMSGSLDPLKSGTGK 359
| | | | | : | : | | | | | : | | | | | : | : | | | : | : | |
DB 271 MKGSGMSVEAFLEBANVMKTLQHDKLVKHAIVYKEBIYIITEYMAAGSLDPLFKSDEGS 330
| | | | | : | : | | | | | : | | | | | : | : | | | : | : | |
QY 360 YLRPLPOLVDAAOIASGMAYVERMYVHRDLRAANIIVGENLVCKVADFGIARLIEDNEY 419
| | | | | : | : | | | | | : | | | | | : | : | | | : | : | |
DB 331 KQPLPKLIDPSAOIABGMATIEQNRTHRDRAANIIVSASLVCKIDFGLARLIEDNEY 390
| | | | | : | : | | | | | : | | | | | : | : | | | : | : | |
QY 420 TABQAKFPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVPPGMVNRVLDQVE 479
| | | | | : | : | | | | | : | | | | | : | : | | | : | : | |
DB 391 TABQAKFPIKMTAPEALINFGSFTIKSDVMSFGILLMEIYVGRIPYPGMSNPEVIRALE 450
| | | | | : | : | | | | | : | | | | | : | : | | | : | : | |
QY 480 RGRMRCPCEPSLHDMCQCRKEBERPTEYLOAFLEDYFTSTPEQY 531
| | | | | : | : | | | | | : | | | | | : | : | | | : | : | |
DB 451 RGYMRBPENCPELYNIMKRCWKNRBERPTEYIOSVLDFYATATESQY 502
| | | | | : | : | | | | | : | | | | | : | : | | | : | : | |

RESULT 2

US-10-505-928-353
/ Sequence 353, Application US/10505928
/ Publication No. US20060088532A1
/ GENERAL INFORMATION:
/ APPLICANT: Ludwig Institute for Cancer Research et al.
/ TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
/ FILE REFERENCE: 28967/39178
/ CURRENT APPLICATION NUMBER: US/10/505, 928
/ PRIOR FILING DATE: 2004-08-27
/ PRIOR APPLICATION NUMBER: US 60/363, 019
/ PRIOR FILING DATE: 2002-03-07
/ NUMBER OF SEQ ID NOS: 866
/ SOFTWARE: PatentIn 3.2
/ SEQ ID NO 353
/ LENGTH: 512
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-505-928-353

Query Match 51.7%; Score 1464; DB 6; Length 512;
Best Local Similarity 53.0%; Pred. No. 7, 4e-73;
Matches 287; Conservative 87; Mismatches 125; Indels 42; Gaps 9;

QY 1 MGSNKSXPDA-----SQRRLSLBPALNVHAGAGAFPASQTPSKPASADGHRGPS 51
| | | | | : | : | | | | | : | | | | | : | : | | | : | : | |
DB 1 MGCISKKGKSDSDDDVDLKTQPVNTERITTYRD-----PISNKKQRFV-----PE 47
| | | | | : | : | | | | | : | | | | | : | : | | | : | : | |
QY 52 AAFAPAAABPKLFGGNSSDVTYTSPORAPLAGGVTTFVALYDESRTETDLSFKKGERL 111
| | | | | : | : | | | | | : | | | | | : | : | | | : | : | |
DB 48 SQLLPQOR-----FQTKD-----PEQGDIV-----VALPYDGIHPDDLSFKKGERM 90
| | | | | : | : | | | | | : | | | | | : | : | | | : | : | |
QY 112 QIVNNTGDMWLAHSISTGOTGYIPSNYVAPSDSIOAEEMYPGKITRRESERILLNAENP 171
| | | | | : | : | | | | | : | | | | | : | : | | | : | : | |
DB 91 KVLBER-HGEVWMAKKSILTYKKEGFIPSNYVAKLNTLETBEWFFPKDITRKDAEROLLAPGNS 149
| | | | | : | : | | | | | : | | | | | : | : | | | : | : | |
QY 172 RGFVLRESEETTKGACLSVSDFDNAKGLNVGHYKIRKLDGSGFYITSTRQFNSLOOLVA 231
| | | | | : | : | | | | | : | | | | | : | : | | | : | : | |
DB 150 AGAFILRESEETTKGACLSVSDFDNAPVGHVYKIKYKIRSLDNGGYISPRITPFCISDMIK 209
| | | | | : | : | | | | | : | | | | | : | : | | | : | : | |
QY 232 YYSKADGLCHRLTVCPSTSKPQTQGLAKDAWEIPRESLRLEVKLGOCGFEVWNGTTRVAIKT 291
| | | | | : | : | | | | | : | | | | | : | : | | | : | : | |
DB 210 HYQKQADGLCRRLKXKCSIPKPO-KPMDKDAWEIPRESITLVKRLAGQGFGEVWNGYNN 268
| | | | | : | : | | | | | : | | | | | : | : | | | : | : | |
QY 292 TTRVAIKTLKPGTMSPEAFLOAQVMKKLRHEKLVOLFAVYSEETIYIVTEYMSGSL 350
| | | | | : | : | | | | | : | | | | | : | : | | | : | : | |
DB 269 STKVAVKTLKPGTMSVOAFLEBANVMKTLQHDKLVRLVAVVATREBEPIYIITEYMAAGSL 328
| | | | | : | : | | | | | : | | | | | : | : | | | : | : | |

QY 351 DPLKGTGKYLRLPOLVDAAOIASGMAYVERMYVHRDLRAANIIVGENLVCKVADFGI 410
| | | | | : | : | | | | | : | | | | | : | : | | | : | : | |
DB 329 DPLKSBGGKVVLLPKLIDPSAOIABGMATIERKNYTHRDRAANIVLSESLMCKIADFGI 388
| | | | | : | : | | | | | : | | | | | : | : | | | : | : | |
QY 411 ARLIEDNEYTARQAKFPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVPPGMV 470
| | | | | : | : | | | | | : | | | | | : | : | | | : | : | |
DB 389 ARVIEDNEYTARQAKFPIKMTAPEALINFGSFTIKSDVMSFGILLMEIYVGRIPYPGRT 448
| | | | | : | : | | | | | : | | | | | : | : | | | : | : | |
QY 471 NREVLQOVRGYMPCPEPESLHDMCQCRKEBERPTEYLOAFLEDYFTSTPEQY 530
| | | | | : | : | | | | | : | | | | | : | : | | | : | : | |
DB 449 NADVMTALSQGYMPPVENCPELYDIMKRCWKEKABERPFYLOSVLDFYATATESQY 508
| | | | | : | : | | | | | : | | | | | : | : | | | : | : | |
QY 531 Q 531
| | | | | : | : | | | | | : | | | | | : | : | | | : | : | |
DB 509 Q 509
| | | | | : | : | | | | | : | | | | | : | : | | | : | : | |

RESULT 3

US-10-511-937-2492
/ Sequence 2492, Application US/10511937
/ Publication No. US2006008836A1
/ GENERAL INFORMATION:
/ APPLICANT: EXPRESSION DIAGNOSTICS, INC.
/ APPLICANT: Wohlgenuth, Jay
/ APPLICANT: Fey, Kirk
/ APPLICANT: Woodward, Robert
/ APPLICANT: Ly, Ngoc
/ APPLICANT: Prentice, James
/ APPLICANT: Morris, MacDonald
/ APPLICANT: Rosenberg, Steven
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
/ TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
/ FILE REFERENCE: 506612000104
/ CURRENT APPLICATION NUMBER: US/10/511, 937
/ PRIOR FILING DATE: 2004-10-19
/ PRIOR APPLICATION NUMBER: PCT/US2003/012946
/ PRIOR FILING DATE: 2003-04-24
/ PRIOR APPLICATION NUMBER: US 10/131, 831
/ PRIOR FILING DATE: 2002-04-24
/ PRIOR APPLICATION NUMBER: US 10/325, 899
/ PRIOR FILING DATE: 2002-12-20
/ NUMBER OF SEQ ID NOS: 3117
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 2492
/ LENGTH: 512
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-511-937-2492

Query Match 51.7%; Score 1464; DB 6; Length 512;
Best Local Similarity 53.0%; Pred. No. 7, 4e-73;
Matches 287; Conservative 87; Mismatches 125; Indels 42; Gaps 9;

QY 1 MGSNKSXPDA-----SQRRLSLBPALNVHAGAGAFPASQTPSKPASADGHRGPS 51
| | | | | : | : | | | | | : | | | | | : | : | | | : | : | |
DB 1 MGCISKKGKSDSDDDVDLKTQPVNTERITTYRD-----PISNKKQRFV-----PE 47
| | | | | : | : | | | | | : | | | | | : | : | | | : | : | |
QY 52 AAFAPAAABPKLFGGNSSDVTYTSPORAPLAGGVTTFVALYDESRTETDLSFKKGERL 111
| | | | | : | : | | | | | : | | | | | : | : | | | : | : | |
DB 48 SQLLPQOR-----FQTKD-----PEQGDIV-----VALPYDGIHPDDLSFKKGERM 90
| | | | | : | : | | | | | : | | | | | : | : | | | : | : | |
QY 112 QIVNNTGDMWLAHSISTGOTGYIPSNYVAPSDSIOAEEMYPGKITRRESERILLNAENP 171
| | | | | : | : | | | | | : | | | | | : | : | | | : | : | |
DB 91 KVLBER-HGEVWMAKKSILTYKKEGFIPSNYVAKLNTLETBEWFFPKDITRKDAEROLLAPGNS 149
| | | | | : | : | | | | | : | | | | | : | : | | | : | : | |
QY 172 RGFVLRESEETTKGACLSVSDFDNAKGLNVGHYKIRKLDGSGFYITSTRQFNSLOOLVA 231
| | | | | : | : | | | | | : | | | | | : | : | | | : | : | |
DB 150 AGAFILRESEETTKGACLSVSDFDNAPVGHVYKIKYKIRSLDNGGYISPRITPFCISDMIK 209
| | | | | : | : | | | | | : | | | | | : | : | | | : | : | |
QY 232 YYSKADGLCHRLTVCPSTSKPQTQGLAKDAWEIPRESLRLEVKLGOCGFEVWNGTTRVAIKT 291
| | | | | : | : | | | | | : | | | | | : | : | | | : | : | |
DB 210 HYQKQADGLCRRLKXKCSIPKPO-KPMDKDAWEIPRESITLVKRLAGQGFGEVWNGYNN 268
| | | | | : | : | | | | | : | | | | | : | : | | | : | : | |


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Qy 292 TTRVAITLKPGTMSPEAFLOEAQVMKKLRHEKLVOLYAAVS-REPIYIYEMSKSIL 350
Db 269 STKAAVATLTPGTMVSQVAFLEBANIMKTLQHDKLVLYAVTREPIYIITETMAKSSLL 328
Qy 351 DFLKSGTKYRLRPLQVDMMAQIASGMAYYERNMYVHRDLRAANILVGENLVCKVADFG 410
Db 329 DFLKSGDKGKVLPLKLDPSAQIAEGMAIYERKXVIRHDLAAANVLVSESLMCKIADPGL 388
Qy 411 ARLIEDNEYIARQCAKFPPIKTAPEALYGRFTIKSDVMSFGIILLTELTKGRVPIYGMV 470
Db 389 ARVIEDNEYIARBEAKFPPIKTAPEALINFGCFTIKSDVMSFGIILLTELTKGRVPIYGMV 448
Qy 471 NRRLDQVERGYRMPCEPCEPSLHDLMOCKRKEPERPFEYLQAFLEDEYFTSTBPQY 530
Db 449 MADVTMLSGQYRMPRVENCPELDYIMKCMKEKAERPTFYDQSVLDDPYATBGOY 508
Qy 531 Q 531
Db 509 Q 509

RESULT 4
US-10-511-937-2467
; Sequence 2467, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Mohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 50661200104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2467
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2467

Query Match 51.6%; Score 1461; DB 6; Length 509;
Best Local Similarity 59.9%; Pred. No. 1.1e-72;
Matches 272; Conservative 80; Mismatches 98; Indels 4; Gaps 3;

Qy 79 AGPLAGVTTVALDYESRTETDLSFKGGERLQIVNTEGDMWLAHSLSTGQGYIPSN 138
Db 58 ASPLQDMLV--IALHSYEPHSDGLGFEKGEPLAILLOS-GEWKAQSLTGGGCFIPFN 114
Qy 139 YVAPSDSIQAEWYFGKITRRESERLLNENPRGTFVRESETTKGAAYCLSVDFNAK 198
Db 115 FVAKANSLPEPMPFKMISRKDAERQLAPGNTGSLFIRESESTAGSFLSVDFDQNG 174
Qy 199 GIANVHKIRKLDGSGGYIISRTQFNSLQOLVAYYSKADGLCHRLTTVCSTSPQOGL 258
Db 175 GSVVKAHKIRKLDGSGGYIISPRITPGIHLVRYHTNASDGLCTRLSPCQYQKPQ-KPW 233
Qy 259 AKDAMEIPRESIRLEVKIGQCGFGEVMMGTWNGTTRVAIKTLKPGTMSPEAFLOEAQVMK 318
Db 234 WBDMEVPRRLVKVERLGAQGFGEVMMGYNGHTTVAIVSLKQGSNSPDAFLAEANIMK 293
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Qy 319 KLAREKLVOLYAAVSEPIYIYTEMKSGSLDPLKSGTKYRLPOLVDMMAQIASGMA 378
Db 294 QLOHQLVRLYAAVTOGPPIYIITTEMKSGSLVLDPLKPSGKIKTLINKLDMMAQIASGMA 353
Qy 379 YVERMNYVHRDLRAANILVGENLVCKVADFGIABLIEDNEYIARQCAKFPPIKTAPEAL 438
Db 354 FIERERNYIHRDLRAANILVSDTISCKIADFGIABLIEDNEYIARBEAKFPPIKTAPEALIN 413
Qy 439 YGRFTIKSDVMSFGIILLTELTKGRVPIYGMVNRRLDQVERGYRMPCEPCEPSLHDL 498
Db 414 YGRFTIKSDVMSFGIILLTELTKGRVPIYGMVNRRLDQVERGYRMPCEPCEPSLHDL 473
Qy 499 CQCKRKEPERPFEYLQAFLEDEYFTSTBPQY 532
Db 474 RLCWKEPERPFEYLDYIRSVLEDEFFATBGOY 507

RESULT 5
US-10-511-937-2593
; Sequence 2593, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Mohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 50661200104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2593
; LENGTH: 659
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2593

Query Match 29.8%; Score 845; DB 6; Length 659;
Best Local Similarity 37.1%; Pred. No. 2.8e-39;
Matches 184; Conservative 96; Mismatches 184; Indels 32; Gaps 13;

Qy 40 KPASADGHRGSAFAFAAPAAEPKLFGGFNSDDYVTSQRAAGPLAGVTT-----FVALYD 94
Db 176 KPQSS--HRTTKKPLPPTPEBDQI-----LKKPLPEPPAAPVSTSELKKVVALYD 224
Qy 95 YESRTETDLSFKGGERLQIVNTEGDMWLAHSLSTGQGYIPSNYVAPS-DSIOAEWYF 153
Db 225 YMPNANADLQARKDDEYFIBLESNLPMWRARD-KNGGBGYIPSNYVLEAESISIMYERYS 283
Qy 154 GKITRRESERLLNENPRGTFVRESETTKGAAYCLSV--SDFNAGLVNKHVKIRKLD 211
Db 284 KHMTRSQAEQ-LLKQEGKEGFIVRDS-SKAGKYVAVFAKSTDDPGV-IRHYVVCSTP 340
Qy 212 SCGYIISRTQFNSLQOLVAYYSKADGLCHRLTTVCSTK-----PQTGLADAVEIP 266
Db 341 QSQYTLKELKLFSTIPILYNHONSAGLISRLK--YVSOQNKMAVSTAGLGYSWEID 398
Qy 267 RESIRLEVKIGQCGFGEVMMGTWNGTTRVAIKTLKPGTMSPEAFLOEAQVMKKLRHEKLV 326
Db 399 PKDLTFLEKLGTOGFVGVYKGMKRGQYDAIKMIKESMSBDEIRIEAKVMMNLSHEKLV 458
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Qy 327 LLYVAVSE--PIVYITETMSKSLVDYDFKGEFGKTLRLPOLVDMAQIUSGAAVERMY 385
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 459 QLYVCCKRRIPIITETEMNAGCLLYNR--EKRHRFQYQQLIEMCKDVCAMEIYESKPF 517
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 386 VHRDLRANILVGENLVCKVADFGIARLIEDNEYTAROGAKPEPIKWTAEBAALYGRFTIK 445
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 518 LHRDLAANCLVNDQGVVKSDFGLSRVYLDDEYTSVGSKEPVMWSPEVLMTYSKFSK 577
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 446 SDVWSFGILLBELTTKGVPYPRGMVREVLDDVEGGRMPCPECPESLHDMCCWRKE 505
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 578 SDIAFGVLMWEIYSLGKMPYERFTNSETAERHIAQGLRLYRPHLASKEYVTYITMYSCKBK 637
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 506 PEERPFEXYLOAFLED 521
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 638 ADERPTFKILLSNILD 653
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 6
US-11-312-958-60
Sequence 60, Application US/11312958
Publication No. US20060100152A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Rosenfeld, Julie Beth
APPLICANT: Sinos-Santiago, Immaculada
TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 9949, 14230, 760, 62553,
TITLE OF INVENTION: 12216, 17719, 41897, 47174, 33408, 10002, 16209, 314, 636,
TITLE OF INVENTION: 27410, 33260, 619, 15985, 69112, 2158, 224, 615, 44373,
TITLE OF INVENTION: 95431, 22245, 2387, 16658, 55054, 16314, 1613, 1675, 9569 OR
FILE REFERENCE: MP102-027P1BIONOMIM
CURRENT APPLICATION NUMBER: US/11/312,958
CURRENT FILING DATE: 2005-12-20
PRIOR APPLICATION NUMBER: US/10/369,022
PRIOR FILING DATE: 2003-02-19
PRIOR APPLICATION NUMBER: US 60/360,495
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/370,121
PRIOR FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: US 60/373,010
PRIOR FILING DATE: 2002-04-16
PRIOR APPLICATION NUMBER: US 60/373,908
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/377,717
PRIOR FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US 60/379,949
PRIOR FILING DATE: 2002-05-13
PRIOR APPLICATION NUMBER: US 60/382,409
PRIOR FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: US 60/385,280
PRIOR FILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: US 60/386,879
PRIOR FILING DATE: 2002-06-06
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 60
LENGTH: 631
TYPE: PRT
ORGANISM: Homo sapiens
US-11-312-958-60

Query Match 29.6%, Score 838.5, DB 7, Length 631,
Best Local Similarity 39.5%, Pred. No. 6,1e-39;
Matches 174; Conservative 91; Mismatches 163; Indels 13; Gaps 9;

Qy 90 VALYDYSRFTETDLSFKKGERLQIVNTEGDMWLAHSLSTGQTGYIIPSNYYA--PSDSIQ 147
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 185 VAMYDFQAAEGHDIRLEKRGQEYLILDKNDVHWWRARD--KYGNEGYIIPSNYYVGGKSSNND 243
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 148 AEEVYFGKITRBSERBLINAEINPFGTFLVARESETTKAYYCLSV--SDPDMAGLAVKHYK 206
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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Db      244 QYEWYCRMNNSKAEO--LLRSEDEKCGFMVADS--SQPGLYTVSLYTKFGEGSSGFRHYH 301
Qy      207 IRKLDG--GYITSRQGFNSLQOLVAAYSAGDGLCHRL---TTVCPTSRQTOGLAKD 261
Db      302 IKETTTSPKYYLLEKNAFGSIPEIIEHKNNAAGLVRLLRPVSVKKNAPTTAGFSYE 361
Qy      262 AMEIPRESLRLEVKLGGCGFCGEVMMGTNGTTRVAIKTLKPGTMSPEAFLOEAQYMKLR 321
Db      362 KWEINPSELTMRRELGSLEFVAVLGLKRAQYKAIAIKIRGAMCEEDFIEBAKYMMLT 421
Qy      322 HEKLVQYAVVSEB--PIYIVTEYMSKSLDFLKGFTGKYLRLPOLVDMAAQIASGMAYV 380
Db      422 HPKLVQYLVGVTQCKPFIYIVTEFMRGCLLNFROQHFER-DVLLSMCDVCGMEYL 480
Qy      381 ERMYVHRDLAANILVGENLVCYVADPGLARLLEDNYYTARQGAKEPIYKTPARALYX 440
Db      481 ERNSFIHRDLAARCLVSEAGVAVVSDGMARYFLDDYTSSGAKFPVKCCPPEVENS 540
Qy      441 RFTKSDVMSFGILLTELTKGRAPVPCMVAREVLQDQERYGMRCPPECESLHDLNCQ 500
Db      541 RFSKSDVMSGVGLMWEVFTGMRPFEXKTYTVEVVTWYTRGHRLYQPKLASNYVEVNLR 600
Qy      501 CWKKEPERPTFEYLAQFLD 521
Db      601 CWGKEPGRPSFEDLRTIDE 621

RESULT 7
US-10-511-937-2959
| Sequence 2959, Application US/10511937
| Publication No. US2006008836A1
| GENERAL INFORMATION:
|   APPLICANT: EXPRESSION DIAGNOSTICS, INC.
|   APPLICANT: Wohlgenuth, Jay
|   APPLICANT: Fry, Kirk
|   APPLICANT: Woodward, Robert
|   APPLICANT: Ly, Ngoc
|   APPLICANT: Prentice, James
|   APPLICANT: Morris, MacDonald
|   APPLICANT: Rosenberg, Steven
|   TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
|   TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
|   FILE REFERENCE: 506612000104
|   CURRENT APPLICATION NUMBER: US/10/511,937
|   CURRENT FILING DATE: 2004-10-19
|   PRIOR APPLICATION NUMBER: PCT/US2003/012946
|   PRIOR FILING DATE: 2003-04-24
|   PRIOR APPLICATION NUMBER: US 10/131,831
|   PRIOR FILING DATE: 2002-04-24
|   PRIOR APPLICATION NUMBER: US 10/325,899
|   PRIOR FILING DATE: 2002-12-20
|   NUMBER OF SEQ ID NOS: 3117
|   SOFTWARE: PatentIn version 3.2
|   SEQ ID NO 2959
|   LENGTH: 620
|   TYPE: PRT
|   ORGANISM: Homo sapiens
US-10-511-937-2959

Query Match      28.2%; Score 800.5; DB 6; Length 620;
Best Local Similarity 34.6%; Pred. No. 6.7e-37;
Matches 176; Conservative 93; Mismatches 181; Indels 59; Gaps 14

Qy      19  EPAENVAGAGGAPASQTSKPASADGHRGPSAFAFMAAPKLFGGFNSDVTYSFOR 78
Db      147 DPTGN-----ASKPLRPPIEDNR-----PLMEEBE 173

Qy      79  AGPLAGVTTFVALYDYESRTETDLSFKGGERLOIVNTEGDWMLIASHLSTGQGYIPSN 138
Db      174  -----TVIALYDYQINDPQELALRNBEYCYLDSSEITHMWRVDP-RNGHEGYVPS 224

Qy      139 YVAA--DSIOAEWYFGKTRRSREULLNAENPRGFFLVRSBETTGAAYCLASVSDPN 196
Db      139  -----DSTIOAEWYFGKTRRSREULLNAENPRGFFLVRSBETTGAAYCLASVSDPN 196

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Db 225 YLVEKSPNNLETYEMWYKNSISRDKAEKLLDT--GKEGAFWVRDSRTA--GTYTVSV--FTK 280
Qy 197 A----KGLANYKHYKIRLDSG--GFYITSRTOFNSLQGLVAYYSKHDGCHRLT--TVC- 248
Db 281 AVVSENNPCIKHNYIKETNDNPKRYIAEKVFPDSITLINTYHOHNGGLVTRLRVYCF 340
Qy 249 -PTSKPOTOGIADKAMEIPRESLRLEVKGCGCFGEVMMGTWNTTVAIKTLKPGTMS 307
Db 341 GRQKAPYTAGIRYKQWVIDSELPFVQEISGCGFGLVHLGYMLKDKVAIKTIEGAMSE 400
Qy 308 EAPLQEAQVWKGLRHEKLVOLYAVVSEE--PIYITEYMSKGLDLPLKGETGKYLRLPQL 366
Db 401 EDFIEAEFVMMKLSHPKLVOLYGVCLQAPICLVFEEMEGCLSDYLRTQGLF--AAETL 459
Qy 367 VDMAAQIASGMAYVERNNYVHRDLRANILVGENLVCKVADFGIARLIEDNEYTARQAK 426
Db 460 LGNCLDCEBMAALEACVIRDLAARNCLVGENQVAKVSDPGMTRVLDQYYSSTGTX 519
Qy 427 FPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGHVPYGMVNRVLDQVERGYMPC 486
Db 520 FPKYMASPEVPSRYSKSDVMSFGLVMEVSEBGKIPYENRNSVEVEDISTGRLYX 579
Qy 487 PPECPSLHDLWCOCWRKEBERPTEPYL 515
Db 580 PRLASTHYQIMNHCWKERPEDRAPAFSRL 608

RESULT 8
US-11-302-678-2
; Sequence 2, Application US/11302678
; Publication No. US2006008881A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Sileo-Santiago, Immaculada
; APPLICANT: Venkateswarlu, Karichela
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46556, 62553, 302, 323,
; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 518, 2058 OR 6351 MOLECULES.
; FILE REFERENCE: MEI02-012P1NM OMNI
; CURRENT APPLICATION NUMBER: US/11/302,678
; CURRENT FILING DATE: 2005-12-14
; PRIOR APPLICATION NUMBER: US/10/345,680
; PRIOR FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/349,511
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/360,500
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/365,041
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/374,063
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/403,468
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 60/414,262
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/419,986
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/423,809
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/429,797
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 983
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-11-302-678-2

Qy 61 PKLFGFNSSDVTYSPQAPPLAGVTTFVALYDSESTEDLSFKKGERLQIVNNTG 120
Db 384 PRQFGLINTVYVY-----DLAHTNNTFE-----IDAVNGVS-- 416
Qy 121 WMLHSLSTGQTCY----IPSNVAPSDSIQAEEMWFGKLTRESEKLLNAENPRGTF 176
Db 417 -----ELSSPPROFAVSIITNOAAPSPLVTLK---DRTSRNSISLSWQEPHEPNIGIL 468
Qy 177 -----VASEETTGAYCLSVSDPDNAKGLVK-----HKIRKLDGCGYIISRT 221
Db 469 DYEVKYYEKOQETSYTIL-----RARGTVNTISSLPDITTYVQIARTRAGYGTNSRK 523
Qy 222 -OFNS-----LOOLVAYSKH-AD----- 238
Db 524 FEFETSPDSISIGESSQVMMIAISAVALIILTVYIVYLIGRPGYKSGHGDKEKHLF 583
Qy 239 -----GLCHRLTYVCP--TSKPGOTGLAKDAMEIPRESLRLEVKGCGCFGEVMMGTW 289
Db 584 GNGLKLPGL---RTYVDPTHYEDPTQAVHEFAKELDATNISIIDKVAGAGFEGVCSGRL 640
Qy 290 NGTTR---VAIKTLKPGTMSPEA--FLQEAQVWKGLRHEKLVOLYAVVSE--EPIYITE 342
Db 641 KLSKKEISVAIKTLKVYTEKORRDFLGEASIMGQPDHNNIIRLEGVYTKSKPMIVTE 700
Qy 343 YMSKGLDLPLKGETGKYLRLPOLYDMAAQIASGMAYVERNNYVHRDLRANILVGENLV 402
Db 701 YMENGSLDSFLRKHDAQFTVI--QLVGLRGLASGMKYLSDMGVYHRDLAARNILINSNV 759
Qy 403 CKVADFGIARLIEDN---EYTAQGAKEPIKMTAPEALYGRFTIKSDVMSFGILLTEL 459
Db 760 CKVSDPGLSVLDEDDPEAAVTTTR--GKIPIMTSPKALIAVKFTPSADVMSYGLVBEVM 818
Qy 460 TKGVRVPYGMVNRVLDQVERGYMPCPPECPSLHDLWCOCWRKEBERPTEPYLQAF 519
Db 819 SYGRRPYEMSNQDVIRKAVDEGYRLPEPMDCPALYOLMDQWQKORNNRPKFOIVSIL 878
Qy 520 E 520
Db 879 D 879

RESULT 9
US-11-303-935-12
; Sequence 12, Application US/11303935
; Publication No. US20060099708A1
; GENERAL INFORMATION:
; APPLICANT: Closssek, Thomas
; APPLICANT: Ullrich, Axel
; APPLICANT: Millaue, Birgit
; TITLE OF INVENTION: METHODS FOR DIAGNOSIS
; AND TREATMENT OF MDK1
; SIGNAL TRANSDUCTION
; DISORDERS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/303,935
; FILING DATE: 19-Dec-2005
; CLASSIFICATION: 435

Query Match 20.7%; Score 586; DB 7; Length 983;
Best Local Similarity 31.4%; Pred. No. 4.3e-25;
Matches 170; Conservative 82; Mismatches 163; Indels 126; Gaps 20;

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/073,064
FILING DATE: 12-Feb-2002
APPLICATION NUMBER: US/08/438,265
FILING DATE: MAY 9, 1995
APPLICATION NUMBER: US/08/368,776
FILING DATE: January 3, 1995
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Wardburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 994 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-11-303-935-12

Query Match 20.2%; Score 573; DB 7; Length 994;
Best Local Similarity 28.4%; Pred. No. 2,8e-24;
Matches 179; Conservative 82; Mismatches 187; Indels 182; Gaps 23;
QY 31 APPASQTPSKPAADG-HRGS-----AAPAPAAEPKLCGPNSSDPTVS----- 75
DB 300 SFSDRSGSSKCECEDGYRAPSDPPYACTRPPAPONTL--FVINQTVSLEKSPADN 357
QY 76 -----PORAGPLAGVYTFVAL-----YDYESRT 99
DB 358 GGRNDVYTRILCKRCSWEGECVPCGSGNIGMPQGTLENNYVYVMDLLAHANTTFEVEA 417
QY 100 ETDLS-FKKGRLQIVNNTGDMWLAHSLSTGQTGYPSNYVAPS--DSIOAEWYFGKI 156
DB 418 VNGVSDLSRSQRL-----FAAVSITTGQ-----AAPSQVSGWKE-----RV 454
QY 157 TRESEERLLMANPRG-----TLVRESEETTKGAYCISVSDPDNAG 199
DB 455 LQRSVQLSWQEPHPNGVITEYEIKYKQKQRETTSTLTKSTS-----ASINLKP 507
QY 200 LANKHYKIRLDSGGF-YITSRTQFNSLQOLVAVYSGHADQLCHRLTTY----- 247
DB 508 GIVYVQIRAVTAAGVGNISPRLDVATLEE-----ASGKMFATAVSSEQNPIITA 559
QY 248 -----CPTSKPQTQ-----LAKDAMEIPRES-- 269
DB 560 VVAVAGTIIIVFWFGFIIGRBHGVSKADQEGDEBELYFCHCTKYIDPEYTEEDPNRAVHQ 619
QY 270 -----LRLVGLGQCGFGEYWMG-----TNGGTRVAIKTLKGTMSPEA--FLQEA 314
DB 620 FAKELDASCIKIRIVGAGEFGEVCSGRLKLPQORDVAVAIKTLKGYTEKQRDFCEA 679
QY 315 QVKKLRLHEKLYOLYAVNSE-EPYIYITEYMSKSLDFLKGFTGKRLRLOLVDMAOI 373
DB 680 SINGQDHPVNVILLEGVYTRGKPMYIEFMENGALDAFRKIDGQTTV--QLVGMIRGI 738
QY 374 ASGMAYVERNNVYHRLRAANILVGENLVCKVADFGIARLLIEDNE--YTARQAKFPIK 430
DB 739 AAGMRVLADMGVYHRLDAANILVNSLVCKVSDFGLSRIEDDPAVYTT--TGKRIPIR 797
QY 431 WTRPEALYGRFTIKSDVMSFGILLTELTTKGAVPIPGMVRNRYLDQVERGCMPCPPEC 490
DB 798 WTRPEALYGRFTIKSDVMSFGILLTELTTKGAVPIPGMVRNRYLDQVERGCMPCPPEC 490
QY 491 PESTLHLMCOCKMRKEPERPTFEYLAFL 520

DB 858 PAGIHLMLDCWQKDRAPRPFQIVGILD 887
RESULT 10
US-11-303-935-2
Sequence 2, Application US/11303935
Publication No. US20060099708A1
GENERAL INFORMATION:
APPLICANT: Ciossek, Thomas
Ulrich, Axel
Mullauer, Birgit
TITLE OF INVENTION: METHODS FOR DIAGNOSIS
AND TREATMENT OF MDK1
SIGNAL TRANSDUCTION
DISORDERS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/303,935
FILING DATE: 19-Dec-2005
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/073,064
FILING DATE: 12-Feb-2002
APPLICATION NUMBER: US/08/438,265
FILING DATE: MAY 9, 1995
APPLICATION NUMBER: US/08/368,776
FILING DATE: January 3, 1995
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Wardburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 998 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-11-303-935-2
Query Match 20.1%; Score 571; DB 7; Length 998;
Best Local Similarity 30.3%; Pred. No. 2,8e-24;
Matches 164; Conservative 76; Mismatches 165; Indels 137; Gaps 19;
QY 76 PORAGPLAGVYTFVAL-----YDYESRTETDS-FKKGRLQIVNNTGDMWLAHSLSTG 130
DB 390 POGTGLIEDNYVYVMDLLAHANTTFEVEAVNGVSDLSRSQRL-----FAAVSITTG 439
QY 131 QNGYIPSNVAPS--DSIOAEWYFGKITRRESERLLMANENPRG----- 173
DB 440 Q-----AAPSQVSGWKE-----RVLQRSVQLSWQEPHPNGVITEYEIKYKQKR 486

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OY 174 --TFVRSBETRKGAACLSVSDPDNAKGLNVKIKYIKRLKDSGGF--YITSOTGNSJLOOLV 230
Db 487 ENTYSTLKTKTS-----ASINLKPCTIVYFOIRAVTAAGYKNTSPRLDVATLEF-- 537
OY 231 AYSKHAODGLCHRLTIV-----CPTSKPOTQ 256
Db 538 -----ASGKMEATVASEQNPVITIAVAVAGTIIIVPMVFGTIGRRHCYGSKADQ 591
OY 257 G-----LAKDAEIPRES-----LMEYVLTGGCGCGEYWMG-- 287
Db 552 GDEELYFHFKPFGTKTYIDPEYEDENRRAHOFAKELDASCITIERVIGAGEGGEVCSGR 651
OY 288 --TWNGTTRVAIKTLKPGTMSBEA--FIOEAOVMKKLRHEKULVOLUAVSE--EPIYIVT 341
Db 652 LKLPGQROVAVALIKTLKVGYTEKQGRDFCEASIMQPOHPNNVHLEGVITRKPWIV 711
OY 342 EYMSKGSLLDFLKGFTGKYLRLPOLYDMAAQIASGAAVYERNMYVHRDLPAANILYGENL 401
Db 712 EFMENGALDAFAFRKHDGQFTVI--QLVGMRLGIAAGKRYIADMKYVHRDLPAARILVNSNL 770
OY 402 VCKVADFGIARLIBENB--YTAROGAKFPIKMTAPEALYGRFTIKSDVMSFGILLTEL 458
Db 771 VCKVSDFGISRIEDDPEAVYTT--TGKXIPVKTALPEALOYRKFTASDVMSGIVWMEV 829
OY 459 TTKGVPPYGVAVREVLDOVERGYRMCPEPECESILHDMCOCWRKPEEERPTFEYLOAF 518
Db 830 MSYGERPAMDMSNOVITKALEEGYRLPAPMDCPAGIHOJLMDCWQDRAPRPFEOVLGI 889
OY 519 LE 520
Db 890 LD 891

```

RESULT 11
 US-11-303-935-11
 ; Sequence 11, Application US/11303935
 ; Publication No. US20060097708A1
 ; GENERAL INFORMATION:
 APPLICANT: Closesek, Thomas
 Ulrich, Axel
 Milauner, Birgit
 TITLE OF INVENTION: METHODS FOR DIAGNOSIS
 AND TREATMENT OF MDK1
 SIGNAL TRANSDUCTION
 DISORDERS
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSER: Lyon & Lyon
 STREET: 633 West Fifth Street
 Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 MB
 Storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/11/303,935
 FILING DATE: 19-Dec-2005
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/10/073,064
 FILING DATE: 12-Feb-2002
 APPLICATION NUMBER: US/08/438,265
 FILING DATE: MAY 9, 1995
 APPLICATION NUMBER: US/08/368,776
 FILING DATE: January 3, 1995
 APPLICATION NUMBER: <Unknown>
 FILING DATE: <Unknown>

```

1  ATTORNEY/AGENT INFORMATION:
2      NAME: Warburg, Richard J.
3      REGISTRATION NUMBER: 32,327
4      REFERENCE/DOCKET NUMBER: 208/007
5
6  TELECOMMUNICATION INFORMATION:
7      TELEPHONE: (213) 489-1600
8      TELEFAX: (213) 955-0440
9      TELEX: 67-3510
10
11 INFORMATION FOR SEQ ID NO: 11:
12     SEQUENCE CHARACTERISTICS:
13         LENGTH: 993 amino acids
14         TYPE: amino acid
15         STRANDEDNESS: single
16         TOPOLOGY: linear
17     MOLECULE TYPE: peptide
18     SEQUENCE DESCRIPTION: SEQ ID NO: 11:
19     SS-11-303-935-11

```

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Query March 20.1% Score 569.5, DB 7; Length 993;
Batch Local Similarity 32.6%; Pred. No. 3,4e-24;
Matches 151; Conservative 67; Mismatches 172; Indels 73; Gaps 14;

QY      84 GGVTFV-VALYDYSRTEETDLSFKKGRRLQIVNNT-EDMWLAHSLSTQGTGYISPNYYA 141
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB      471 GVITEVEIKYKXKQDRERTYSTLKTSYASINNLKPGTVVYFQJRAVTAAGY--GNYSP 528

QY      142 PSDSIQAEWYFGKITTRESEERLLMANPRGTFLVRSBETTKGAYCLSVDPDNAGLN 201
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB      529 RLDAVTEEASATAVSSSEQNPIIIVAVAVAGTILL-----VFVWFGFI----IG 574

QY      202 VKHYKIRLSDSG-----PYTSRTOFNSLQOLVAYYSKADGLCHRLTVV 247
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB      575 RRHGGYKADQEGDEBELYFHKKPFGTKYIIDET-YEDPNRAVHQPAKELDASC----- 627

QY      248 CPTSKPQTQSLAKAMEIPRESRLRLVXLGGCGCFGEVWVG-----TWNGTTRVAIKTLKKG 303
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB      628 -----IKIERVITGAGEFGEVCSGRKLKPGORDVAVAIKTLKVG 665

QY      304 TMSDEA--FLOEAOVMKCLRHEKVLQVLAVYSE--EPITYVEYMSKGSLLDLKSETGKY 360
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB      666 YTEKQORDFLCEASIMQGFDPHPNVVTHLEGVVTRGPWAVIEFWMNGALDALRKHDGQF 725

QY      361 LRLPOLVDMAQIISGMAYVERMNVYHRDLPAANILVGENIVYCKAADFGLARLEIDNE-- 418
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB      726 TVI-QVGLMRLGIAGMRYYLADMGVYHRDLAARNILVNSNLVCKVSDGLSLVIEDDEPA 784

QY      419 -YTAQGAKEPIKWTAPAPALYGRFTIKSDVMSFGILLTELTKGRVPYPGVNRREVLQ 477
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB      785 VYTT-TGGKIPVMTAPPAIQRKFTSASDVMSYGVIMVEVMSYGERPFYDMSNDVIXA 843

QY      478 VERGYRMPCEPEPESLHDMCCCKRKEPERPRTEVYQAPLE 520
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB      844 IEESGYRLPAPMDCPAGLHQLMLDCMKQARERPKFEQIVGLID 886

RESULT 12
US-11-312-958-52
; Sequence 52, Application US/11312958
; Publication No. US20060100152A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Rosenfeld, Julie Beth
; APPLICANT: Siles-Santiago, Inmaculada
; TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 9949, 14230, 760, 62553,
; TITLE OF INVENTION: 12216, 17719, 41897, 47174, 33408, 10002, 16209, 314, 636,
; TITLE OF INVENTION: 27410, 33260, 619, 15985, 69112, 2158, 224, 615, 44373,
; TITLE OF INVENTION: 95431, 22245, 2387, 16658, 55054, 16314, 1613, 1675, 9569 OR
; TITLE OF INVENTION: 13424 MOLECULES
; FILE REFERENCE: MP102-027P1RNONMIM
; CURRENT APPLICATION NUMBER: US/11/312, 958
; CURRENT FILING DATE: 2005-12-20
; PRIOR APPLICATION NUMBER: US/10/369, 022

```

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; PRIOR FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: US 60/360,495
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/370,121
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/373,010
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US 60/373,908
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/377,717
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US 60/379,949
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/382,409
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/385,280
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 60/386,879
; PRIOR FILING DATE: 2002-06-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 1130
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-312-958-52

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Query Match      19.7%; Score 558.5; DB 7; Length 1130;
Best Local Similarity 30.3%; Pred. No. 1.5e-23;
Matches 176; Conservative 67; Mismatches 179; Indels 159; Gaps 20;

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```

QY 61 PKLFGFNSSDTTSQORAPLAGGYTTPALYDEBRTDLSFKKGERLQVNNTEGD 120
DB 522 PKPF-----TAIVTTTODAPSLG-----VVRKDWASONSIALS----- 556
QY 121 WMLAHLSTGQTGYISNYVAFSDSIOAEEMVFGK-----ITRRESRLLNENPR 172
DB 557 -WQAPFNSGAL-----LDYEIKYEKEHEOLTYSSTSKASVITIGLKPA 602
QY 173 GTFVLESETTKGAYCLVSDF-----DNAGLNVRKHKIRKLDSE--GG----- 214
DB 603 TKVVFHVRRTANGYGYSGKFEFETGDETSDMAEQQLVIATAVGGFTLLVILTF 662
QY 215 FYTTSKTP-----NSLOQVAVYSKHA--DGLCHRLTTPVC--TSKPTQGL 258
DB 663 FLTGRCSWYIKAKMKSEKRRNHLQ-----NGHLRFPGI--KTYIDDTYEDPSLAV 713
QY 259 AADAMEIPRESLLEVKLGCGCFGEVWMTGNCTTR-----VAIKTLKPGTMSDEA--FLQ 312
DB 714 HEPAKEIDPSRIEIVIGAGEFGEVCSGRKLTGPKREIIVALIKTLKGHMDRQRDFLR 773
QY 313 EAQVMKKLRHEKLVOLYAVVSE----- 334
DB 774 BASIMGQFPHNPIIRLEGVYTKRSPFAIGVEAFCCPSFLRAGFLNSIOAPHVPGGSLRP 833
QY 335 -----EPIYIVVEYMKSGSLDLPLKGETGKYRLPOLVYMAAQIAGSMAYVERMNTYHRD 389
DB 834 RLPAGRPWMIIVEMYENGSLDSFLRKIDGHFTVI--QLVGLRGIASGMKLSDMGYHRD 892
QY 390 LBAANLVGENLVCKYADFGRLARLIEDNEYTA--ROGAKFPIMKTAPEALYGRFTIKSD 447
DB 893 LAARNLVSNLVCKVSDFLGSVLEBDPEAAVTTTGCKIPRMVTAPEALYARKFESASD 952
QY 448 VMSFGILLTELTKGVVPGMNVREVLDOVERGYRMPCCPECSLSHDLMOCKWEKEPE 507
DB 953 AMSYGIIVMVEVMSYGRPIWEMSGNOVILSIEBGYRLPAMGCPASIHQMLHMCWKERN 1012
QY 508 ERPFETYLQAF-----EDYFTSTEPQYQGE 534
DB 1013 HRPKFTDIVSFLDKLIRNPSALHTLVEDLWME--SPGE 1050

```

```

RESULT 13
US-11-251-465-21
; Sequence 21, Application US/11251465
; Publication No. US20060094061A1
; GENERAL INFORMATION:
; APPLICANT: Blye, Reginald
; APPLICANT: Vandeghinste, Nick
; APPLICANT: Tonne, Peter
; APPLICANT: Klaassen, Hubertus
; TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The
; TITLE OF INVENTION: Same, Useful In The Treatment Of Joint Degenerative And
; FILE REFERENCE: P30,172-A USA
; CURRENT FILING DATE: 2005-10-14
; PRIOR APPLICATION NUMBER: US/11/251,465
; PRIOR FILING DATE: 2004-10-15
; NUMBER OF SEQ ID NOS: 880
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21
; LENGTH: 894
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-251-465-21

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```

Query Match      17.4%; Score 492; DB 7; Length 894;
Best Local Similarity 29.1%; Pred. No. 4.7e-20;
Matches 162; Conservative 72; Mismatches 216; Indels 106; Gaps 21;

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QY 18 LBAENVNHA--GGGAPASQTPSPKPSAD--GHRGPSAAPPAALPKLFGGFNSSDTV 73
DB 334 LGPPENISATRNQSGAFVHMOBPRAVLQSTLLGYR---LAV--GGQDTPEVLMDIGLRQEV 389
QY 74 TSPQAPAGPLAGGYTTPVVALYDEBRTDLSFKKGERLQVNNTEGDMLANSLSGQG 133
DB 390 TTELQDGSVSNLTYCVAAVYTAAG-----DGPMSLPPVLEAMRPG 429
QY 134 YI--PSNYVAPSDSIOAEW-----YFGKITRRESRLLNENPRGTFPV--RESSTKG 185
DB 430 QAPVHQVLKPESTPAPFSPMWTVLGAVVAACVIL-----ALFLVHRKKETRRYG 482
QY 186 AYCLSVSDPDNAKGLNVKHKIRKLDGSGFYITSRTQFNSLOQLVAVYSKADGLCHRLT 245
DB 483 ---EVFEPVTERGELVAVRYVRKYSRR---TTEATLNSL----- 516
QY 246 TVCPSTSKPOTQGIADAME-----IPRESLLEVKLGCGCFGEVWMTGN--GTTRYA 256
DB 517 -----GISBELKEKLRDVMVDRHKVALGKTLGEGEFGAVNEGQLNODDSILKYA 565
QY 297 IKTLKPG--TMSF--BAFLQEAQVMKKLRHEKLVOLYAVV--SEEDPY-----IVTEYMSK 346
DB 566 VKTMKAICTRSLELPELSEAVCKMEFDHPNVWRLLGVCFOGSEERSFAPVVIIEFPMKH 625
QY 347 GSLDLPL-----KGETGKYRLPOLVYMAAQIAGSMAYVERMNTYHRDLPAAVLENTLV 402
DB 626 GDHSLFLVSRIGDDQVYVLPQMLVYFMADIASGWEYLSKGFIRHDLAARNOMLNENMS 685
QY 403 CKYADFGRLARLIEDNEYTRPG--AKFPKMTAPEALYGRFTIKSDVMSFGILLTELTT 460
DB 686 VCVADFGLSKTIYNGDY--YROGRIAMPVYKMAIBSLADRVYTSKSDVMSFGTWMELIT 744
QY 461 KGRVPRPGMNVREVLDOVERGYRMPCCPECSLSHDLMOCKWEKEERPTPEYLQAFLE 520
DB 745 RGQTPYGVENSEIYLYLQGRNKLQAPADCLDGLVLMKRCWELNDQDRPSFTLEKEDLE 804
QY 521 DYFTSTEPQYQGENL 536
DB 805 NTLKALPAPGEPDEL 820

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RESULT 14
US-10-505-928-432
; Sequence 432, Application US/10505928

```

```
Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig, Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 432
; LENGTH: 885
; TYPE: PRN
; ORGANISM: Homo sapiens
; US-10-505-928-432

Query Match      17.1% Score 485.5; DB 6; Length 885;
Best Local Similarity 29.2%; Pred. No. 1e-19;
Matches 161; Conservative 72; Mismatches 212; Indels 107; Gaps 21;

Qy      18 LEPANVHGA--GGGAPASQTPSKPASAD--GHRGSAAPAPAAEPKLFGEFNSDPTV 73
      334 LGPPNISATRNQSAFVHMQEPRAPIQGTLLGYR---LAY-QGQDTPVLMDIGLROEV 389
Qy      74 TSPQAGPLAGGVTTFVYALDYBSRTETDLSFKKGERLQIVNTEGDMWLAHSLSTGQTG 133
      390 TLEIQGGSVSNLTVCVAAYTAAG-----DGPWSLVPLEAMRPV 429
Qy      134 YIPSNVAPSDSIQAEWY--FGKITRRESERLLNENPRGTPLV--RESETTKAVCL 189
      430 KEPS-----TPAFSPMWYVLLGAVVAAACVLL-----ALPLVHRKKETRYG--- 473
Qy      190 SVSPDNAGKLVNHYKIRKLDGSGFYITSTRTOFNSIQOLVAYYSKADGLCHRLTYCP 249
      474 EVFEPYTERGELVYRVKRSYSRR---TTEATINSL----- 507
Qy      250 TSKPQTQGLANDWE-----IPRESLRLEVKLGQCGFGEVWMTGN---GTRVAIKTL 300
      508 -----GISELKEKLDVWVDRHKVALGKTLGEGFGAVMEGQLNODDSILKVAVXTM 560
Qy      301 KPG--TWSP--EAFLOEAQVMKQLRHEKLVOLYAVV---SEEPY---ITYEYNSKSL 350
      561 KIAICTRSELEDPLSEAVCKMEFDPHVMRLIGVCFQGESERESPAPAVIILPFMKHGDILH 620
Qy      351 DFL----KGETGKYLRLPOLVDMAAQIASGMAYYERNVYVRDLRAANIIVGENLVCKVA 406
      621 SFLLYSRLGDPVYLPQMLVKFMADIASGMEYISTKRFIRDLAARCMLENMNSVCVA 680
Qy      407 DFGIARLIEDNEYTARQG--AKPFIKWTAPPAALYGRFTISKDVWSFGIILLTELTTKRV 464
      681 DFGISKIYNGDY-YRQGRIAKMPVKIAIESLADRYVTSKDVWSFGVTMMEIATRGQT 739
Qy      465 PYPGMNVREVLDOYERGYRMECPPECPSLHDLMOCCMRKEPERPTEYIQAFLDEYFT 524
      740 PYPGVENSEIYDIYRQGNRLKQPADCLDGLYALMSRCMELNPDRPSTELREDLENTLK 799
Qy      525 STEPOYQGENL 536
      : : : : :
Db      800 ALPPAQBDEITL 811

RESULT 15
US-11-251-465-20
; Sequence 20, Application US/11251465
; Publication No. US20060094061A1
; GENERAL INFORMATION:
; APPLICANT: Blye, Reginald
; APPLICANT: Vandeghinste, Nick
; APPLICANT: Toume, Peter
; APPLICANT: Klaassen, Hubertus
; TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The
; TITLE OF INVENTION: Same, Useful In The Treatment Of Joint Degenerative And
```

```

; TITLE OF INVENTION: Inflammatory Diseases
; FILE REFERENCE: P30,172-A USA
; CURRENT APPLICATION NUMBER: US/11/251,465
; CURRENT FILING DATE: 2005-10-14
; PRIOR APPLICATION NUMBER: 60/619,384
; PRIOR FILING DATE: 2004-10-15
; NUMBER OF SEQ ID NOS: 860
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20
; LENGTH: 885
; TYPE: PRN
; ORGANISM: Homo sapiens
; US-11-251-465-20

Query Match      17.1% Score 485.5; DB 7; Length 885;
Best Local Similarity 29.2%; Pred. No. 1e-19;
Matches 161; Conservative 72; Mismatches 212; Indels 107; Gaps 21;

Qy      18 LEPANVHGA--GGGAPASQTPSKPASAD--GHRGSAAPAPAAEPKLFGEFNSDPTV 73
      334 LGPPNISATRNQSAFVHMQEPRAPIQGTLLGYR---LAY-QGQDTPVLMDIGLROEV 389
Qy      74 TSPQAGPLAGGVTTFVYALDYBSRTETDLSFKKGERLQIVNTEGDMWLAHSLSTGQTG 133
      390 TLEIQGGSVSNLTVCVAAYTAAG-----DGPWSLVPLEAMRPV 429
Qy      134 YIPSNVAPSDSIQAEWY--FGKITRRESERLLNENPRGTPLV--RESETTKAVCL 189
      430 KEPS-----TPAFSPMWYVLLGAVVAAACVLL-----ALPLVHRKKETRYG--- 473
Qy      190 SVSPDNAGKLVNHYKIRKLDGSGFYITSTRTOFNSIQOLVAYYSKADGLCHRLTYCP 249
      474 EVFEPYTERGELVYRVKRSYSRR---TTEATINSL----- 507
Qy      250 TSKPQTQGLANDWE-----IPRESLRLEVKLGQCGFGEVWMTGN---GTRVAIKTL 300
      508 -----GISELKEKLDVWVDRHKVALGKTLGEGFGAVMEGQLNODDSILKVAVXTM 560
Qy      301 KPG--TWSP--EAFLOEAQVMKQLRHEKLVOLYAVV---SEEPY---ITYEYNSKSL 350
      561 KIAICTRSELEDPLSEAVCKMEFDPHVMRLIGVCFQGESERESPAPAVIILPFMKHGDILH 620
Qy      351 DFL----KGETGKYLRLPOLVDMAAQIASGMAYYERNVYVRDLRAANIIVGENLVCKVA 406
      621 SFLLYSRLGDPVYLPQMLVKFMADIASGMEYISTKRFIRDLAARCMLENMNSVCVA 680
Qy      407 DFGIARLIEDNEYTARQG--AKPFIKWTAPPAALYGRFTISKDVWSFGIILLTELTTKRV 464
      681 DFGISKIYNGDY-YRQGRIAKMPVKIAIESLADRYVTSKDVWSFGVTMMEIATRGQT 739
Qy      465 PYPGMNVREVLDOYERGYRMECPPECPSLHDLMOCCMRKEPERPTEYIQAFLDEYFT 524
      740 PYPGVENSEIYDIYRQGNRLKQPADCLDGLYALMSRCMELNPDRPSTELREDLENTLK 799
Qy      525 STEPOYQGENL 536
      : : : : :
Db      800 ALPPAQBDEITL 811

Search completed: June 5, 2006, 17:43:31
Job time : 7.95244 secs
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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 5, 2006, 17:01:34 ; Search time 118.626 Seconds
(without alignments)
2085.165 Million cell updates/sec

Title: US-10-691-079-3
Perfect score: 2859
Sequence: 1 MSGNSKSPKADASQRRSLP.....AFLEDTFTSTPEQYQECNL 541

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues
Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_8:.*
1: geneseqp1980s:.*
2: geneseqp1990s:.*
3: geneseqp2000s:.*
4: geneseqp2001s:.*
5: geneseqp2002s:.*
6: geneseqp2003as:.*
7: geneseqp2003bs:.*
8: geneseqp2004s:.*
9: geneseqp2005s:.*
10: geneseqp2006s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2859	100.0	541	6	ABP57261 Mouse src
2	2859	100.0	541	8	ADY84077 Murine Src
3	2820.5	98.7	542	5	ABR97339 Novel hum
4	2820.5	98.7	542	8	ADY84075 Human Src
5	2778.5	97.2	536	2	AAR39706 Human pp6
6	2778.5	97.2	536	5	ABG95123 Human v-s
7	2778.5	97.2	536	5	AAU78678 Human SH2
8	2778.5	97.2	536	6	ABP57260 Human src
9	2778.5	97.2	536	7	AD120072 Human c-S
10	2778.5	97.2	536	8	AD122904 Human MP2
11	2778.5	97.2	536	8	ADQ88400 Human wll
12	2778.5	97.2	536	8	ADQ97772 Human can
13	2778.5	97.2	536	8	ADU04517 Protein c
14	2778.5	97.2	536	8	ADY84076 Human Src
15	2778.5	97.2	536	9	ADV94834 Human wll
16	2778.5	97.2	536	9	AEA35914 Human src
17	2778.5	97.2	536	8	ADY84080 Human Src
18	2773.5	97.0	535	7	ADP45087 Human kin
19	2773.5	97.0	535	7	AEED21154 Human non
20	2745.5	96.0	530	8	ADQ88402 Human mut
21	2745.5	96.0	530	8	ADV94836 Human mut
22	2645	92.5	533	3	AAV44447 Wild-type
23	2645	92.5	533	4	ABR84661 Amino aci

24	2645	92.5	533	9	ABR07192 Chicken c
25	2641	92.4	533	3	AAV44449 Mutant ch
26	2640	92.3	533	2	AAR39705 Chicken p
27	2639	92.3	533	3	AAV44451 Mutant ch
28	2463.5	86.2	523	9	ABR07190 Rous sarc
29	2389	83.6	565	4	ABG23778 Novel hum
30	2238	78.3	423	8	ADQ97769 Mouse can
31	2111	73.8	543	4	ABR84663 Amino aci
32	2111	73.8	543	4	ABG10302 Novel hum
33	2111	73.8	543	6	ADA00843 Human Src
34	2111	73.8	543	7	ADP45099 Human kin
35	2111	73.8	543	8	AD122913 Human MP2
36	2111	73.8	543	8	AD019329 Human PRO
37	2111	73.8	543	8	AD019331 Human PRO
38	2111	73.8	543	8	ADQ26047 v-yes-1 y
39	2111	73.8	543	8	ADU06318 Novel bro
40	2111	73.8	543	9	ADW78761 Human Yam
41	2111	73.8	543	9	ADY19868 PRO polyP
42	2111	73.8	543	9	AEA33955 Human PRO
43	2111	73.8	543	9	AEA35915 Human Yes
44	2111	73.8	543	9	AE011122 Human c-x
45	2103	73.6	543	2	AAV24421 Human Yes

ALIGNMENTS

RESULT 1	ABP57261	standard; protein; 541 AA.
ID	ABP57261	
XX	ABP57261	
AC	ABP57261	
XX	17-APR-2003	(first entry)
DE	Mouse src-c protein SEQ ID NO:10.	
XX		
XX	Mouse, src-c; tyrosine kinase; src-c inhibitor; cytosolic; osteopathic;	AB07192 Chicken c
KW	antiinflammatory; antibacterial; antisense therapy; vaccine; cancer;	AAV4449 Mutant ch
KW	antisense oligonucleotide; aberrant bone remodeling; breast cancer;	AAR39705 Chicken p
KW	hyperproliferative disorder; pancreatic cancer; lung cancer; tumour;	AAV4451 Mutant ch
KW	ovarian cancer; oesophageal cancer; neuroblastoma; retinoblastoma;	AB07190 Rous sarc
KW	Kaposi's sarcoma; infection; inflammation; tumour formation.	ABG23778 Novel hum
XX		ADQ97769 Mouse can
XX	Mus musculus.	ABR84663 Amino aci
XX		ABG10302 Novel hum
PN	WO200295053-A2.	ADA00843 Human Src
PD	28-NOV-2002.	ADP45099 Human kin
XX		AD122913 Human MP2
PF	16-MAY-2002; 2002WO-US015684.	AD019329 Human PRO
PR	18-MAY-2001; 2001US-00860473.	AD019331 Human PRO
XX	(ISIS-) ISIS PHARM INC.	ADQ26047 v-yes-1 y
PA		ADU06318 Novel bro
PI	Bennett FC, Watt AT;	ADW78761 Human Yam
XX	WPI; 2003-120806/11.	ADY19868 PRO polyP
DR	N-PSDB; ABZ59389.	AEA33955 Human PRO
XX		AEA35915 Human Yes
PT	New antisense oligonucleotides targeted to nucleic acids encoding src-c,	AE011122 Human c-x
PT	useful for diagnosing, treating or preventing diseases associated with	AAV24421 Human Yes
PT	the expression of src-c, e.g. cancer or inflammation, and in research	
XX	applications.	
XX	Example 13; Page 101-103; 137pp; English.	
XX	The present invention describes a compound (I) that is 8-50 nucleobases	
CC	in length targeted to a nucleic acid molecule encoding a 5'UTR, 3'UTR,	
CC	coding region, intron region, stop codon, intron:exon	
CC	junction, exon:exon junction, or 5' mRNA variant of src-c, and which	
CC	specifically hybridises with and inhibits the expression of src-c. (1)	

CC have cytosolic, antiinflammatory, osteopathic and antibacterial
 CC activities, and can be used in antisense therapy and in vaccines. The
 CC antisense compound (I) can be used for modulating the expression of src-
 CC c and for treating diseases or conditions associated with expression of
 CC src-c, e.g. aberrant bone remodeling or hyperproliferative disorders,
 CC particularly cancer, such as breast cancer, pancreatic cancer, lung
 CC cancer, ovarian cancer, oesophageal cancer, neuroblastoma, retinoblastoma
 CC or Kaposi's sarcoma. (I) are also useful for diagnostics, therapeutics,
 CC prophylaxis, e.g. to prevent or delay infection, inflammation or tumour
 CC formation, as research reagents and kits, and in distinguishing between
 CC functions of various members of a biological pathway. The present
 CC sequence represents mouse src-c, which is used in an example from the
 CC present invention

XX Sequence 541 AA;

Query Match 100.0%; Score 2859; DB 6; Length 541;
 Best Local Similarity 100.0%; Pred. No. 7,2e-241;
 Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSNKKPKDASQRRSLSESENVHAGAGAFPAASQTPSKPASADGHRGSAAFVPPAEP 60
 DB 1 MGSNKKPKDASQRRSLSESENVHAGAGAFPAASQTPSKPASADGHRGSAAFVPPAEP 60
 QY KLFGEFNSDPTVSPORAGALAGVTFVALYVESRTETDLSFKGERLQIVNTRKVD 120
 DB KLFGEFNSDPTVSPORAGALAGVTFVALYVESRTETDLSFKGERLQIVNTRKVD 120
 QY 121 VREGDWMLAHSLSSTGQGYIPSNVYAPSDSIQAEWYFGKITRRESERLLNENPRGTF 180
 DB 121 VREGDWMLAHSLSSTGQGYIPSNVYAPSDSIQAEWYFGKITRRESERLLNENPRGTF 180
 QY 181 LVRESSTTGAYCLSVSDPDNAKGLNVKHKIRKLDGSGFYITSRTQFNSLQOLVAAYYSK 240
 DB 181 LVRESSTTGAYCLSVSDPDNAKGLNVKHKIRKLDGSGFYITSRTQFNSLQOLVAAYYSK 240
 QY 241 HADGLCHRLTTVCPSTKPTQGLAKDAWEIPRESLRLEVLGQCGEGVMGTWNGTTRV 300
 DB 241 HADGLCHRLTTVCPSTKPTQGLAKDAWEIPRESLRLEVLGQCGEGVMGTWNGTTRV 300
 QY 301 AIKTLKPGTMSPEAFLOEAQVMKKLRHEKLVOLYAVVSEBPIYIYTEYNNKSLDLFLKG 360
 DB 301 AIKTLKPGTMSPEAFLOEAQVMKKLRHEKLVOLYAVVSEBPIYIYTEYNNKSLDLFLKG 360
 QY 361 ETGKYLRLPOLVMSAQIASGMAVVERMNVYHDLRAANILVGENLVCKVADFGRLRLIE 420
 DB 361 ETGKYLRLPOLVMSAQIASGMAVVERMNVYHDLRAANILVGENLVCKVADFGRLRLIE 420
 QY 421 DNEYTAROGAKFPFKWTAPAEALYGRFTIKSDVMSFGILLTELTTKGRVPPGMVNRVYL 480
 DB 421 DNEYTAROGAKFPFKWTAPAEALYGRFTIKSDVMSFGILLTELTTKGRVPPGMVNRVYL 480
 QY 481 DOVERGYRMPCEPCEBSLHDLWCQCKRKEPERPTEFYLAFLBEDYFTSTEPQOYGEN 540
 DB 481 DOVERGYRMPCEPCEBSLHDLWCQCKRKEPERPTEFYLAFLBEDYFTSTEPQOYGEN 540
 QY 541 L 541
 DB 541 L 541

RESULT 2
 ADY84077
 ID ADY84077 standard; protein; 541 AA.

XX ADY84077;
 XX
 XX
 DT 02-JUN-2005 (first entry)
 XX
 XX Murine Src protein SEQ ID NO:3.
 XX
 XX pharmaceutical; Alzheimers disease; neuroprotective; nootropic;
 KW Src tyrosine kinase.

XX Mus sp.
 XX
 XX EPI413887-A1.
 XX
 XX 28-APR-2004.
 XX
 XX 22-OCT-2002; 2002EP-00292608.
 XX
 XX 22-OCT-2002; 2002EP-00292608.
 XX
 XX (AVET) AVENTIS PHARMA SA.
 XX
 XX Mercken L, Zambrano N, Ruoso T;
 XX
 XX WPI, 2004-332834/31.
 XX
 PT Identifying therapeutic compound for treating Alzheimer's disease,
 PT involves providing Src protein and determining inhibitory effect of
 PT compound on Src activity.

XX Claim 4; SEQ ID NO 3; 45pp; English.

XX The invention relates to a novel method for identifying (M1) a
 CC therapeutic compound for the treatment of Alzheimer's disease, involving
 CC providing a Src protein and determining the inhibitory effect of a
 CC compound on the Src activity. The method optionally involves providing a
 CC sequence which regulates Src expression and determining if a compound
 CC inhibits the expression of Src protein. A compound of the invention has
 CC neuroprotective and nootropic activity. The compound identified by the
 CC method of the invention is useful for preparing a pharmaceutical for
 CC treating Alzheimer's disease. The present sequence represents murine Src
 CC protein.

XX Sequence 541 AA;

Query Match 100.0%; Score 2859; DB 8; Length 541;
 Best Local Similarity 100.0%; Pred. No. 7,2e-241;
 Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSNKKPKDASQRRSLSESENVHAGAGAFPAASQTPSKPASADGHRGSAAFVPPAEP 60
 DB 1 MGSNKKPKDASQRRSLSESENVHAGAGAFPAASQTPSKPASADGHRGSAAFVPPAEP 60
 QY 61 KLFGEFNSDPTVSPORAGALAGVTFVALYVESRTETDLSFKGERLQIVNTRKVD 120
 DB 61 KLFGEFNSDPTVSPORAGALAGVTFVALYVESRTETDLSFKGERLQIVNTRKVD 120
 QY 121 VREGDWMLAHSLSSTGQGYIPSNVYAPSDSIQAEWYFGKITRRESERLLNENPRGTF 180
 DB 121 VREGDWMLAHSLSSTGQGYIPSNVYAPSDSIQAEWYFGKITRRESERLLNENPRGTF 180
 QY 181 LVRESSTTGAYCLSVSDPDNAKGLNVKHKIRKLDGSGFYITSRTQFNSLQOLVAAYYSK 240
 DB 181 LVRESSTTGAYCLSVSDPDNAKGLNVKHKIRKLDGSGFYITSRTQFNSLQOLVAAYYSK 240
 QY 241 HADGLCHRLTTVCPSTKPTQGLAKDAWEIPRESLRLEVLGQCGEGVMGTWNGTTRV 300
 DB 241 HADGLCHRLTTVCPSTKPTQGLAKDAWEIPRESLRLEVLGQCGEGVMGTWNGTTRV 300
 QY 301 AIKTLKPGTMSPEAFLOEAQVMKKLRHEKLVOLYAVVSEBPIYIYTEYNNKSLDLFLKG 360
 DB 301 AIKTLKPGTMSPEAFLOEAQVMKKLRHEKLVOLYAVVSEBPIYIYTEYNNKSLDLFLKG 360
 QY 361 ETGKYLRLPOLVMSAQIASGMAVVERMNVYHDLRAANILVGENLVCKVADFGRLRLIE 420
 DB 361 ETGKYLRLPOLVMSAQIASGMAVVERMNVYHDLRAANILVGENLVCKVADFGRLRLIE 420
 QY 421 DNEYTAROGAKFPFKWTAPAEALYGRFTIKSDVMSFGILLTELTTKGRVPPGMVNRVYL 480
 DB 421 DNEYTAROGAKFPFKWTAPAEALYGRFTIKSDVMSFGILLTELTTKGRVPPGMVNRVYL 480
 QY 481 DOVERGYRMPCEPCEBSLHDLWCQCKRKEPERPTEFYLAFLBEDYFTSTEPQOYGEN 540
 DB 481 DOVERGYRMPCEPCEBSLHDLWCQCKRKEPERPTEFYLAFLBEDYFTSTEPQOYGEN 540

Db 481 DQVGRGTRMPCPECPESLHDLMCQCRKEPERPTEFYLAFLIEDYFTSTBPQYQGE 540
QY 541 L 541
Db 541 L 541

RESULT 3
ABB97339
ID ABB97339 standard; protein; 542 AA.
AC ABB97339;
XX
XX 27-JUN-2002 (first entry)
DT
DE Novel human protein SEQ ID NO: 607.
XX
XX Human; antihaemic; vulnerary; antiinflammatory; immunomodulator;
KM antiinfertility; cerebroprotective; cytosstatic; rheumatic; gene therapy;
KM neuroprotective; antiparkinsonian; protein therapy; EST;
KM expressed sequence tag.
XX
XX Homo sapiens.
OS
XX W0200222660-A2.
PN
XX 21-MAR-2002.
PD
XX 10-SEP-2001; 2001WO-US026015.
PF
XX 11-SEP-2000; 2000US-00659671.
PR
XX (HYSE-) HYSEQ INC.
PA
XX Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F,
PI Xue AJ, Yang Y, Mehrman T, Drmanac RT;
XX WPI; 2002-292408/33.
DR N-PSDB; ABN32525.
XX
XX An isolated polynucleotide for treating diseases associated with its
PT encoded polypeptide such as cancer and multiple sclerosis.
XX
XX Example 2; SEQ ID NO 607; 509pp; English.
XX
XX The present invention provides the protein and coding sequences of 444
CC novel human proteins. These were isolated from expressed sequences tags
CC (ESTs). They can be used to stimulate cell growth, to regulate
CC haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth
CC e.g. in burn treatment, to regulate the immune system e.g. to treat
CC multiple sclerosis, to regulate activin or inhibin e.g. to treat
CC infertility, to regulate haemostasis or thrombolysis e.g. to treat
CC and cancer, to screen for drugs, to treat inflammatory conditions e.g.
CC rheumatoid arthritis, and to treat nervous system disorders e.g.
CC Parkinson's disease. The present sequence is a protein of the invention
XX
XX Sequence 542 AA;
SQ

Query Match 98.7%; Score 2820.5; DB 5; Length 542;
Best Local Similarity 98.7%; Pred. No. 1.7e-237;
Matches 535; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 1 MGSNKSFKPDASQRRSLSEPSENVGA-GGAPFASQTPSKPASADGHRGSPAALVPPAAE 59
DB 1 MGSNKSFKPDASQRRSLSEPSENVGA-GGAPFASQTPSKPASADGHRGSPAALVPPAAE 60
QY 60 PKLFGFNSSDPTVTSPPQAGALAGCVTTFVALYYESTETETDLSFKKGERLQIVNTRKV 119
DB 61 PKLFGFNSSDPTVTSPPQAGALAGCVTTFVALYYESTETETDLSFKKGERLQIVNTRKV 120
QY 120 DVREGDWMLHSLSTGQTGYIPSNVYAPSDSIQAEWYFGKITRRESRLLNENPRGT 179

Db 121 DVREGDWMLHSLSTGQTGYIPSNVYAPSDSIQAEWYFGKITRRESRLLNENPRGT 180
QY 180 FLVRESSTTGAYCLSVSDPDNAGLNVKHYKIRKLDSSGGFYITSRQFNSLOOLVAYYS 239
Db 181 FLVRESSTTGAYCLSVSDPDNAGLNVKHYKIRKLDSSGGFYITSRQFNSLOOLVAYYS 240
QY 240 KHADELCHRLTTVCPTSKPOTQGLAKDAWEIPRESLRLLEVYLGQCGEVMGTMNGTTR 299
Db 241 KHADELCHRLTTVCPTSKPOTQGLAKDAWEIPRESLRLLEVYLGQCGEVMGTMNGTTR 300
QY 300 VAIKTLKPGTMSPEAFIQEAQVMKQLHREKLVOLYAVVSEBPIYITEYNNKGSLLDPLK 359
Db 301 VAIKTLKPGTMSPEAFIQEAQVMKQLHREKLVOLYAVVSEBPIYITEYNNKGSLLDPLK 360
QY 360 GETCKYLRPLPOLVDMASQIASGNAVYERRNRYVRDLDAANILVGENLVCKRADGLARLI 419
Db 361 GETCKYLRPLPOLVDMASQIASGNAVYERRNRYVRDLDAANILVGENLVCKRADGLARLI 420
QY 420 EDNEYTAROGAKKPEIKMTAPPAALYGRFTIKSDVMSFGILLTETTKGRVVPYPGMVRREV 479
Db 421 EDNEYTAROGAKKPEIKMTAPPAALYGRFTIKSDVMSFGILLTETTKGRVVPYPGMVRREV 480
QY 480 LDQVGRGYRMPCEPECPESLHDLMCQCRKEPERPTEFYLAFLIEDYFTSTBPQYQGE 539
Db 481 LDQVGRGYRMPCEPECPESLHDLMCQCRKEPERPTEFYLAFLIEDYFTSTBPQYQGE 540
QY 540 NL 541
Db 541 NL 542

RESULT 4
ADY84075
ID ADY84075 standard; protein; 542 AA.
XX
XX ADY84075;
AC
XX 02-JUN-2005 (first entry)
DT
XX Human Src protein isoform 1 SEQ ID NO:1.
DE
XX pharmaceutical; Alzheimer's disease; neuroprotective; nootropic;
KM Src tyrosine kinase.
XX
XX Homo sapiens.
OS
XX EP1413887-A1.
XX
XX 28-APR-2004.
PD
XX 22-OCT-2002; 2002EP-00292608.
PF
XX 22-OCT-2002; 2002EP-00292608.
PR
XX (AVET) AVENTIS PHARMA SA.
PA
XX Mercken L, Zambrano N, Russo T;
XX
XX WPI; 2004-332834/31.
DR
XX
XX Identifying therapeutic compound for treating Alzheimer's disease,
PT involves providing Src protein and determining inhibitory effect of
PT compound on Src activity.
XX
XX Claim 4; SEQ ID NO 1; 45pp; English.
XX
XX The invention relates to a novel method for identifying (MI) a
CC therapeutic compound for the treatment of Alzheimer's disease, involving
CC providing a Src protein and determining the inhibitory effect of a
CC compound on the Src activity. The method optionally involves providing a
CC sequence which regulates Src expression and determining if a compound
CC inhibits the expression of Src protein. A compound of the invention has
CC neuroprotective and nootropic activity. The compound identified by the

CC method of the invention is useful for preparing a pharmaceutical for
 CC treating Alzheimer's disease. The present sequence represents isoform 1
 CC of human Src protein.

XX Sequence 542 AA:

Query Match 98.7%; Score 2820.5; DB 8; Length 542;

Best Local Similarity 98.7%; Pred. No. 1,7e-237; Mismatches 3; Indels 1; Gaps 1;

Matches 535; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

1 MSNKKSPKQASQRRSLSESENVHGA-GGAPASQTPSKPASADGHRGSAFVPPAAE 59
 1 MSNKKSPKQASQRRSLSESENVHGA-GGAPASQTPSKPASADGHRGSAFVPPAAE 60
 60 PKLFGFNSDVTYSPQAGALAGVTTFFVALDYESTRTDLSFKKGERLQIVNNTKV 119
 61 PKLFGFNSDVTYSPQAGALAGVTTFFVALDYESTRTDLSFKKGERLQIVNNTKV 120
 120 DVREGDWMHLAHSSTQGTGYIPSNVYAPSDSIQAEEMYPFKITRRESERLLNAENPRGT 179
 121 DVREGDWMHLAHSSTQGTGYIPSNVYAPSDSIQAEEMYPFKITRRESERLLNAENPRGT 180
 180 FLVRESEITTKGAYCLSVSDPDNAKGLNVKXKIKRLDSSGFFYITSRTQFNSLQQLVAYYS 239
 181 FLVRESEITTKGAYCLSVSDPDNAKGLNVKXKIKRLDSSGFFYITSRTQFNSLQQLVAYYS 240
 240 KXADGLCHRLTTYCPTSKPQTQGLADAMEIPRESLRLEVKLGQGCGEVWMTGNQTTT 299
 241 KXADGLCHRLTTYCPTSKPQTQGLADAMEIPRESLRLEVKLGQGCGEVWMTGNQTTT 300
 300 VAIKTLKPGTMSBEALQEAQVWKKLRHEKLVOLYAVVSEBPIYIYTEYNSKSLDPLK 359
 301 VAIKTLKPGTMSBEALQEAQVWKKLRHEKLVOLYAVVSEBPIYIYTEYNSKSLDPLK 360
 360 GETGKTLRLPOLVDMAAOIASGMAVYERMYVHRDLRAANILVGENLVCKVADFGRLRI 419
 361 GETGKTLRLPOLVDMAAOIASGMAVYERMYVHRDLRAANILVGENLVCKVADFGRLRI 420
 420 EDNEYTARQAKPPIKMTAPEALYGRFTTKSDVMSFGILLTELTTKGRVPGMVNREV 479
 421 EDNEYTARQAKPPIKMTAPEALYGRFTTKSDVMSFGILLTELTTKGRVPGMVNREV 480
 480 LDQVERGYMPCPEPCESLHDLCCQWKKEBERPTEFYLOAFLEDDYFTSTEPQVOPGE 539
 481 LDQVERGYMPCPEPCESLHDLCCQWKKEBERPTEFYLOAFLEDDYFTSTEPQVOPGE 540
 540 NL 541
 541 NL 542

RESULT 5
 AAR39706 standard; protein; 536 AA.

XX AAR39706;
 XX 25-MAR-2003 (revised)
 XX 23-DEC-1993 (first entry)
 XX Human pp60 c-src protein.
 XX Endohelital; tyrosine kinase protein; pp60 c-src; BE.
 XX Homo sapiens.
 XX WO9314193-A1.
 XX 22-JUL-1993.
 XX 05-JAN-1993; 93WO-US000445.
 XX 06-JAN-1992; 92US-00820011.

XX (UYVA) UNIV YALE.

XX Bell L, Madri JA, Warren SL, Luthringer DJ;

XX WPI; 1993-243209/30.

XX P-PSDB; AAR39705.

PT Genetically engineered endothelial cells - which exhibit enhanced cell
 PT migration, urokinase-type plasminogen activator activity, and reduced
 PT mononuclear cell adhesion and fibronectin prodn.

PS Disclosure; Page 75-77; 91pp; English.

CC The DNA encoding a portion or (more preferably) the entire pp60 c-src
 CC polypeptide (given in A046688) is used to transform endothelial cells.
 CC Transformed cells produce increased amounts of pp60 c-src and have
 CC improved therapeutic properties. They migrate at faster rates than non-
 CC transformed counterparts; have an enhanced ability to inhibit the
 CC formation of thrombi and/or dissolve thrombi once they have formed and
 CC exhibit reduced mononuclear cell adhesion. They can also be used to
 CC improve the success of surgical procedures such as coronary angioplasty,
 CC heart bypass surgery, vessel graft and stent implantation. (Updated on 25
 CC -MAR-2003 to correct PN field.)

XX Sequence 536 AA:

Query Match 97.2%; Score 2778.5; DB 2; Length 536;

Best Local Similarity 97.6%; Pred. No. 8e-234; Mismatches 3; Indels 7; Gaps 2;

Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;

1 MSNKKSPKQASQRRSLSESENVHGA-GGAPASQTPSKPASADGHRGSAFVPPAAE 59

1 MSNKKSPKQASQRRSLSESENVHGA-GGAPASQTPSKPASADGHRGSAFVPPAAE 60

60 PKLFGFNSDVTYSPQAGALAGVTTFFVALDYESTRTDLSFKKGERLQIVNNTKV 119

61 PKLFGFNSDVTYSPQAGALAGVTTFFVALDYESTRTDLSFKKGERLQIVNNTKV 117

120 DVREGDWMHLAHSSTQGTGYIPSNVYAPSDSIQAEEMYPFKITRRESERLLNAENPRGT 179

118 ---EGDWMHLAHSSTQGTGYIPSNVYAPSDSIQAEEMYPFKITRRESERLLNAENPRGT 174

180 FLVRESEITTKGAYCLSVSDPDNAKGLNVKXKIKRLDSSGFFYITSRTQFNSLQQLVAYYS 239

175 FLVRESEITTKGAYCLSVSDPDNAKGLNVKXKIKRLDSSGFFYITSRTQFNSLQQLVAYYS 234

240 KXADGLCHRLTTYCPTSKPQTQGLADAMEIPRESLRLEVKLGQGCGEVWMTGNQTTT 299

235 KXADGLCHRLTTYCPTSKPQTQGLADAMEIPRESLRLEVKLGQGCGEVWMTGNQTTT 294

300 VAIKTLKPGTMSBEALQEAQVWKKLRHEKLVOLYAVVSEBPIYIYTEYNSKSLDPLK 359

295 VAIKTLKPGTMSBEALQEAQVWKKLRHEKLVOLYAVVSEBPIYIYTEYNSKSLDPLK 354

360 GETGKTLRLPOLVDMAAOIASGMAVYERMYVHRDLRAANILVGENLVCKVADFGRLRI 419

355 GETGKTLRLPOLVDMAAOIASGMAVYERMYVHRDLRAANILVGENLVCKVADFGRLRI 414

420 EDNEYTARQAKPPIKMTAPEALYGRFTTKSDVMSFGILLTELTTKGRVPGMVNREV 479

415 EDNEYTARQAKPPIKMTAPEALYGRFTTKSDVMSFGILLTELTTKGRVPGMVNREV 474

480 LDQVERGYMPCPEPCESLHDLCCQWKKEBERPTEFYLOAFLEDDYFTSTEPQVOPGE 539

475 LDQVERGYMPCPEPCESLHDLCCQWKKEBERPTEFYLOAFLEDDYFTSTEPQVOPGE 534

540 NL 541

535 NL 536

RESULT 6

ABG95123
 ID ABG95123 standard; protein; 536 AA.
 XX AC ABG95123;
 XX DT 04-DEC-2002 (first entry)
 XX DE Human v-src isoform.
 XX KM Chromosome aberration; oncogenic fusion protein; cancer; oncogene;
 KM proliferative disease; cellular protein isoform; heat shock protein 90;
 KM HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
 KM T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
 KM acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
 KM acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
 KM papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
 KM rhabdomyosarcoma; synovial sarcoma; viral infection.
 XX OS Homo sapiens.
 XX EN MO200269900-A2.
 XX PD 12-SEP-2002.
 XX PF 01-MAR-2002; 2002MO-US006518.
 XX PR 01-MAR-2001; 2001US-0272751P.
 XX PA (CONF-) CONFORMA THERAPEUTICS CORP.
 XX PI Fritz LC, Burrows FJ;
 XX DR WPI; 2002-698710/75.
 XX DR N-PSDB; ABS73324.
 XX PT Treating genetically-defined disease associated with chromosomal
 PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
 PT diseases, involves administering an inhibitor of heat shock protein 90.
 XX PS Disclosure; Page 310-312; 389pp; English.
 XX CC The invention describes a method of treating genetically-defined disease
 CC associated with chromosomal aberrations yielding oncogenic fusion
 CC proteins (I); treating cancerous cells containing (I) in a heterogeneous
 CC cell population, treating proliferative diseases associated with mutant
 CC protein or cellular protein isoforms (II) dependent on heat shock protein
 CC (HSP)-90, or selectively treating cells expressing (II) involving
 CC administering HSP90-inhibitor. The method is useful for treating
 CC genetically-defined disease with chromosomal aberration yielding
 CC oncogenic fusion protein, treating cancerous cells containing fusion
 CC protein in heterogeneous cell population, treating proliferative disease
 CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
 CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
 CC p53), or selectively treating cells expressing mutant protein or cellular
 CC protein isoform in a patient heterozygous for (II). The method is useful
 CC for treating a disease e.g. haematopoietic disorder such as T or B cell
 CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CMML,
 CC or a disease characterised by a solid tumour such as papillary thyroid
 CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
 CC synovial sarcoma. The method is also useful for treating viral
 CC infections. This is the amino acid sequence of a human oncogenic protein
 XX
 XX Sequence 536 AA;
 SQ
 Query Match 97.2%; Score 2778.5; DB 5; Length 536;
 Best Local Similarity 97.6%; Pred. No. 8e-234;
 Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;

QY 1 MGSNKSFKPKDASQRRSLSPSENVHGA-GGAFPAQTPSPKPSADGHRGSPSAFVPAAE 59
 DB 1 MGSNKSFKPKDASQRRSLSPSENVHGA-GGAFPAQTPSPKPSADGHRGSPSAFVPAAE 60
 QY 60 PKLFGFNSSDVTYTSPPQAGLAGCVTTFFVALYYESTERTDLSFKGGERLQIVNTRKV 119

DB 61 PKLFGFNSSDVTYTSPPQAGLAGCVTTFFVALYYESTERTDLSFKGGERLQIVNTRKV 117
 QY 120 DVREGDWMLAHSLSGTGTGYIPSNVYAPSDSIQABEWFYFKITRRESRRLILNENPRGT 179
 DB 118 ---EGDWMLAHSLSGTGTGYIPSNVYAPSDSIQABEWFYFKITRRESRRLILNENPRGT 174
 QY 180 FLVRESEETTKGAYCLYSDDPNMAGLVNKHKIRKLDSGGFYITSRQFNSLQOLVAAYS 239
 DB 175 FLVRESEETTKGAYCLYSDDPNMAGLVNKHKIRKLDSGGFYITSRQFNSLQOLVAAYS 234
 QY 240 KHADGLCHRLTTPVPTSPKPTQGLAKDAWEIPRESLRLEVVLGGCFGEVMWGTWNGTTR 299
 DB 235 KHADGLCHRLTTPVPTSPKPTQGLAKDAWEIPRESLRLEVVLGGCFGEVMWGTWNGTTR 294
 QY 300 VAIKTLKPTWSPFAFLQEAQVMKKLRHEKLVQLYAVVSEEPYIVTERYMKSGSLDFLK 359
 DB 295 VAIKTLKPTWSPFAFLQEAQVMKKLRHEKLVQLYAVVSEEPYIVTERYMKSGSLDFLK 354
 QY 360 GETGKYLRLPOLVMSAQIASGMAVVERMNVYHRDLAANILVGENLVCKVADGFLARLI 419
 DB 355 GETGKYLRLPOLVMSAQIASGMAVVERMNVYHRDLAANILVGENLVCKVADGFLARLI 414
 QY 420 EDNEYTAROGAKFPDKMTAPPAALYGRFTIKSDVMSFGILLTETTKGRVVPYPGVNRV 479
 DB 415 EDNEYTAROGAKFPDKMTAPPAALYGRFTIKSDVMSFGILLTETTKGRVVPYPGVNRV 474
 QY 480 LDQVERGYRMPCPPECPSLHDLMCQCRKKEPERPTEFYLAQFLQFSTEPYQDGE 539
 DB 475 LDQVERGYRMPCPPECPSLHDLMCQCRKKEPERPTEFYLAQFLQFSTEPYQDGE 534
 QY 540 NL 541
 DB 535 NL 536
 RESULT 7
 AAU78678
 ID AAU78678 standard; protein; 536 AA.
 XX AC AAU78678;
 XX DT 18-JUN-2002 (first entry)
 XX DE Human SH2/SH3 domain containing protein, v-src.
 XX KM Protein profiling; c-src; SH2; SH3; antibody microarray;
 KM protein microarray; DNA microarray; expression profiling; immunology;
 KM protein analysis; proteome analysis; human; protein expression profiling.
 XX OS Homo sapiens.
 XX EN MO200214667-A2.
 XX PD 21-FEB-2002.
 XX PF 13-AUG-2001; 2001MO-US041709.
 XX PR 11-AUG-2000; 2000US-0224939P.
 XX PR 12-APR-2001; 2001US-0283498P.
 XX PA (AGIL-) AGILIX CORP.
 XX PI Chait BT, Lattimer DR, Lizardi PM, Kershner ER, Morrow JS;
 XX PI Roch ME, Matthesich WJ, McConnell KJ;
 XX DR WPI; 2002-304072/34.
 XX PT Detecting multiple analytes by separating a set of reporter signals
 PT having common property from molecules lacking common property, altering
 PT signal, detecting and distinguishing altered forms of signal from each
 PT other.

PS Disclosure; Page 224; 341pp; English.

XX The invention relates to detecting (M1) multiple analytes involving
CC separating a set of reporter signals (RS), where each RS has a common
CC property, from molecules lacking the common property, altering the RS,
CC and detecting and distinguishing the altered forms of the RS from each
CC other. The method (M1) is useful for detecting multiple analytes M1 is
CC useful for detection of analytes and biomolecules, (such as proteins,
CC peptides and protein fragments), preferably for multiplex detection and
CC analysis of analytes and biomolecules. M1 is useful to detect a specific
CC analyte (in a specific sample or in multiple samples) or multiple
CC analytes (in a single sample or multiple samples), and to gather and
CC catalogue information about unknown analytes. M1 is useful as a detection
CC system in a number of fields, including antibody or protein microarrays,
CC DNA microarrays, expression profiling, comparative genomics, immunology,
CC diagnostic assay and quality control. M1 is useful as a detection and
CC analysis system for protein analysis, proteome analysis, proteomic,
CC protein expression profiling, de novo protein discovery, functional
CC genomics and protein detection. M1 increases the sensitivity and accuracy
CC of detection of analytes of interest, and allows a complex sample of
CC analytes to be quickly and easily catalogued in a reproducible manner. M1
CC is compatible with techniques involving cleavage, treatment or
CC fragmentation of a bulk sample in order to simplify the sample prior to
CC introduction into the first stage of a multistage detection system. M1 is
CC also compatible with any desired sample, including raw extracts and
CC fractionated samples. The present sequence is human c-src whose SH3/SH2
CC domains are detected in a sample, using the method of the invention
XX

Sequence 536 AA:

Query Match 97.2%; Score 2778.5; DB 5; Length 536;

Best Local Similarity 97.6%; Pred. No. 8e-234; Indels 7; Gaps 2;

Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;

1 MGSNKKSPDASGRRSLSPSENVHGA-GGAPPASQTPSPKPSADGHRGSAAFVPPAAE 59
1 MGSNKKSPDASGRRSLSPSENVHGA-GGAPPASQTPSPKPSADGHRGSAAFVPPAAE 60
60 PKLFGFNSSDVTSPQAGALAGVTTFVALDYESRTETDLSFKKGERLQIVNTRKV 119
61 PKLFGFNSSDVTSPQAGALAGVTTFVALDYESRTETDLSFKKGERLQIVNTRKV 117
120 DVEEGDMWLHLSSTQGTGYIPSNVYVAPSDIOAEEMYPFKITRRESEERLLNAENRGT 179
118 ---EGMWMHLHLSSTQGTGYIPSNVYVAPSDIOAEEMYPFKITRRESEERLLNAENRGT 174
180 FLVRESEETTKGAYCLSVSDPDNAKGLNVKXKIKRKLDSGGFYITSRTQFNSLQOLVAYYS 239
175 FLVRESEETTKGAYCLSVSDPDNAKGLNVKXKIKRKLDSGGFYITSRTQFNSLQOLVAYYS 234
240 KPADGICHLRTTYCPTSPKPTQGLADWAEIPRESRLRYKLGQGGCGEYVWMTWGTTR 239
235 KPADGICHLRTTYCPTSPKPTQGLADWAEIPRESRLRYKLGQGGCGEYVWMTWGTTR 234
300 VAIKTLKPGTMSPEAFLOEAQWVKLRHEQLVOLYAVVSEPIYIVTEYNNKSLDLPLK 359
295 VAIKTLKPGTMSPEAFLOEAQWVKLRHEQLVOLYAVVSEPIYIVTEYNNKSLDLPLK 354
360 GETGKYLRLPOLVDMSAQIASGMAVYERNYVHRDLRAANILVGENLVCFVADFGLARLI 419
355 GETGKYLRLPOLVDMSAQIASGMAVYERNYVHRDLRAANILVGENLVCFVADFGLARLI 414
420 EDNEIYAROGAKPPIKWTAPAEALYGRFTIKSDVWSGILLTETLTGGRIPYEGMNNREV 479
415 EDNEIYAROGAKPPIKWTAPAEALYGRFTIKSDVWSGILLTETLTGGRIPYEGMNNREV 474
480 LDQVERGYNRPCEPCESLHDLMLCCMKRKEPERPFETYLQFLBEDYFTSTEQYOPGE 539
475 LDQVERGYNRPCEPCESLHDLMLCCMKRKEPERPFETYLQFLBEDYFTSTEQYOPGE 534
540 NL 541
535 NL 536

RESULT 8

ABP57260

ID ABP57260 standard; protein; 536 AA.

AC ABP57260;

DT 17-APR-2003 (first entry)

DE Human src-c protein SEQ ID NO:3.

XX Human; src-c; tyrosine kinase; src-c inhibitor; cytosolic; osteopathic;

XX antiinflammatory; antibacterial; antisense therapy; vaccine; cancer;

XX antisense oligonucleotide; aberrant bone remodeling; breast cancer;

XX hyperproliferative disorder; pancreatic cancer; lung cancer; tumour;

XX ovarian cancer; oesophageal cancer; neuroblastoma; retinoblastoma;

XX Kaposi's sarcoma; infection; inflammation; tumour formation.

XX Homo sapiens.

XX 16-MAY-2002; 2002MO-US015684.

XX 18-MAY-2001; 2001US-00860473.

XX (ISIS-) ISIS PHARM INC.

XX Bennett FC, Walt AT;

XX WPI, 2003-120806/11.

XX N-PSDB; ABZ59382.

XX New antisense oligonucleotides targeted to nucleic acids encoding src-c,

XX useful for diagnosing, treating or preventing diseases associated with

XX the expression of src-c, e.g. cancer or inflammation, and in research

XX applications.

XX Example 13; Page 97-100; 137pp; English.

XX The present invention describes a compound (I) that is 8-50 nucleobases

XX in length targeted to a nucleic acid molecule encoding a 5'UTR, 3'UTR,

XX coding region, intron region, exon region, stop codon, intron:exon

XX junction, exon:exon junction, or 5' mRNA variant of src-c, and which

XX specifically hybridizes with and inhibits the expression of src-c. (I)

XX have cytosolic, antiinflammatory, osteopathic and antibacterial

XX activities, and can be used in antisense therapy and in vaccines. The

XX antisense compounds (I) can be used for modulating the expression of src-

XX c and for treating diseases or conditions associated with expression of

XX src-c, e.g. aberrant bone remodeling or hyperproliferative disorders,

XX particularly cancer, such as breast cancer, pancreatic cancer, lung

XX cancer, ovarian cancer, oesophageal cancer, neuroblastoma, retinoblastoma

XX or Kaposi's sarcoma. (I) are also useful for diagnostics, therapeutics,

XX prophylaxis, e.g. to prevent or delay infection, inflammation or tumour

XX formation, as research reagents and kits, and in distinguishing between

XX functions of various members of a biological pathway. The present

XX sequence represents human src-c, which is used in an example from the

Sequence 536 AA:

Query Match 97.2%; Score 2778.5; DB 6; Length 536;

Best Local Similarity 97.6%; Pred. No. 8e-234; Indels 7; Gaps 2;

Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;

1 MGSNKKSPDASGRRSLSPSENVHGA-GGAPPASQTPSPKPSADGHRGSAAFVPPAAE 59
1 MGSNKKSPDASGRRSLSPSENVHGA-GGAPPASQTPSPKPSADGHRGSAAFVPPAAE 60
60 PKLFGFNSSDVTSPQAGALAGVTTFVALDYESRTETDLSFKKGERLQIVNTRKV 119

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Db      61 PKLFGFNSSDVTYVSPRAGLAGVTFVALYDSESTETDLSFKKGERLQIVNNT--- 117
Qy      120 DVREGDWMLAHSLSSTGQGYIPSNYVAPSDSIQAEEMVFGKITRRESERLLLNENPRGT 179
Db      118 ---EGDWMLAHSLSSTGQGYIPSNYVAPSDSIQAEEMVFGKITRRESERLLLNENPRGT 174
Qy      180 FLVRESSTTGAYCLSVSDPNAKGLNVKHKIRKLDGSGFYITSRTQFNSLQQLVAYYS 239
Db      175 FLVRESSTTGAYCLSVSDPNAKGLNVKHKIRKLDGSGFYITSRTQFNSLQQLVAYYS 234
Qy      240 KHADGLCHRLTYVCPTRSKPOTQGLAKDAWEIPRESLLEVLGCGCGEYVWGTMNGTTR 299
Db      235 KHADGLCHRLTYVCPTRSKPOTQGLAKDAWEIPRESLLEVLGCGCGEYVWGTMNGTTR 294
Qy      300 VAIKTLKPGTMSPEAFLOEAOVMKGLRHEKLVQLYAVVSEEPYIYVTEYNNKSGSLDPLK 359
Db      295 VAIKTLKPGTMSPEAFLOEAOVMKGLRHEKLVQLYAVVSEEPYIYVTEYNNKSGSLDPLK 354
Qy      360 GETGKYLRPLPOLVDMASQIASGMAVYERMMYVHRDLRAANILVGENLVCKVADFGRLRI 419
Db      355 GETGKYLRPLPOLVDMASQIASGMAVYERMMYVHRDLRAANILVGENLVCKVADFGRLRI 414
Qy      420 EDNEYTARQGAKEPIKWTAPBAALYGRFTIKSDVMSFGILLTELTTGKRVYPCGMVNRV 479
Db      415 EDNEYTARQGAKEPIKWTAPBAALYGRFTIKSDVMSFGILLTELTTGKRVYPCGMVNRV 474
Qy      480 LDVERGYRMPCEPECSLHDLMCQCKRKEPERPFEYLQAFLEDFYFSTEPQYOPGE 539
Db      475 LDVERGYRMPCEPECSLHDLMCQCKRKEPERPFEYLQAFLEDFYFSTEPQYOPGE 534
Qy      540 NL 541
Db      535 NL 536

RESULT 9
ID      ADI20072 standard; protein; 536 AA.
AC      ADI20072;
DT      22-APR-2004 (first entry)
DE      Human c-Src.
XX      specific-binding agent; Src; Cytostatic; Cardiant; Src-positive tumor;
XX      heart disease.
XX      Homo sapiens.
XX      WO2003057238-A1.
XX      17-JUL-2003.
XX      27-DEC-2002; 2002MO-US041564.
XX      28-DEC-2001; 2001US-0345888P.
XX      (UYOR-) UNIV OREGON HEALTH SCI.
XX      Schmitt JM, Stork PJ5;
XX      WPI; 2003-587076/55.
XX      N-PSDB; ADI20071.
XX      New specific-binding agent which specifically binds to Src when Src is
XX      phosphorylated at serine-17 (Ser17) but does not detectably bind to Src
XX      when Ser17 is not phosphorylated; useful for identifying abnormal cell
XX      proliferation.
XX      Disclosure; SEQ ID NO 2; 40pp; English.

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CC      The present invention relates to a specific-binding agent which
CC      specifically binds to Src when Src is phosphorylated at serine at
CC      position 17 (Ser17) but does not detectably bind to Src when Ser17 is not
CC      phosphorylated. The specific-binding agent is useful as a diagnostic
CC      agent. The agent and the methods may also be used for treating Src-
CC      positive tumors or heart disease. The present sequence represents human c-
CC      Src.
XX      Sequence 536 AA;
SQ      Query Match          97.2%; Score 2778.5; DB 7; Length 536;
        Best Local Similarity 97.6%; Pred. No. 8e-234;
        Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;

Qy      1 MGSNKSXPKQASQRRRLSEPSBENTHGA-GGAFPASQTPSPKASADGHRGSAATVPPAAE 59
Db      1 MGSNKSXPKQASQRRRLSEPSBENTHGA-GGAFPASQTPSPKASADGHRGSAATVPPAAE 60
Qy      60 PKLFGFNSSDVTYVSPRAGLAGVTFVALYDSESTETDLSFKKGERLQIVNNTRKV 119
Db      61 PKLFGFNSSDVTYVSPRAGLAGVTFVALYDSESTETDLSFKKGERLQIVNNT--- 117
Qy      120 DVREGDWMLAHSLSSTGQGYIPSNYVAPSDSIQAEEMVFGKITRRESERLLLNENPRGT 179
Db      118 ---EGDWMLAHSLSSTGQGYIPSNYVAPSDSIQAEEMVFGKITRRESERLLLNENPRGT 174
Qy      180 FLVRESSTTGAYCLSVSDPNAKGLNVKHKIRKLDGSGFYITSRTQFNSLQQLVAYYS 239
Db      175 FLVRESSTTGAYCLSVSDPNAKGLNVKHKIRKLDGSGFYITSRTQFNSLQQLVAYYS 234
Qy      240 KHADGLCHRLTYVCPTRSKPOTQGLAKDAWEIPRESLLEVLGCGCGEYVWGTMNGTTR 299
Db      235 KHADGLCHRLTYVCPTRSKPOTQGLAKDAWEIPRESLLEVLGCGCGEYVWGTMNGTTR 294
Qy      300 VAIKTLKPGTMSPEAFLOEAOVMKGLRHEKLVQLYAVVSEEPYIYVTEYNNKSGSLDPLK 359
Db      295 VAIKTLKPGTMSPEAFLOEAOVMKGLRHEKLVQLYAVVSEEPYIYVTEYNNKSGSLDPLK 354
Qy      360 GETGKYLRPLPOLVDMASQIASGMAVYERMMYVHRDLRAANILVGENLVCKVADFGRLRI 419
Db      355 GETGKYLRPLPOLVDMASQIASGMAVYERMMYVHRDLRAANILVGENLVCKVADFGRLRI 414
Qy      420 EDNEYTARQGAKEPIKWTAPBAALYGRFTIKSDVMSFGILLTELTTGKRVYPCGMVNRV 479
Db      415 EDNEYTARQGAKEPIKWTAPBAALYGRFTIKSDVMSFGILLTELTTGKRVYPCGMVNRV 474
Qy      480 LDVERGYRMPCEPECSLHDLMCQCKRKEPERPFEYLQAFLEDFYFSTEPQYOPGE 539
Db      475 LDVERGYRMPCEPECSLHDLMCQCKRKEPERPFEYLQAFLEDFYFSTEPQYOPGE 534
Qy      540 NL 541
Db      535 NL 536

RESULT 10
ADL22904
ID      ADL22904 standard; protein; 536 AA.
AC      ADL22904;
DT      20-MAY-2004 (first entry)
DE      Human MP2153 polypeptide sequence SEQ ID NO: 24.
XX      human; MP2153; p21; p53; cancer.
XX      Homo sapiens.
XX      WO2004015069-A2.
XX      19-FEB-2004.

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PF 06-AUG-2003; 2003WO-US024505.
 XX 07-AUG-2002; 2002US-0401701P.
 PR 16-SEP-2002; 2002US-0411017P.
 PR 30-DEC-2002; 2002US-0437107P.
 XX
 PA (EXEL-) EXELIXIS INC.
 XX
 PI Francis-Iang H, Friedman L, Kidd T, Roche S, Belvin M;
 PI Ploman GD, Lickteig K, Zhang H, Amundsen CD;
 XX
 DR MPI; 2004-180653/17.
 DR N-PSDB; ADL22887.
 XX
 PT Identifying a candidate p21 or p53 pathway modulating agent using an
 PT assay system having a modulator of p21 or p53 (MP2153) polypeptide or
 PT nucleic acid, useful for diagnosing or treating cancer, such as colon or
 PT breast cancer.
 XX
 PS Example 3; Page 87-90; 110pp; English.

CC The present invention relates to a method of identifying a candidate p21
 CC or p53 pathway modulating agent. This comprises providing an assay system
 CC comprising a modulator of p21 or p53 (MP2153) polypeptide or nucleic
 CC acid, contacting the assay system with a test agent, where in its
 CC presence the system provides a reference activity, and detecting a test
 CC agent-biased activity of the assay system, wherein a difference between
 CC the test agent-biased activity and the reference activity identifies the
 CC test agent as a candidate p21 or p53 pathway modulating agent. The
 CC methods and compositions of the present invention are useful for the
 CC diagnosis and/or treatment of diseases or conditions associated with
 CC aberrant expression or activity of the p21 or p53 pathway, such as
 CC cancer, preferably colon or head and neck cancer. The present sequence is
 CC a human MP2153 protein sequence of the invention.
 XX
 SQ Sequence 536 AA;

Query Match 97.2%; Score 2778.5; DB 8; Length 536;

Best Local Similarity 97.6%; Pred. No. 8e-234; Indels 7; Gaps 2;

Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;

QY 1 MGSNKSXPDAQRRSLRSPSENVHGA-GGAPASQTPSKPASADGHRPSAFAVPAAE 59
 DB 1 MGSNKSXPDAQRRSLRSPSENVHGA-GGAPASQTPSKPASADGHRPSAFAVPAAE 60
 QY 60 PKLFGFNSSDVTYSPQAGALAGVTTVALYDYSRTETDLSFKKGERLQIVNNTKV 119
 DB 61 PKLFGFNSSDVTYSPQAGALAGVTTVALYDYSRTETDLSFKKGERLQIVNNTKV 117
 QY 120 DVREGDMWLAHSLSTGQGTIPSNVYAPSDSIQAEEMWFGKTRRSERLLNAENPRGT 179
 DB 118 ---EGDMWLAHSLSTGQGTIPSNVYAPSDSIQAEEMWFGKTRRSERLLNAENPRGT 174
 QY 180 FLVRESETTKGAAYCLSVSPFDNAKGLNVKHYKIRKLDGSGFYITSRTQFNSLQOLVAAYS 239
 DB 175 FLVRESETTKGAAYCLSVSPFDNAKGLNVKHYKIRKLDGSGFYITSRTQFNSLQOLVAAYS 234
 QY 240 KAADGICHLITTYCPTSPKPTQGLADANEIPRESIRLEVKLQGGCGEGEWMGTNGTTR 299
 DB 235 KAADGICHLITTYCPTSPKPTQGLADANEIPRESIRLEVKLQGGCGEGEWMGTNGTTR 294
 QY 300 VAIKTLKPGTMSBEALQEAQWVKLRHEKLVOLYVAVSEEPYIYTEVYNGSLDLDFLK 359
 DB 295 VAIKTLKPGTMSBEALQEAQWVKLRHEKLVOLYVAVSEEPYIYTEVYNGSLDLDFLK 354
 QY 360 GETGKYLRLPOLVDMSAQIASGMAVYERMYVYRDRAANILVGENLVCKVADFGARLIL 419
 DB 355 GETGKYLRLPOLVDMSAQIASGMAVYERMYVYRDRAANILVGENLVCKVADFGARLIL 414
 QY 420 EBNETYARQAGKFPIMWTAPEALYGRFTTKSDVMSFGILLTELTKGRVPIYGMVNRREV 479
 DB 415 EBNETYARQAGKFPIMWTAPEALYGRFTTKSDVMSFGILLTELTKGRVPIYGMVNRREV 474

QY 480 LDQVERGYMPCBPCEPESLHDLMLCOCKWKEPEREPTFEYLQAFLEDDYFTSTEPYQPGS 539
 DB 475 LDQVERGYMPCBPCEPESLHDLMLCOCKWKEPEREPTFEYLQAFLEDDYFTSTEPYQPGS 534
 QY 540 NL 541
 DB 535 NL 536

RESULT 11

ADQ88400
 ID ADQ88400 standard; protein; 536 AA.

XX ADQ88400;

AC 07-OCT-2004 (first entry)

DE Human wild-type tyrosine kinase protein pp60.

KM Cellular oncogene Src; c-Src; tyrosine kinase protein pp60; cancer;

XX infection; inflammation; tumour; gene therapy; human.

OS Homo sapiens.

PN US6764833-B1.

PD 20-JUL-2004.

PF 24-NOV-1999; 99US-00444711.

PR 24-NOV-1999; 99US-00444711.

XX (UYSF-) UNITV SOUTH FLORIDA.

XX Yeatman TJ, Irby RB;

DR MPI; 2004-532511/51.

XX N-PSDB; ADQ88399.

PT New isolated c-Src tyrosine kinase polynucleotide, useful for treating

PT diseases associated or caused by mutant Src, cancer, or for preventing

PS infection, inflammation, or tumor formation.

XX disclosure; SEQ ID NO 2; 29pp; English.

CC The invention relates to novel mutant cellular oncogene Src (c-Src) which

CC codes for mutant tyrosine kinase protein pp60. c-Src sequences are useful

CC for treating diseases which are associated or caused by mutant Src. They

CC are useful for treating cancer, to delay or prevent infection,

CC inflammation or tumor formation. The invention is also useful in gene

CC therapy. The present sequence is human wild-type tyrosine kinase protein

CC pp60.
 XX

SQ Sequence 536 AA;

Query Match 97.2%; Score 2778.5; DB 8; Length 536;

Best Local Similarity 97.6%; Pred. No. 8e-234; Indels 7; Gaps 2;

Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;

QY 1 MGSNKSXPDAQRRSLRSPSENVHGA-GGAPASQTPSKPASADGHRPSAFAVPAAE 59
 DB 1 MGSNKSXPDAQRRSLRSPSENVHGA-GGAPASQTPSKPASADGHRPSAFAVPAAE 60
 QY 60 PKLFGFNSSDVTYSPQAGALAGVTTVALYDYSRTETDLSFKKGERLQIVNNTKV 119
 DB 61 PKLFGFNSSDVTYSPQAGALAGVTTVALYDYSRTETDLSFKKGERLQIVNNTKV 117
 QY 120 DVREGDMWLAHSLSTGQGTIPSNVYAPSDSIQAEEMWFGKTRRSERLLNAENPRGT 179
 DB 118 ---EGDMWLAHSLSTGQGTIPSNVYAPSDSIQAEEMWFGKTRRSERLLNAENPRGT 174
 QY 180 FLVRESETTKGAAYCLSVSPFDNAKGLNVKHYKIRKLDGSGFYITSRTQFNSLQOLVAAYS 239
 DB 175 FLVRESETTKGAAYCLSVSPFDNAKGLNVKHYKIRKLDGSGFYITSRTQFNSLQOLVAAYS 234

Db 175 FLVRESEETTKGAYCLSVSDPDNAKGLNVKHKYIKRLKLDGSGFYITSRTQFNSLQQLVAIYS 234
QY 240 KHADGLCHRLTTCPTSKPQTQGLAKDAWEI PRESLELVKLGCGCGEVMGTMNGTTR 299
Db 235 KHADGLCHRLTTCPTSKPQTQGLAKDAWEI PRESLELVKLGCGCGEVMGTMNGTTR 294
QY 300 VAIKTLKPGTMSPEAFLOBAQVMKGLRHEKLVOLYAVVSEEPYIYVTEYNSKSLDPLK 359
Db 295 VAIKTLKPGTMSPEAFLOBAQVMKGLRHEKLVOLYAVVSEEPYIYVTEYNSKSLDPLK 354
QY 360 GETGKYLRPLQVDMASQIASGMAVVERMNVHRDLAANILVGENLVCKVADGGLARLI 419
Db 355 GETGKYLRPLQVDMASQIASGMAVVERMNVHRDLAANILVGENLVCKVADGGLARLI 414
QY 420 EDNEYTAROGAKPEIKMTAPEALYGRFTIKSDVMSFGILLTELTTGKRVVPQGVNREV 479
Db 415 EDNEYTAROGAKPEIKMTAPEALYGRFTIKSDVMSFGILLTELTTGKRVVPQGVNREV 474
QY 480 LDQVERGYRMPCEPCEBSLHDLMCQCRKEPEREPFEYLQAFLEDFYFSTEPQYQGE 539
Db 475 LDQVERGYRMPCEPCEBSLHDLMCQCRKEPEREPFEYLQAFLEDFYFSTEPQYQGE 534
QY 540 NL 541
Db 535 NL 536

RESULT 12

ADQ97772
ID ADQ97772 standard; protein; 536 AA.

AC ADQ97772;

DT 07-OCT-2004 (first entry)

XX Human cancer associated sequence HPI0-043, SEQ ID 749.

KW Cytostatic; Gene Therapy; cancer; leukemia; lymphoma; Human.

OS Homo sapiens.

PN WO2004060304-A2.

PD 22-JUL-2004.

PF 22-DEC-2003; 2003WO-US041389.

PR 27-DEC-2002; 2002US-00330773.

PA (SAGR-) SAGRES DISCOVERY INC.

PI Morris DW, Malandro MS;

DR WPI; 2004-543781/52.

XX New isolated cancer associated nucleic acids comprising at least 10

PT contiguous nucleotides, useful for diagnosing, preventing and/or treating

XX cancers such as leukemia and lymphoma.

PS Claim 1, SEQ ID NO 749; 199pp; English.

XX The present invention relates to cancer associated sequences (ADQ97025-

CC ADQ98004). The sequences are useful for the diagnosis, prevention and/or

CC treatment of cancer, such as leukemia and lymphoma. Note: The sequence

CC data for this patent did not form part of the printed specification, but

CC was obtained in electronic formate directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 536 AA;

XX Query Match 97.2%; Score 2778.5; DB 8; Length 536;

XX Best Local Similarity 97.6%; Pred. No. 8e-234; Mismatches 3; Indels 7; Gaps 2;

QY 1 MGSNKSXPKQASORRRLBPSENVHGA-GGAFPASOTPSKRPASADGHRGSPAAPPAE 59
Db 1 MGSNKSXPKQASORRRLBPSENVHGA-GGAFPASOTPSKRPASADGHRGSPAAPPAE 60
QY 60 PKLFGFNSSDVTYSPQAGLAGVTTFVALYDESRTETDLSFKKGERLQIVNNTKRV 119
Db 61 PKLFGFNSSDVTYSPQAGLAGVTTFVALYDESRTETDLSFKKGERLQIVNNTKRV 117
QY 120 DVREGDWWLAHSSTGOTGYIPSNYVAPSDSIQAEENYFGKITRSEBRLLNENRGT 179
Db 118 ---EGDWMHLAHSSTGOTGYIPSNYVAPSDSIQAEENYFGKITRSEBRLLNENRGT 174
QY 180 FLVRESEETTKGAYCLSVSDPDNAKGLNVKHKYIKRLKLDGSGFYITSRTQFNSLQQLVAIYS 239
Db 175 FLVRESEETTKGAYCLSVSDPDNAKGLNVKHKYIKRLKLDGSGFYITSRTQFNSLQQLVAIYS 234
QY 240 KHADGLCHRLTTCPTSKPQTQGLAKDAWEI PRESLELVKLGCGCGEVMGTMNGTTR 299
Db 235 KHADGLCHRLTTCPTSKPQTQGLAKDAWEI PRESLELVKLGCGCGEVMGTMNGTTR 294
QY 300 VAIKTLKPGTMSPEAFLOBAQVMKGLRHEKLVOLYAVVSEEPYIYVTEYNSKSLDPLK 359
Db 295 VAIKTLKPGTMSPEAFLOBAQVMKGLRHEKLVOLYAVVSEEPYIYVTEYNSKSLDPLK 354
QY 360 GETGKYLRPLQVDMASQIASGMAVVERMNVHRDLAANILVGENLVCKVADGGLARLI 419
Db 355 GETGKYLRPLQVDMASQIASGMAVVERMNVHRDLAANILVGENLVCKVADGGLARLI 414
QY 420 EDNEYTAROGAKPEIKMTAPEALYGRFTIKSDVMSFGILLTELTTGKRVVPQGVNREV 479
Db 415 EDNEYTAROGAKPEIKMTAPEALYGRFTIKSDVMSFGILLTELTTGKRVVPQGVNREV 474
QY 480 LDQVERGYRMPCEPCEBSLHDLMCQCRKEPEREPFEYLQAFLEDFYFSTEPQYQGE 539
Db 475 LDQVERGYRMPCEPCEBSLHDLMCQCRKEPEREPFEYLQAFLEDFYFSTEPQYQGE 534
QY 540 NL 541
Db 535 NL 536

RESULT 13

ADU04517
ID ADU04517 standard; peptide; 536 AA.

AC ADU04517;

DT 13-JAN-2005 (first entry)

XX Protein tyrosine kinase Src.

XX Protein tyrosine kinase; Src; proto-oncogene; phosphorylation;

XX protein structure; enzyme; EC_2.7.1.112.

XX Unidentified.

XX Key Location/Qualifiers

FT Modified-site 216 /note= "Tyr phosphorylation site"

FT Modified-site 419 /note= "Tyr phosphorylation site"

FT Modified-site 530 /note= "Tyr phosphorylation site"

XX WO2004092703-A2.

XX 28-OCT-2004.

XX 09-APR-2004; 2004WO-US010834.

XX 11-APR-2003; 2003US-0462083P.

XX 11-APR-2003; 2003US-0462472P.

PR 25-JUL-2003; 2003US-0490057P.
 PR 08-MAR-2004; 2004US-055131P.
 PR 19-MAR-2004; 2004US-0554701P.
 PR 08-APR-2004; 2004US-00821231.
 XX
 PA (PURDUE RES FOUND.
 XX
 PI Zhang D, Amotz B, Xie Y, Davison VJ, Mrozek M, Ortiz C;
 XX
 DR WPI, 2004-784629/77.
 XX
 PT Obtaining structural characteristic information for separation and
 PT detection of e.g. proteins comprises irradiating a region formed by
 PT evaporating specimen-containing solvent in a droplet on planar solvo-
 PT phobic sample support.
 XX
 XX
 PS Example C; Page 25; 91pp; English.
 XX
 CC The present sequence is that of proto-oncogene protein tyrosine kinase
 CC Src (p60-src, c-src). The invention relates to the combined use of solid
 CC substrates, micro-deposition techniques, spectral imaging methods, and
 CC data processing to facilitate the concentration and separate detection of
 CC biological molecules including proteins, peptides, polysaccharides,
 CC glycans and nucleotides, in a liquid mixture, using spectral analysis
 CC such as normal Raman spectroscopy, infrared spectroscopy and matrix-
 CC assisted laser desorption/ionisation (MALDI) time-of-flight mass
 CC spectrometry. The methods were demonstrated in examples from the high
 CC invention using peptide fragments of Src. These demonstrated the high
 CC level of analyte discrimination that can be achieved and that the method
 CC can be used to detect and quantify Tyr phosphorylation in tryptic digests
 CC of physiologically important proteins.
 XX
 SQ Sequence 536 AA;
 Query Match 97.2%; Score 2778.5; DB 8; Length 536;
 Best Local Similarity 97.6%; Pred. No. 8e-234;
 Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;
 QY 1 MGSNKKPKPDASQRRRLSPSENVHGA-GGAPASQTPSPKPSADGHRGSAAFVPPAAE 59
 DB 1 MGSNKKPKPDASQRRRLSPSENVHGA-GGAPASQTPSPKPSADGHRGSAAFVPPAAE 60
 QY PKLFGFNSSDVTYTSPOKAGALAGVTTFVALYDYESRTETDLSFKKGERLQIVNNTRKY 119
 DB 61 PKLFGFNSSDVTYTSPOKAGALAGVTTFVALYDYESRTETDLSFKKGERLQIVNNTRKY 117
 QY 120 DVREGDWMLAHSLSTGQTYIPSNVYAPSDSIQAEEMVFGKTRRSEERLLNAENPRGT 179
 DB 118 ---EGDWMMLAHSLSTGQTYIPSNVYAPSDSIQAEEMVFGKTRRSEERLLNAENPRGT 174
 QY 180 FLVRESEETTKGAYCLSVSPFDNAKGLNVGHYKIRKLDGSGFYITTSRTQNSLQOLVAYYS 239
 DB 175 FLVRESEETTKGAYCLSVSPFDNAKGLNVGHYKIRKLDGSGFYITTSRTQNSLQOLVAYYS 234
 QY 240 KPADGCHRLTTCYCPSTKSPOTQGLADAMEIPRESRLRYKLGCGCGEYVMGMNGTTR 229
 DB 235 KPADGCHRLTTCYCPSTKSPOTQGLADAMEIPRESRLRYKLGCGCGEYVMGMNGTTR 234
 QY 300 VAIKTLKPGTMSPEAFLOEAQVWKKLHREKLVOLYAVVSEEPYIYIVTEYNNKSLDLFLK 359
 DB 295 VAIKTLKPGTMSPEAFLOEAQVWKKLHREKLVOLYAVVSEEPYIYIVTEYNNKSLDLFLK 354
 QY 360 GETGKYLRLPOLVDMSAQIASGMAVYERMYVHARDLPAANILVGENLVCKVADFGLARLI 419
 DB 355 GETGKYLRLPOLVDMSAQIASGMAVYERMYVHARDLPAANILVGENLVCKVADFGLARLI 414
 QY 420 EDNEVYARAGAKRPIKMTAPEALYGRFTIKSDVMSFGILLTELTKGRVPYGMNREV 439
 DB 415 EDNEVYARAGAKRPIKMTAPEALYGRFTIKSDVMSFGILLTELTKGRVPYGMNREV 474
 QY 480 LDQVGVGYMPCPECPESLHDLMOCKWRKEPEREPTFEYLQAFLEDYFTSTEPQYOPGE 539
 DB 475 LDQVGVGYMPCPECPESLHDLMOCKWRKEPEREPTFEYLQAFLEDYFTSTEPQYOPGE 534

QY 540 NL 541
 DB 535 NL 536
 RESULT 14
 ID ADY84076 standard; protein; 536 AA.
 XX
 AC ADY84076;
 XX
 DT 02-JUN-2005 (first entry)
 XX
 DE Human Src protein isoform 2 SEQ ID NO:2.
 XX
 XX pharmaceutical; Alzheimers disease; neuroprotective; nootropic;
 KW Src tyrosine kinase.
 XX
 OS Homo sapiens.
 XX
 PN EP1413887-A1.
 XX
 PD 28-APR-2004.
 XX
 PF 22-OCT-2002; 2002EP-00292608.
 XX
 PR 22-OCT-2002; 2002EP-00292608.
 XX
 PA (AVET) AVENTIS PHARMA SA.
 XX
 PI Mercken L, Zambrano N, Russo T;
 XX
 DR WPI, 2004-332834/31.
 XX
 PT Identifying therapeutic compound for treating Alzheimer's disease,
 PT involves providing Src protein and determining inhibitory effect of
 PT compound on Src activity.
 XX
 PS Claim 4; SEQ ID NO 2; 45pp; English.
 XX
 CC The invention relates to a novel method for identifying (M1) a
 CC therapeutic compound for the treatment of Alzheimer's disease, involving
 CC providing a Src protein and determining the inhibitory effect of a
 CC compound on the Src activity. The method optionally involves providing a
 CC sequence which regulates Src expression and determining if a compound
 CC inhibits the expression of Src protein. A compound of the invention has
 CC neuroprotective and nootropic activity. The compound identified by the
 CC method of the invention is useful for preparing a pharmaceutical for
 CC treating Alzheimer's disease. The present sequence represents isoform 2
 CC of human Src protein.
 XX
 SQ Sequence 536 AA;
 Query Match 97.2%; Score 2778.5; DB 8; Length 536;
 Best Local Similarity 97.6%; Pred. No. 8e-234;
 Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;
 QY 1 MGSNKKPKPDASQRRRLSPSENVHGA-GGAPASQTPSPKPSADGHRGSAAFVPPAAE 59
 DB 1 MGSNKKPKPDASQRRRLSPSENVHGA-GGAPASQTPSPKPSADGHRGSAAFVPPAAE 60
 QY PKLFGFNSSDVTYTSPOKAGALAGVTTFVALYDYESRTETDLSFKKGERLQIVNNTRKY 119
 DB 61 PKLFGFNSSDVTYTSPOKAGALAGVTTFVALYDYESRTETDLSFKKGERLQIVNNTRKY 117
 QY 120 DVREGDWMLAHSLSTGQTYIPSNVYAPSDSIQAEEMVFGKTRRSEERLLNAENPRGT 179
 DB 118 ---EGDWMMLAHSLSTGQTYIPSNVYAPSDSIQAEEMVFGKTRRSEERLLNAENPRGT 174
 QY 180 FLVRESEETTKGAYCLSVSPFDNAKGLNVGHYKIRKLDGSGFYITTSRTQNSLQOLVAYYS 239
 DB 175 FLVRESEETTKGAYCLSVSPFDNAKGLNVGHYKIRKLDGSGFYITTSRTQNSLQOLVAYYS 234

QY 240 KHADELCHRLITVCPPTSKPOTQGLAKDAMEI PRESLELEVYLGCGCGEVMGTMNGTTR 299
 DB 235 KHADELCHRLITVCPPTSKPOTQGLAKDAMEI PRESLELEVYLGCGCGEVMGTMNGTTR 294
 QY 300 VAIKTLKPGTMSPEAFLOEAQVMKQLRHEKLVOLYAVSEEPYIYTEYNNKSLDPLK 359
 DB 295 VAIKTLKPGTMSPEAFLOEAQVMKQLRHEKLVOLYAVSEEPYIYTEYNNKSLDPLK 354
 QY 360 GETGKYLRPLQVLDVMAQIASGMAVVERMNVYHDLPAANILVGENIVCKVADFGIARLI 419
 DB 355 GETGKYLRPLQVLDVMAQIASGMAVVERMNVYHDLPAANILVGENIVCKVADFGIARLI 414
 QY 420 EDNEYTARQGAKEPIKMTAPBAALYGRFTTKSDVMSFGILITLTTGGRVYPGMVNRV 479
 DB 415 EDNEYTARQGAKEPIKMTAPBAALYGRFTTKSDVMSFGILITLTTGGRVYPGMVNRV 474
 QY 480 LDQVERGYRMPCEPCEPSLHDLMCQCRKEPERPTEFYLOAFLEDFYFTSTEPQYQGE 539
 DB 475 LDQVERGYRMPCEPCEPSLHDLMCQCRKEPERPTEFYLOAFLEDFYFTSTEPQYQGE 534
 QY 540 NL 541
 DB 535 NL 536

RESULT 15
 ADV94834
 ID ADV94834 standard; protein; 536 AA.
 XX
 AC ADV94834;
 XX
 DT 10-MAR-2005 (first entry)
 XX
 DE Human wild type c-Src protein.
 XX
 KM Cytostatic; gene therapy; mutagenesis; tumor; sarcoma; neuroblastoma;
 KM breast carcinoma; c-Src; tyrosine kinase inhibitor; enzyme.
 XX
 OS Homo sapiens.
 XX
 PN US2004261142-A1.
 XX
 PD 23-DEC-2004.
 XX
 PF 09-JUL-2004; 2004US-00887588.
 XX
 PR 24-NOV-1999; 99US-00444711.
 XX
 PA (YEAT/) YEATMAN T J.
 PA (IRBY/) IRBY R B.
 PI Yeatman TJ, Irby RB;
 XX
 DR MPI: 2005-038810/04.
 DR N-PSDB; ADV94833.
 XX
 PT New truncated c-Src polypeptide, useful for treating and/or preventing
 PT clinical conditions associated with or caused by Src mutation, e.g.
 PT tumors.
 XX
 PS Disclosure; SEQ ID NO 2; 28bp; English.
 XX
 CC The invention relates to a truncated c-Src polypeptide comprising a
 CC sequence of 530 amino acids given in the specification. The polypeptide,
 CC composition and method are useful for treating and/or preventing clinical
 CC conditions associated with or caused by Src mutation e.g. tumors
 CC (sarcoma, neuroblastoma, breast carcinoma). This sequence corresponds to
 CC the wild type c-Src protein.
 XX
 SQ Sequence 536 AA;
 Query Match 97.2%; Score 2778.5; DB 9; Length 536;

Best Local Similarity 97.6%; Pred. No. 8e-234;
 Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;
 QY 1 MGSNKSXPCKASQRRRLBPEENVHGA-GGAFPASQTPSPKASADGHRGSAFVPPAAE 59
 DB 1 MGSNKSXPCKASQRRRLBPEENVHGA-GGAFPASQTPSPKASADGHRGSAFVPPAAE 60
 QY 60 PKLFGGNSSDTVTSPPQAGLGGVTFVALYVSEETEDLSFKGGERLQIVNNT-- 119
 DB 61 PKLFGGNSSDTVTSPPQAGLGGVTFVALYVSEETEDLSFKGGERLQIVNNT-- 117
 QY 120 DVREGDWMLAHSLSGTQGYIPSNYVAPSDSIQAEWYFGKITRSEERLLNENPRGT 179
 DB 118 ---BGDMMLAHSLSGTQGYIPSNYVAPSDSIQAEWYFGKITRSEERLLNENPRGT 174
 QY 180 FLVRESSTTGAYCYLSVDFDNAGLVKHYKIRKLDGSGFYITSRTQFNSLQQLVAYS 239
 DB 175 FLVRESSTTGAYCYLSVDFDNAGLVKHYKIRKLDGSGFYITSRTQFNSLQQLVAYS 234
 QY 240 KHADELCHRLITVCPPTSKPOTQGLAKDAMEI PRESLELEVYLGCGCGEVMGTMNGTTR 299
 DB 235 KHADELCHRLITVCPPTSKPOTQGLAKDAMEI PRESLELEVYLGCGCGEVMGTMNGTTR 294
 QY 300 VAIKTLKPGTMSPEAFLOEAQVMKQLRHEKLVOLYAVSEEPYIYTEYNNKSLDPLK 359
 DB 295 VAIKTLKPGTMSPEAFLOEAQVMKQLRHEKLVOLYAVSEEPYIYTEYNNKSLDPLK 354
 QY 360 GETGKYLRPLQVLDVMAQIASGMAVVERMNVYHDLPAANILVGENIVCKVADFGIARLI 419
 DB 355 GETGKYLRPLQVLDVMAQIASGMAVVERMNVYHDLPAANILVGENIVCKVADFGIARLI 414
 QY 420 EDNEYTARQGAKEPIKMTAPBAALYGRFTTKSDVMSFGILITLTTGGRVYPGMVNRV 479
 DB 415 EDNEYTARQGAKEPIKMTAPBAALYGRFTTKSDVMSFGILITLTTGGRVYPGMVNRV 474
 QY 480 LDQVERGYRMPCEPCEPSLHDLMCQCRKEPERPTEFYLOAFLEDFYFTSTEPQYQGE 539
 DB 475 LDQVERGYRMPCEPCEPSLHDLMCQCRKEPERPTEFYLOAFLEDFYFTSTEPQYQGE 534
 QY 540 NL 541
 DB 535 NL 536

Search completed: June 5, 2006, 17:07:39
 Job time : 121.626 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 5, 2006, 17:08:03 ; Search time 21.7202 Seconds
(without alignments)
2396.538 Million cell updates/sec

Title: US-10-691-079-3

Perfect score: 2859

Sequence: 1 MGSNKSXPKDASQRRSLRP.....AFLEDYFTSTPEQYQENL 541

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: p1r1:*
- 2: p1r2:*
- 3: p1r3:*
- 4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2859	100.0	541	A43610	protein-tyrosine k
2	2820.5	98.7	542	1 TVHUSC	protein-tyrosine k
3	2643	92.4	533	1 TVCHS	protein-tyrosine k
4	2603	91.0	587	1 TVFVPR	protein-tyrosine k
5	2596	90.8	568	1 TVFVSR	protein-tyrosine k
6	2581	90.3	357	1 TVFVS2	protein-tyrosine k
7	2498	87.4	526	1 TVFV60	protein-tyrosine k
8	2479	86.7	526	2 S20808	protein-tyrosine k
9	2473	86.5	526	1 OKFYR	protein-tyrosine k
10	2465	86.3	526	2 S15582	protein-tyrosine k
11	2463	86.1	526	1 TVFVR	protein-tyrosine k
12	2448	85.6	526	2 S26420	protein-tyrosine k
13	2444.5	85.5	532	1 B34104	protein-tyrosine k
14	2442.5	85.4	532	1 A34104	protein-tyrosine k
15	2431	85.0	545	2 S52313	protein-tyrosine k
16	2428	84.9	546	2 S52314	protein-tyrosine k
17	2399.5	83.9	523	1 TVFVMT	protein-tyrosine k
18	2122	74.2	537	1 A45501	protein-tyrosine k
19	2111	73.8	541	1 TVHUS	protein-tyrosine k
20	2108	73.7	541	2 S31645	protein-tyrosine k
21	2103	73.6	541	1 TVCHS	protein-tyrosine k
22	2052	71.8	544	2 S15193	protein-tyrosine k
23	2032	71.1	528	1 TVFVGR	protein-tyrosine k
24	1965.5	68.7	534	1 A44991	protein-tyrosine k
25	1947	68.1	537	2 S15192	protein-tyrosine k
26	1942.5	67.9	534	1 S33568	protein-tyrosine k
27	1929.5	67.4	537	1 TVHUSY	protein-tyrosine k
28	1928	66.9	542	2 A49114	protein-tyrosine k
29	1913	66.9	542	2 A49114	protein-tyrosine k

30	1910.5	66.8	539	2 B49114	protein-tyrosine k
31	1904	66.6	537	1 A43806	protein-tyrosine k
32	1847.5	64.6	529	1 TVHUR	protein-tyrosine k
33	1829.5	64.0	517	2 A43807	protein-tyrosine k
34	1793.5	62.7	517	2 S24547	protein-tyrosine k
35	1589	55.6	663	1 TVMVRR	protein-tyrosine k
36	1581.5	55.3	509	1 TVHAST	protein-tyrosine k
37	1568	54.8	392	2 S04205	protein-tyrosine k
38	1526	53.4	503	1 JQ1321	protein-tyrosine k
39	1523	53.3	503	1 TVMSHC	protein-tyrosine k
40	1515.5	53.0	505	1 TVHUSC	protein-tyrosine k
41	1488	52.0	507	1 A39939	protein-tyrosine k
42	1462.5	51.2	512	1 TVHULY	protein-tyrosine k
43	1455	50.9	509	1 OKHUK	protein-tyrosine k
44	1453.5	50.8	512	1 S56160	protein-tyrosine k
45	1447.5	50.6	509	1 I48845	protein-tyrosine k

ALIGNMENTS

RESULT 1
A43610 protein-tyrosine kinase (BC 2.7.1.112) src, neuronal [similarity] - mouse
N:Alternate names: Rouse sarcoma oncogene
C:Species: Mus musculus (house mouse)
C:Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 05-Oct-2004
C:Accession: A43610
R:Martinez, R.; Mathey-Prevot, B.; Bernards, A.; Baltimore, D.
Science 237, 411-415, 1987
A:Title: Neuronal pp60(c-src) contains a six-amino acid insertion relative to its non-ne
A:Reference number: A43610; MUID:87263406; PMID:2440106
A:Accession: A43610
A:Molecule type: mRNA
A:Residues: 1-541 <MAR>
A:Cross-references: UNIPROT:P05480; UNIPARC:UPI0000161D19; GB:M17031; NID:9201056; PIDN:
C:Comment: The neuronal c-src has an 6 residue insertion of RLNVNR within the amino-term
C:Genetics:
A:Gene: Src
A:Cross-references: MGI:98397
A:Map position: 2:91.0
C:Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C:Keywords: ATP; autophosphorylation; blocked amino end; lipidprotein; myristylation; pho
F:156-253/Domain: SH3 homology <SH3>
F:156-253/Domain: SH2 homology <SH2>
F:273-531/Domain: protein kinase homology <KIN>
F:281-289/Region: protein kinase ATP-binding motif
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:303/Active site: Lys #status predicted
F:424,535/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 100.0%; Score 2859; DB 1; Length 541;
Best Local Similarity 100.0%; Pred. No. 2.4e-136;
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSNKSXPKDASQRRSLRPSENVHAGAPPAASQTPSKPAADGHRGPAAPPAEP 60
Db 1 MGSNKSXPKDASQRRSLRPSENVHAGAPPAASQTPSKPAADGHRGPAAPPAEP 60

QY 61 KLREGFNSDPTVSPQAGALAGAGVTFVALYDRESHTENDLSFKGKERLQIVNTRKVD 120
Db 61 KLREGFNSDPTVSPQAGALAGAGVTFVALYDRESHTENDLSFKGKERLQIVNTRKVD 120

QY 121 VREGDWWLAHSLSTGQTGYIPSNVVA PSDSIQAEWYFGKITRRESRLILNAENPGTF 180
Db 121 VREGDWWLAHSLSTGQTGYIPSNVVA PSDSIQAEWYFGKITRRESRLILNAENPGTF 180

QY 181 LVRESFTTKAAYCLISVDPNNAKLVNKHKKIRKLDGSGGYITTSRTQFNSLQQLVAYYSK 240
Db 181 LVRESFTTKAAYCLISVDPNNAKLVNKHKKIRKLDGSGGYITTSRTQFNSLQQLVAYYSK 240

QY 241 HAQGLCHRLTTVQPTSPKQOGLAKDAWEI PRESLRLEVLLGQCGFGVMMGVTNGTTRV 300
Db 241 HAQGLCHRLTTVQPTSPKQOGLAKDAWEI PRESLRLEVLLGQCGFGVMMGVTNGTTRV 300

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Dh 241 HADGLCHRLTTVCPTSPKQTOGLAKDAWEIPRESRLRLVKLGQCGFGEVMGWTNGTTRV 300
Qy 301 AITLTKPGTMSPEAFLOEAQVMKLRHKKIYQLYAVVSEEPYIVTEYMKSGSLDPLKG 360
Db 301 AITLTKPGTMSPEAFLOEAQVMKLRHKKIYQLYAVVSEEPYIVTEYMKSGSLDPLKG 360
Qy 361 ETGKYLRLPOLVDMASQIASGMAVVERMNVYHRDLRAANILVGENLVCKVADFGIARLI 420
Db 361 ETGKYLRLPOLVDMASQIASGMAVVERMNVYHRDLRAANILVGENLVCKVADFGIARLI 420
Qy 421 DNEYTARQAGAKPPIKMTAPBALYGRFTIKSDVMSFGILLTELTKGRVPYPGMNVREV 480
Db 421 DNEYTARQAGAKPPIKMTAPBALYGRFTIKSDVMSFGILLTELTKGRVPYPGMNVREV 480
Qy 481 DQVERGYRMPCCPECPESLHDLMOCCMKRKEPERFTPEYLOAFLEDYFTSTEPQYOPGE 540
Db 481 DQVERGYRMPCCPECPESLHDLMOCCMKRKEPERFTPEYLOAFLEDYFTSTEPQYOPGE 540
Qy 541 L 541
Db 541 L 541

RESULT 2
TVHUSC
protein-tyrosine kinase (EC 2.7.1.112) src, neuronal - human
C/Date: 30-Jun-1989 #sequence_revision 07-Oct-1994 #text_change 05-Oct-2004
C/Accession: A26891; A61083; B61083; A23287; A28833; B34704
R/Tanaka, A.; Glibbs, C.P.; Archur, R.R.; Anderson, S.K.; Kung, H.J.; Fujita, D.J.
Mol. Cell. Biol. 7, 1978-1983, 1987
A/Title: DNA sequence encoding the amino-terminal region of the human c-src protein: img
A/Reference number: A26891; MUID:87257903; PMID:3299057
A/Accession: A26891
A/Molecule type: mRNA
A/Residues: 1-117/124-191 <TAN>
A/Cross-references: UNIPROT: P12931; UNIPARC: UP10000172578; UNIPARC: UP10000172579; GB: M16
R/Pyper, J.M.; Bolen, J.B.
J. Neurosci. Res. 24, 89-96, 1989
A/Title: Neuron-specific splicing of C-SRC RNA in human brain.
A/Reference number: A61083; MUID:9040882; PMID:2681803
A/Accession: A61083
A/Molecule type: mRNA
A/Residues: 98-145 <PYP>
A/Cross-references: UNIPARC: UP1000017257A
A/Accession: B61083
A/Molecule type: mRNA
A/Residues: 98-117/124-145 <PY2>
A/Cross-references: UNIPARC: UP1000017257A
R/Anderson, S.K.; Glibbs, C.P.; Tanaka, A.; Kung, H.J.; Fujita, D.J.
Mol. Cell. Biol. 5, 1122-1129, 1985
A/Title: Human cellular src gene: Nucleotide sequence and derived amino acid sequence of
A/Reference number: A23287; MUID:85213483; PMID:2582238
A/Accession: A23287
A/Molecule type: mRNA
A/Residues: 192-542 <AND>
A/Cross-references: UNIPARC: UP1000016B068; GB: X02647; NID: g36588; PID: CA26485.1; PID: G
R/Parker, R.C.; Maroon, G.; Lebo, R.V.; Varmus, H.E.; Bishop, J.M.
Mol. Cell. Biol. 5, 831-838, 1985
A/Title: Isolation of duplicated human c-src genes located on chromosomes 1 and 20.
A/Reference number: A28832; MUID:85187981; PMID:2581127
A/Accession: A28832
A/Molecule type: mRNA
A/Residues: 382-542 <PAR>
A/Cross-references: UNIPARC: UP1000017257D
R/Pyper, J.M.; Bolen, J.B.
Mol. Cell. Biol. 10, 2035-2040, 1990
A/Title: Identification of a novel neuronal C-SRC exon expressed in human brain.
A/Reference number: A34704; MUID:90220588; PMID:1651439
A/Accession: B34704
A/Molecule type: mRNA
A/Residues: 118-123 <PY3>
A/Cross-references: UNIPARC: UP1000017257E
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C/Genetics:
A:Gene: GDB:SRC
A:Cross-references: GDB:120750; OMIM:190090
A:Map position: 20q11.2-20q11.2
A:Insertions: 84/1; 117/2; 123/2; 156/2; 191/1; 241/1; 293/1; 353/1; 378/3; 430/1; 474/1
C/Function:
A:Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
C:Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology,
C/Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; phos
F/1-542/Product: protein-tyrosine kinase src, neuronal #status predicted <Mat>
F/1-117/124-542/Product: protein-tyrosine kinase src, short form #status predicted <Mat>
F/91-146/Domain: SH3 homology <SH2>
F/157-254/Domain: SH2 homology <SH2>
F/274-532/Domain: protein kinase homology <Kin>
F/282-390/Region: protein kinase ATP-binding motif
F/2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F/3/Active site: Lys #status predicted
F/425/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predi

Query Match 98.7%; Score 2820.5; DB 1; Length 542;
Best Local Similarity 98.7%; Pred. No. 26-134; 3; Indels 1; Gaps 1;
Matches 535; Conservative 3; Mismatches 3;

Qy 1 MGSNKSXPXDAQGRRLSPSENVGA-GGAPASQTPSKPASADGHRGSAFVPPAAE 59
Db 1 MGSNKSXPXDAQGRRLSPSENVGA-GGAPASQTPSKPASADGHRGSAFVPPAAE 60
Qy 60 PKLFGFNSSDYTSQRRAGALAGYTTVALYDYSRRTDLSFKKGRLOIVNNTRKY 119
Db 61 PKLFGFNSSDYTSQRRAGALAGYTTVALYDYSRRTDLSFKKGRLOIVNNTRKY 120
Qy 120 DVEGGMWLASHSTQGTGTPSNVYAPSDIOAEEMYGKTRRESERLLNAENPRGT 179
Db 121 DVEGGMWLASHSTQGTGTPSNVYAPSDIOAEEMYGKTRRESERLLNAENPRGT 180
Qy 180 FLVRESEETTKGAYCLSVSPDNAGLVNHYKIRKLDGGFYTSRTQFNSLQQLVAYYS 239
Db 181 FLVRESEETTKGAYCLSVSPDNAGLVNHYKIRKLDGGFYTSRTQFNSLQQLVAYYS 240
Qy 240 KHADGCHRLTTVCPTSPKQTOGLAKDAWEIPRESRLRLVKLGQCGFGEVMGWTNGTTR 259
Db 241 KHADGCHRLTTVCPTSPKQTOGLAKDAWEIPRESRLRLVKLGQCGFGEVMGWTNGTTR 300
Qy 300 VAITKLKPGTMSPEAFLOEAQVMKLRHKKIYQLYAVVSEEPYIVTEYMKSGSLDPLK 359
Db 301 VAITKLKPGTMSPEAFLOEAQVMKLRHKKIYQLYAVVSEEPYIVTEYMKSGSLDPLK 360
Qy 360 GETGKYLRLPOLVDMASQIASGMAVVERMNVYHRDLRAANILVGENLVCKVADFGIARLI 419
Db 361 GETGKYLRLPOLVDMASQIASGMAVVERMNVYHRDLRAANILVGENLVCKVADFGIARLI 420
Qy 420 EDNEYTARQAGAKPPIKMTAPBALYGRFTIKSDVMSFGILLTELTKGRVPYPGMNVREV 479
Db 421 EDNEYTARQAGAKPPIKMTAPBALYGRFTIKSDVMSFGILLTELTKGRVPYPGMNVREV 480
Qy 480 LDQVERGYRMPCCPECPESLHDLMOCCMKRKEPERFTPEYLOAFLEDYFTSTEPQYOPGE 539
Db 481 LDQVERGYRMPCCPECPESLHDLMOCCMKRKEPERFTPEYLOAFLEDYFTSTEPQYOPGE 540
Qy 540 NL 541
Db 541 NL 542

RESULT 3
TVHUSC
protein-tyrosine kinase (EC 2.7.1.112) src - chicken
N/Alternate names: kinase-related transforming protein src
C/Species: Gallus gallus (chicken)
C/Date: 19-Feb-1984 #sequence_revision 07-Oct-1994 #text_change 05-Oct-2004
C/Accession: A00630; I50217; A41256; C35650; A32432
R/Takeya, T.; Hanafusa, H.
Cell 32, 881-890, 1983
```

A>Title: Structure and sequence of the cellular gene homologous to the RSV sec gene and
A/Reference number: A00630; MUID:83155664; PMID:6299580
A/Accession: A00630
A/Molecule type: DNA
A/Residues: 1-500; 'R', 502-533 <TAK>
A/Cross-references: UNIPROT:P00523; UNIPROT:Q90993; UNIPARC:UPI000017257F; GB:J00844; NT
R:Takeya, T.; Hanafusa, H.
Cell 34, 319, 1983
A/Reference number: A90838
A/Content: annotation; erratum, correct translation of residue 526
R:Takeya, T.; Hanafusa, H.
J. Virol. 44, 12-18, 1982
A>Title: DNA sequence of the viral and cellular src gene of chickens: II comparison of t
A/Reference number: I50217; MUID:83059861; PMID:6292480
A/Accession: I50217
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-7 <TA2>
A/Cross-references: UNIPARC:UPI0000118887; GB:J00908; NID:g211690; PIDN:AA48732.1; PID:
A/Note: the authors translated the codons AAC and CAG for residues 301 and 526 as Thr an
R:Dora, T.; Levy, J.B.; Kang, L.; Brugge, J.S.; Wang, L.H.
Mol. Cell. Biol. 11, 4165-4176, 1991
A>Title: Analysis of cDNAs of the proto-oncogene c-src: heterogeneity in 5' exons and pc
A/Reference number: A41256; MUID:91304409; PMID:1712905
A/Accession: A41256
A/Molecule type: mRNA
A/Residues: 484-533 <DOR1>
A/Cross-references: UNIPARC:UPI0000171468; GB:S43579; NID:g167964; PIDN:AA19353.1; PID:
A/Note: the authors translated the codon CAG for residue 527 as Glu
R:Dora, T.; Wang, L.H.
Mol. Cell. Biol. 10, 4068-4079, 1990
A>Title: An alternative non-tyrosine protein kinase product of the c-src gene in chicken
A/Reference number: A35650; MUID:90318371; PMID:2115117
A/Accession: C35650
A/Molecule type: mRNA
A/Residues: 1-182; 'DPCIPPLSLC', <DOR2>
A/Cross-references: UNIPARC:UPI000008F03A4; GB:M57290; NID:g212703; PIDN:AA49078.1; PID:
A/Note: alternatively spliced mRNA exclusively replaces the long form in skeletal muscle
R:Shenoy, S.; Choi, J.K.; Bagrodia, S.; Copeland, T.D.; Waller, J.L.; Shalloway, D.
Cell 57, 763-774, 1989
A>Title: Purified maturation promoting factor phosphorylates pp60(c-src) at the sites ph
A/Reference number: A32432; MUID:8924341; PMID:2470512
A/Accession: A32432
A/Molecule type: protein
A/Residues: 2-88 <SH2>
A/Cross-references: UNIPARC:UPI0000172580
A/Note: 34-Thr, 46-Thr, and 72-Ser are phosphorylated during mitosis
C/Genetics:
A/Gene: src
C/Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C/Keywords: alternative splicing; ATP; autophosphorylation; blocked amino end; lipoprote
F:88-137/Domain: SH3 homology <SH3>
F:148-245/Domain: SH2 homology <SH2>
F:265-523/Domain: protein kinase homology <KIN>
F:273-281/Region: protein kinase ATP-binding motif
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:12,48/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F:17/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted
F:34,46/Binding site: phosphate (Thr) (covalent) #status experimental
F:72/Binding site: phosphate (Ser) (covalent) #status experimental
F:25/Active site: Lys #status predicted
F:416,527/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 92.4%; Score 2643; DB 1; Length 533;
Best Local Similarity 92.0%; Pred. No. 1.5e-125;
Matches 503; Conservative 12; Mismatches 18; Indels 8; Gaps 2;

Qy 1 MGSNKSXPXKASQRRRLSPSENVHAGAPASQTSKPSASDGHGSPSAFVPPAEP 60
Db 1 MGSNKSXPXKASQRRRLSPSENVHAGAPASQTSKPSASDGHGSPSAFVPPAEP 58
Qy 61 KLFQGFNSPDTVTSPOAGALAGVTTFFVALLYDRESRTETDLSPKGERLQIVNTRKVD 120
Db 61 KLFQGFNSPDTVTSPOAGALAGVTTFFVALLYDRESRTETDLSPKGERLQIVNTRKVD 120

Db 59 KLFQGFNSPDTVTSPOAGALAGVTTFFVALLYDRESRTETDLSPKGERLQIVNTRKVD 114
Qy 121 VREGDWLHSLSTGQTGYIPSNVAPSDSIQAEEMTFGKTRRESERLLMAENPGTF 180
Db 115 --EGDWLHSLSTGQTGYIPSNVAPSDSIQAEEMTFGKTRRESERLLMAENPGTF 172
Qy 181 LVRESSTTKAAYCLSVSDPNNAGLNVKHYKIRLDSGGFFITSRTPNSLQQLVAYYSK 240
Db 173 LVRESSTTKAAYCLSVSDPNNAGLNVKHYKIRLDSGGFFITSRTPNSLQQLVAYYSK 232
Qy 241 HADGLCHRLTTCPTSPQOTGLAKDAMEIPRESLRLEVLKGGCFSEVWNGTNGTTRV 300
Db 233 HADGLCHRLTTCPTSPQOTGLAKDAMEIPRESLRLEVLKGGCFSEVWNGTNGTTRV 292
Qy 301 AIKTLKPGTMSPEAFLOEAOVMKKLRHEKLVQLYAVVSEBPIYVTEYMKGSLLDPLKG 360
Db 293 AIKTLKPGTMSPEAFLOEAOVMKKLRHEKLVQLYAVVSEBPIYVTEYMKGSLLDPLKG 352
Qy 361 ETGKYLRLPOLVDMASQIAGSMAYVERMYVHRDLRANLIVGNNVCKVADFGRLALIE 420
Db 353 EMGKYLRLPOLVDMASQIAGSMAYVERMYVHRDLRANLIVGNNVCKVADFGRLALIE 412
Qy 421 DNEYTAQGAKEPIKMTAPREALYGRFTIKSDVMSFGILLTELTKGRVPYPGWNEEVL 480
Db 413 DNEYTAQGAKEPIKMTAPREALYGRFTIKSDVMSFGILLTELTKGRVPYPGWNEEVL 472
Qy 481 DOVERGYRMPCEPCEPSLDLMQCWRKBEERPTFEYLQAFLEDYFTSTEPQYQGEN 540
Db 473 DOVERGYRMPCEPCEPSLDLMQCWRKBEERPTFEYLQAFLEDYFTSTEPQYQGEN 532
Qy 541 L 541
Db 533 L 533

RESULT 4
TVFPR
protein-tyrosine kinase (EC 2.7.1.112) src - avian sarcoma virus PR2257
C/Species: avian sarcoma virus PR2257
C/Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 05-Oct-2004
C/Accession: A30174
R:Geryk, J.; Dezelic, P.; Barnier, J.V.; Svoboda, J.; Nehyba, J.; Karakoz, I.; Rynditch,
J. Virol. 63, 481-492, 1989
A>Title: Transduction of the cellular src gene and 3' adjacent sequences in avian sarcom
A/Reference number: A30174; MUID:89094972; PMID:2463376
A/Accession: A30174
A/Molecule type: DNA
A/Residues: 1-587 <GER>
A/Cross-references: UNIPROT:P15054; UNIPARC:UPI0000135F23; GB:M21526; NID:g210264; PIDN:
A/Gene: src
C/Genetics:
C/Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C/Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; onc
F:88-137/Domain: SH3 homology <SH3>
F:148-245/Domain: SH2 homology <SH2>
F:265-523/Domain: protein kinase homology <KIN>
F:273-281/Region: protein kinase ATP-binding motif
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:12/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:25/Active site: Lys #status predicted
F:416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 91.0%; Score 2603; DB 1; Length 587;
Best Local Similarity 91.1%; Pred. No. 1.7e-123;
Matches 496; Conservative 12; Mismatches 17; Indels 8; Gaps 2;

Qy 1 MGSNKSXPXKASQRRRLSPSENVHAGAPASQTSKPSASDGHGSPSAFVPPAEP 60
Db 1 MGSNKSXPXKASQRRRLSPSENVHAGAPASQTSKPSASDGHGSPSAFVPPAEP 58
Qy 61 KLFQGFNSPDTVTSPOAGALAGVTTFFVALLYDRESRTETDLSPKGERLQIVNTRKVD 120
Db 59 KLFQGFNSPDTVTSPOAGALAGVTTFFVALLYDRESRTETDLSPKGERLQIVNTRKVD 114

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QY 121 VREGDWMWLAHSLSTGGTGYIPSNVVAAPSISIOAEWYFGKITRRESERLLNAENPAGTF 180
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 115 --EGDWMWLAHSLTTGGTGYIPSNVVAAPSISIOAEWYFGKITRRESERLLNAENPAGTF 172
QY 181 LVRESSETTGAYCLSVDFPDNAKGLNVKHKIRKLDGSGFYITSRTOFNSLQOLVAAYSK 240
Db 173 LVRESSETTGAYCLSVDFPDNAKGLNVKHKIRKLDGSGFYITSRTOFNSLQOLVAAYSK 232
QY 241 HADGCHRLTTCVPTSPKPTQGLAKDAWEIPRESLRLEVKLGCGCGEVMWGMGTGTRV 300
Db 233 HADGCHRLTTCVPTSPKPTQGLAKDAWEIPRESLRLEVKLGCGCGEVMWGMGTGTRV 292
QY 301 AIKTLPGTSPAPFOEAOVMKKLRHEKLVOLYAVVSEPIYIVTEYNNKSLDPLK 360
Db 293 AIKTLPGTSPAPFOEAOVMKKLRHEKLVOLYAVVSEPIYIVTEYNNKSLDPLK 352
QY 361 ETGKYLRLPOLVDMASQIASGMAYVERMNYVHRDLRAANILVGENLVCKVADFGLARLIE 420
Db 353 EMGKYLRLPOLVDMASQIASGMAYVERMNYVHRDLRAANILVGENLVCKVADFGLARLIE 412
QY 421 DNEYTRAQAKFPKIKTAPBAALYGRFTIKSDVWSGILLTELTTGGRVPYPMVNRREV 480
Db 413 DNEYTRAQAKFPKIKTAPBAALYGRFTIKSDVWSGILLTELTTGGRVPYPMVNRREV 472
QY 481 DOVERGYRMPCEPCEPSLHDLMCQCKRKEPERPFEYLOAFLEDFYFTSTP 533
Db 473 DOVERGYRMPCEPCEPSLHDLMCQCKRKEPERPFEYLOAFLEDFYFTSTP 525

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RESULT 5

TVFVS1

protein-tyrosine kinase (EC 2.7.1.112) src - avian sarcoma virus S1

C/Species: avian sarcoma virus S1

C/Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 05-Oct-2004

C/Accession: A25375

R/Ikawa, S.; Hagino-Yamagishi, K.; Kawai, S.; Yamamoto, T.; Toyoshima, K.

Mol. Cell. Biol. 6, 2420-2428, 1986

A/Title: Activation of the cellular src gene by transducing retrovirus.

A/Reference number: A25375; PMID:87064539; PMID:3097513

A/Residues: 1-568 <IKA>

A/Molecule type: DNA

A/Cross-references: UNIPROT:P14084; UNIPARC:UPI0000135F25

C/Genetic:

A/Gene: src

C/Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology

C/Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; phd

F/148-245/Domain: SH3 homology <SH3>

F/148-245/Domain: SH2 homology <SH2>

F/273-281/Region: protein kinase ATP-binding motif

F/2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted

F/295/Active site: Lys #status predicted

F/416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 90.8%; Score 2596; DB 1; Length 568;
 Best Local Similarity 92.7%; Pred. No. 3.7e-123;
 Matches 494; Conservative 14; Mismatches 17; Indels 8; Gaps 2;

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QY 1 MGSNKSXPDAOSRRSLSEPSENVHAGAGAPASQTPSPKASADGHRGSAFVPPAEP 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MGSNKSXPDPORRRSLSEPPDSTH--HGFPASQTPNKTAADTHRTSPRSRGVATP 58
QY 61 KLFPGFNSSDVTYSPORAGALAGVTTFVALYDYESRTETDLSFKKGERLQIVNNTKVD 120
Db 59 KLFPGFNSTDTYSPORAGALAGVTTFVALYDYESRTETDLSFKKGERLQIVNNT---- 114
QY 121 VREGDWMWLAHSLSTGGTGYIPSNVVAAPSISIOAEWYFGKITRRESERLLNAENPAGTF 180
Db 115 --EGDWMWLAHSLTTGGTGYIPSNVVAAPSISIOAEWYFGKITRRESERLLNAENPAGTF 172
QY 181 LVRESSETTGAYCLSVDFPDNAKGLNVKHKIRKLDGSGFYITSRTOFNSLQOLVAAYSK 240

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Db 173 LVRESSETTGAYCLSVDFPDNAKGLNVKHKIRKLDGSGFYITSRTOFNSLQOLVAAYSK 232
QY 241 HADGCHRLTTCVPTSPKPTQGLAKDAWEIPRESLRLEVKLGCGCGEVMWGMGTGTRV 300
Db 233 HADGCHRLTTCVPTSPKPTQGLAKDAWEIPRESLRLEVKLGCGCGEVMWGMGTGTRV 292
QY 301 AIKTLPGTSPAPFOEAOVMKKLRHEKLVOLYAVVSEPIYIVTEYNNKSLDPLK 360
Db 293 AIKTLPGTSPAPFOEAOVMKKLRHEKLVOLYAVVSEPIYIVTEYNNKSLDPLK 352
QY 361 ETGKYLRLPOLVDMASQIASGMAYVERMNYVHRDLRAANILVGENLVCKVADFGLARLIE 420
Db 353 EMGKYLRLPOLVDMASQIASGMAYVERMNYVHRDLRAANILVGENLVCKVADFGLARLIE 412
QY 421 DNEYTRAQAKFPKIKTAPBAALYGRFTIKSDVWSGILLTELTTGGRVPYPMVNRREV 480
Db 413 DNEYTRAQAKFPKIKTAPBAALYGRFTIKSDVWSGILLTELTTGGRVPYPMVNRREV 472
QY 481 DOVERGYRMPCEPCEPSLHDLMCQCKRKEPERPFEYLOAFLEDFYFTSTP 533
Db 473 DOVERGYRMPCEPCEPSLHDLMCQCKRKEPERPFEYLOAFLEDFYFTSTP 525

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RESULT 6

TVFVS2

protein-tyrosine kinase (EC 2.7.1.112) src - avian sarcoma virus S2

C/Species: avian sarcoma virus S2

C/Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 05-Oct-2004

C/Accession: B25375

R/Ikawa, S.; Hagino-Yamagishi, K.; Kawai, S.; Yamamoto, T.; Toyoshima, K.

Mol. Cell. Biol. 6, 2420-2428, 1986

A/Title: Activation of the cellular src gene by transducing retrovirus.

A/Reference number: A25375; PMID:87064539; PMID:3097513

A/Residues: 1-557 <IKA>

A/Molecule type: DNA

A/Cross-references: UNIPROT:P14085; UNIPARC:UPI0000135F26

C/Genetic:

A/Gene: src

C/Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology;

C/Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; onc

F/148-245/Domain: SH3 homology <SH3>

F/148-245/Domain: SH2 homology <SH2>

F/273-281/Region: protein kinase ATP-binding motif

F/2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted

F/295/Active site: Lys #status predicted

F/416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 90.3%; Score 2581; DB 1; Length 557;
 Best Local Similarity 88.7%; Pred. No. 2.1e-122;
 Matches 495; Conservative 16; Mismatches 21; Indels 26; Gaps 3;

```

QY 1 MGSNKSXPDAOSRRSLSEPSENVHAGAGAPASQTPSPKASADGHRGSAFVPPAEP 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MGSNKSXPDPORRRSLSEPPDSTH--HGFPASQTPNKTAADTHRTSPRSRGVATP 58
QY 61 KLFPGFNSSDVTYSPORAGALAGVTTFVALYDYESRTETDLSFKKGERLQIVNNTKVD 120
Db 59 KLFPGFNSTDTYSPORAGALAGVTTFVALYDYESRTETDLSFKKGERLQIVNNT---- 114
QY 121 VREGDWMWLAHSLSTGGTGYIPSNVVAAPSISIOAEWYFGKITRRESERLLNAENPAGTF 180
Db 115 --EGDWMWLAHSLTTGGTGYIPSNVVAAPSISIOAEWYFGKITRRESERLLNAENPAGTF 172
QY 181 LVRESSETTGAYCLSVDFPDNAKGLNVKHKIRKLDGSGFYITSRTOFNSLQOLVAAYSK 240
Db 173 LVRESSETTGAYCLSVDFPDNAKGLNVKHKIRKLDGSGFYITSRTOFNSLQOLVAAYSK 232
QY 241 HADGCHRLTTCVPTSPKPTQGLAKDAWEIPRESLRLEVKLGCGCGEVMWGMGTGTRV 300
Db 233 HADGCHRLTTCVPTSPKPTQGLAKDAWEIPRESLRLEVKLGCGCGEVMWGMGTGTRV 292

```


QY 301 AIKTLKPGTMSPEAFLOBAQVMKLRHEKLVQLVAVVSEBPIYIVTEYMKSGSLIDFLKG 360
 Db AIKTLKPGTMSPEAFLOBAQVMKLRHEKLVQLVAVVSEBPIYIVTEYMKSGSLIDFLKG 352
 QY 361 ETGYLRLPOLVDMASQIASGMAYVERNNYVHRLRANILVGNLVCKVADFGIARLIE 420
 Db EMGYLRLPOLVDMASQIASGMAYVERNNYVHRLRANILVGNLVCKVADFGIARLIE 412
 QY 421 DNEYTAQAGAKFPIKMTAPAEALYGRFTIKSDVMSFGILLTELTTKGRVPYPMGNVREVL 480
 Db DNEYTAQAGAKFPIKMTAPAEALYGRFTIKSDVMSFGILLTELTTKGRVPYPMGNVREVL 472
 QY 481 DQVERGRMPCCPEPSLHDMQCCKRKEBERPTEFYIQAFLIEDYF----- 528
 Db DQVERGRMPCCPEPSLHDMQCCKRKEBERPTEFYIQAFLIEDYIIGILAMTPWBDKQ 532
 QY 529 -----TSTERQYQGEN 540
 Db 533 EGPRGETASNKQERPGED 550

RESULT 7

TVFV60

protein-tyrosine kinase (EC 2.7.1.112) src - Rous sarcoma virus
 C/Species: Rous sarcoma virus
 C/Date: 22-May-1991 #sequence_revision 17-Dec-1982 #text_change 05-Oct-2004
 C/Accession: A38017; A00631; S02726; A38018
 R/CERN/Jobkey: A.P.; Levinson, A.D.; Varmus, H.E.; Bishop, J.M.; Tischer, E.; Goodman, Nature 301, 726-738, 1983
 A/Title: Corrections to the nucleotide sequence of the src gene of Rous sarcoma virus.
 A/Reference number: A38017; MUID:83141780; PMID:6298633
 A/Accession: A38017
 A/Molecule type: DNA
 A/Residues: 1-526 <CZE>
 A/Cross-references: UNIPROT:P00524; UNIPARC:UPI0000170DC3; GB:L29199; GB:J02018; GB:J020
 R/Experimental source: strain Schmidt-Ruppin
 R/Keya, T.; Hanafusa, H.
 Cell 32, 881-890, 1983
 A/Title: Structure and sequence of the cellular gene homologous to the RSV sec gene and
 A/Reference number: A00630; MUID:83155664; PMID:6299580
 A/Accession: A00631
 A/Molecule type: DNA
 A/Residues: 1-62, 'D', 64-95, 'T', 97-123, 'V', 125-300, 'N', 302-526 <TAK>
 A/Cross-references: UNIPARC:UPI0000172582
 A/Experimental source: strain Schmidt-Ruppin
 R/Barnier, J.V.; Dezelic, P.; Marx, M.; Calochy, G.
 Nucleic Acids Res. 17, 1252, 1989
 A/Title: Nucleotide sequence of the src gene of the Schmidt-Ruppin strain of Rous Sarcom
 A/Reference number: S02726; MUID:89160256; PMID:2537953
 A/Accession: S02726
 A/Molecule type: DNA
 A/Residues: 1-9, 'G', 11-62, 'D', 64-123, 'V', 125-319, 'K', 321-495, 'S', 497-526 <BAR>
 A/Cross-references: UNIPARC:UPI0000135F2C; EMBL:X13745; NID:G61908; PIDN:CAA32012.1; PID
 R/Keya, T.; Feldman, R.A.; Hanafusa, H.
 J. Virol. 44, 1-11, 1982
 A/Title: DNA sequence of the viral and cellular src gene of chickens: I. Complete nucle
 A/Reference number: A38018; MUID:83059858; PMID:6292477
 A/Accession: A38018
 A/Molecule type: DNA
 A/Residues: 1-15, 'C', 17-94, 'RT', 97-116, 'D', 118-337, 'T', 339-526 <TA2>
 A/Cross-references: UNIPARC:UPI0000135F24; GB:K00928; NID:G210187; PIDN:AAA42565.1; PID
 R/Experimental source: strain RASV441
 R/Ngell, J.C.; Ghysdael, J.; Vogt, P.K.; Smart, J.E.
 Nature 291, 675-677, 1981
 A/Title: Homologous tyrosine phosphorylation sites in transformation-specific gene produ
 A/Reference number: A38019; MUID:81220979; PMID:6264320
 A/Contents: annotation; phosphorylation site
 C/Comments: The sequence from the Schmidt-Ruppin strain is shown.
 C/Genetics:
 A/Gene: src
 C/Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
 C/Keywords: ATP; autophosphorylation; blocked amino end; 11pprotein; myristylation; ond
 C/Keywords: ATP; autophosphorylation; blocked amino end; 11pprotein; myristylation; ond

F:88-137/Domain: SH3 homology <SH3>
 F:148-245/Domain: SH2 homology <SH2>
 F:265-523/Domain: protein kinase homology <KIN>
 F:273-281/Region: protein kinase ATP-binding motif
 F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F:295/Active site: Lys #status predicted
 F:416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status experimen

Query Match 87.4%; Score 2498; DB 1; Length 526;

Best Local Similarly 91.2%; Pred. No. 2,86-118;

Matches 478; Conservative 15; Mismatches 23; Indels 8; Gaps 2;

QY 1 MGSNKRKPKASQRRSLRPSENVHAGGAFPAQSQTSKPSADGHRPSAFAFPAPAE 60
 Db 1 MGSSKSRKPKSPQRRSLRPPDSTH--HGFPASQTFNKTRAPDTHTPPSFGTVATSP 58
 QY KLFGFNSSDVTYSPQAGALAGVTFVALYDYESTETDLSFKGGRLOIVNTRKVD 120
 Db KLFGFNSTDTYSPQAGALAGVTFVALYDYESWLETDLSPKGBRLQIVNNT---- 114
 QY 59 KLFGFNSTDTYSPQAGALAGVTFVALYDYESWLETDLSPKGBRLQIVNNT---- 114
 Db 121 VREGDMLANSLSTGQTGYIPSNVAPSDSIQAEWYFGKTRRESERLLIANENPGTF 180
 Db 115 --EGNWMLANSLTGTQGYIPSNVAPSDSIQAEWYFGKTRRESERLLIANENPGTF 172
 QY 181 LVRESFTTKGAYCCLSVSDPNAKGLNHYKIRKLDGSGFITSRTQFNSLQOLVAYYSK 240
 Db 173 LVRESFTTKGAYCCLSVSDPNAKGLNHYKIRKLDGSGFITSRTQFNSLQOLVAYYSK 232
 QY 241 HADGLCHRLTTCVCTSPKQTOGLAKDAWEIPRESLRLEVKLGQCGFVMMGTNNGTTRV 300
 Db 233 HADGLCHRLTTCVCTSPKQTOGLAKDAWEIPRESLRLEVKLGQCGFVMMGTNNGTTRV 292
 QY 301 AIKTLKPGTMSPEAFLOBAQVMKLRHEKLVQLVAVVSEBPIYIVTEYMKSGSLIDFLKG 360
 Db 293 AIKTLKPGTMSPEAFLOBAQVMKLRHEKLVQLVAVVSEBPIYIVTEYMKSGSLIDFLKG 352
 QY 361 ETGYLRLPOLVDMASQIASGMAYVERNNYVHRLRANILVGNLVCKVADFGIARLIE 420
 Db 353 EMGYLRLPOLVDMASQIASGMAYVERNNYVHRLRANILVGNLVCKVADFGIARLIE 412
 QY 421 DNEYTAQAGAKFPIKMTAPAEALYGRFTIKSDVMSFGILLTELTTKGRVPYPMGNVREVL 480
 Db 413 DNEYTAQAGAKFPIKMTAPAEALYGRFTIKSDVMSFGILLTELTTKGRVPYPMGNVREVL 472
 QY 481 DQVERGRMPCCPEPSLHDMQCCKRKEBERPTEFYIQAFLIEDYF----- 528
 Db 473 DQVERGRMPCCPEPSLHDMQCCKRKEBERPTEFYIQAFLIEDYIIGILAMTPWBDKQ 532

RESULT 8

S20808

protein-tyrosine kinase (EC 2.7.1.112) src - Rous sarcoma virus
 C/Species: Rous sarcoma virus
 C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Oct-2004
 C/Accession: S20808; S32774
 R/Bodor, J.; Rozkot, F.; Svoboda, J.
 submitted to the EMBL Data Library, May 1990
 A/Description: Sequence organization of the adjacent chromosomal flanks the LTR.
 A/Reference number: S20808
 A/Accession: S20808
 A/Molecule type: DNA
 A/Residues: 1-526 <BD>
 A/Cross-references: UNIPROT:Q06057; UNIPARC:UPI00001068B2; EMBL:X52822; NID:G49656; PIDN
 R/Experimental source: Mesocricetus auratus (golden hamster) provirus
 C/Genetics:
 A/Gene: src
 C/Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
 C/Keywords: ATP; autophosphorylation; oncogene; phosphoprotein; phosphotransferase; tran
 F:148-245/Domain: SH2 homology <SH2>
 F:265-523/Domain: protein kinase homology <KIN>
 F:273-281/Region: protein kinase ATP-binding motif
 F:295/Active site: Lys #status predicted

F:116/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 86.7%; Score 2479; DB 2; Length 526;

Best Local Similarity 90.6%; Pred. No. 2.5e-117;

Matches 475; Conservative 13; Mismatches 28; Indels 8; Gaps 2;

```
Qy 1 MGSNKSXPQASQRRSLSESENVHAGAFAPASQTPSPKASADGHRGSAAPVPAAP 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MGSNKSXPQASQRRSLSEPDSTH--HGFPASQTPDETAADAHNRPSRSGTVATEP 58
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 61 KLFGEFNSDVTYSPORAGLAGVTTFFVALYDESEETETDLSFKKGERLQIVNNTRKVD 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 59 KLFMGFTSDVTYSPORAGLAGVTTFFVALYDESEETETDLSFKKGERLQIVNNTRKVD 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 121 VREGDWMLHSLSTGQGYI PSNYVAPSDSIQAEEMVFGKITRRESERLLNENPRGTG 180
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 115 --EGDWMLHSLSTGQGYI PSNYVAPSDSIQAEEMVFGKITRRESERLLNENPRGTG 172
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 181 LVRESSTTGAYCLSDPDNAKGLNVKHYKIRKLDGSGFYTSRQFNSLQQLVAYYSK 240
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 173 LVKSESTAKAYCLSDVDPNAGPNVKKIKCLYSGGFYTSRQFNSLQQLVAYYSK 232
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 241 HADGLCHRLTTCPTSPKPTQGLAKDAMEI PRESRLRLEVLGQCGFGEVMMGTNGTTRV 300
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 233 HADGLCHRLTTCPTSPKPTQGLAKDAMEI PRESRLRLEVLGQCGFGEVMMGTNGTTRV 292
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 301 AITLKPGMTSPBAFLQEAQVMKKLRHEKLVOLYAVSEEPYIVTEYNNKSGSLDPLKG 360
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 293 AITLKPGMTSPBAFLQEAQVMKKLRHEKLVOLYAVSEEPYIVTEYNNKSGSLDPLKG 352
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 361 ETGKYRLPOLVMSAQISGMAYVERMYVHRDLRAANILVGENLVCKVADGLARLIE 420
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 353 EMGKYRLPOLVMAAQISGMAYVERMYVHRDLRAANILVGENLVCKVADGLARLIE 412
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 421 DNEYTARQAKAPFIKMTAPEALYGRFTIKSDVWSFGILLTELTTKGRVYPGMVNRVYL 480
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 413 DNEYTARQAKAPFIKMTAPEALYGRFTIKSDVWSFGILLTELTTKGRVYPGMVNRVYL 472
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 481 DOVERGYRMPCEPCEPSLHDLMCQCKRKEPERPFEYLOAFL 524
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 473 DOVERGYRMPCEPCEPSLHDLMCQCKRKEPERPFEYLOAFL 516
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

RESULT 9

OKREYVR

protein-tyrosine kinase (EC 2.7.1.112) src - Rous sarcoma virus (strain H-19)
N/Alternate names: kinase-related transforming protein src
C/Species: Rous sarcoma virus

C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 05-Oct-2004
C/Accession: S09609

R/Bodor, J.; Poljak, E.; Pichrtova, J.; Geryk, J.; Svoboda, J.

Nucleic Acids Res. 17, 8869, 1989

A/Title: Complete nucleotide sequence of LTR, v-src, LTR provirus H-19.

A/Reference number: S09609; PMID:90067864; PMID:2587228

A/Accession: S09609

A/Status: translation not shown

A/Molecule type: DNA

A/Residues: 1-526 <BOD>

A/Cross-references: UNIPROT:P25020; UNIPARC:UPI0000135F2A; EMBL:X15345; NID:961706; PIDN

C/Genetics:

A/Genes: src

C/Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology

C/Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; onc

F:148-245/Domain: SH2 homology <SH2>

F:265-523/Domain: protein kinase homology <KIN>

F:273-281/Region: protein kinase ATP-binding motif

F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted

F:295/Active site: Lys #status predicted

F:116/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 86.5%; Score 2473; DB 1; Length 526;

Best Local Similarity 90.5%; Pred. No. 5e-117;

Matches 474; Conservative 13; Mismatches 29; Indels 8; Gaps 2;

```
Qy 1 MGSNKSXPQASQRRSLSESENVHAGAFAPASQTPSPKASADGHRGSAAPVPAAP 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MGSNKSXPQASQRRSLSEPDSTH--HGFPASQTPDETAADAHNRPSRSGTVATEP 58
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 61 KLFGEFNSDVTYSPORAGLAGVTTFFVALYDESEETETDLSFKKGERLQIVNNTRKVD 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 59 KLFMGFTSDVTYSPORAGLAGVTTFFVALYDESEETETDLSFKKGERLQIVNNTRKVD 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 121 VREGDWMLHSLSTGQGYI PSNYVAPSDSIQAEEMVFGKITRRESERLLNENPRGTG 180
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 115 --EGDWMLHSLSTGQGYI PSNYVAPSDSIQAEEMVFGKITRRESERLLNENPRGTG 172
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 181 LVRESSTTGAYCLSDPDNAKGLNVKHYKIRKLDGSGFYTSRQFNSLQQLVAYYSK 240
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 173 LVKSESTAKAYCLSDVDPNAGPNVKKIKCLYSGGFYTSRQFNSLQQLVAYYSK 232
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 241 HADGLCHRLTTCPTSPKPTQGLAKDAMEI PRESRLRLEVLGQCGFGEVMMGTNGTTRV 300
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 233 HADGLCHRLTTCPTSPKPTQGLAKDAMEI PRESRLRLEVLGQCGFGEVMMGTNGTTRV 292
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 301 AITLKPGMTSPBAFLQEAQVMKKLRHEKLVOLYAVSEEPYIVTEYNNKSGSLDPLKG 360
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 293 AITLKPGMTSPBAFLQEAQVMKKLRHEKLVOLYAVSEEPYIVTEYNNKSGSLDPLKG 352
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 361 ETGKYRLPOLVMSAQISGMAYVERMYVHRDLRAANILVGENLVCKVADGLARLIE 420
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 353 EMGKYRLPOLVMAAQISGMAYVERMYVHRDLRAANILVGENLVCKVADGLARLIE 412
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 421 DNEYTARQAKAPFIKMTAPEALYGRFTIKSDVWSFGILLTELTTKGRVYPGMVNRVYL 480
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 413 DNEYTARQAKAPFIKMTAPEALYGRFTIKSDVWSFGILLTELTTKGRVYPGMVNRVYL 472
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 481 DOVERGYRMPCEPCEPSLHDLMCQCKRKEPERPFEYLOAFL 524
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 473 DOVERGYRMPCEPCEPSLHDLMCQCKRKEPERPFEYLOAFL 516
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

RESULT 10

S15582

protein-tyrosine kinase (EC 2.7.1.112) src - Rous sarcoma virus (strain Prague A)

C/Species: Rous sarcoma virus

A/Variety: strain Prague A

C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 05-Oct-2004

C/Accession: S15582; S09665

R/Alu, Z.; Hackett, P.B.

Nucleic Acids Res. 17, 3986, 1989

A/Title: Sequence variation of the Rous sarcoma virus PTA src gene.

A/Reference number: S15582; PMID:89282411; PMID:2543959

A/Accession: S15582

A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-526 <LIU>

A/Cross-references: UNIPROT:Q64994; UNIPROT:Q92806; UNIPROT:Q60567; UNIPROT:Q07461; UNIP

A/Experimental source: strain Prague A

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1989

A/Note: only a list of differences from sequence S09665 is given; however, the list is in

R./Fincham, V.J.; Wyke, J.A.

J. Virol. 58, 694-699, 1986

A/Title: Localization of temperature-sensitive transformation mutations and back mutator

A/Reference number: S09665; PMID:86200422; PMID:3009882

A/Accession: S09665

A/Status: nucleic acid sequence not shown

A/Molecule type: DNA

A/Residues: 231-241, 'TH', '244-287', 'G', '289-463', 'P', '465-501', 'N', '503-526 <FIN>

A/Cross-references: UNIPARC:UPI00001755F1

C/Genetics:

A/Genes: src

C/Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology;

C/Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; onc

F:148-245/Domain: SH2 homology <SH2>

F/265-523/Domain: protein kinase homology <KIN>
F/273-281/Region: protein kinase ATP-binding motif
F/2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F/295/Active site: lys #status predicted
F/416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 86.3%; Score 2466; DB 2; Length 526;
Best Local Similarity 90.1%; Pred. No. 1,66-116;
Matches 473; Conservative 13; Mismatches 31; Indels 8; Gaps 2;

```
QY 1 MGSNKSFKPDASQRRRLSEENVHAGAFPPASQTSKPSADGHRGSAAPFPAAEP 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MGSNKSFKPDSPQRRLSEPDSTH--HGSPASQTDDETAAPDAHPNPSRSFGTVATEP 58
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 KLGGFNSSDTVMSPQAGALAGGVTFVALVYDESRETDLSFKGERLQIVNNTKVD 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 59 KLFWGFNTSDTVSPQAGALAGGVTFVALVYDESRETDLSFKGERLQIVNNTKVD 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 VREGDWMIAHSLSTGQGYIPSNVVA PSDSIQAEEMWFGKITRRESRLILNAENPGTF 180
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 115 --EGDWMIAHSLTTGQGYIPSNVVA PSDSIQAEEMWFGKITRRESRLILNAENPGTF 172
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 181 LVRESETTKAGYCLSVDFPNAGKLVNKHKKRLDSGFFYITSRTQFNSIQQLVAYYSK 240
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 173 LVKSEETTKAGYCLSVDFPNAGKLVNKHKKRYLYLGSGFYITSRTQFNSIQQLVAYYSK 232
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 241 HADGLCHRLTTVCPTSPQOTQGLAKDAMEIPRESRLIEVLGQCCFGEVMMGTNNTTV 300
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 233 HADGLCHRLANVCPTSPQOTQGLAKDAMEIPRESRLIEVLGQCCFGEVMMGTNNTTV 292
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 301 AIKTLKPGTMSPEAFLOEAQVMKKLRHEKLVQVAVVSEBPIYLVTEYNNKSLIDFLKG 360
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 293 AIKTLKPGTMSPEAFLOEAQVMKKLRHEKLVQVAVVSEBPIYLVTEYNNKSLIDFLKG 352
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 361 ETGKYTLRLPOLVMSAQIASGMAYVERMYVHRDLRAANILVGENLVCKVADFGIARLIE 420
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 353 EMGKYTLRLPOLVMAAQIASGMAYVERMYVHRDLRAANILVGENLVCKVADFGIARLIE 412
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 421 DNEYTARQAGKFPKWTAPAPALYGRFTIKSDWVSFEILLTELTKRVPVPGVNNREVL 480
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 413 DNEYTARQAGKFPKWTAPAPALYGRFTIKSDWVSFEILLTELTKRVPVPGVNNREVL 472
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 481 DVERGYRMPCPPECESLHDLMOQCWKRPESRPTEYLOAFL 524
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 473 DVERGYRMPCPPECESLHDLMOQCWKRPESRPTEYLOAFL 516
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

RESULT 11

TVFVR protein-tyrosine kinase (EC 2.7.1.112) src - Rous sarcoma virus (strain Prague C)

C/Species: Rous sarcoma virus
C/Date: 01-Sep-1981 #sequence_revision 17-Dec-1982 #text_change 05-Oct-2004
C/Accession: A00632

R/Schwarz, D.; Tizard, R.; Gilbert, W.

submitted to the Nucleic Acid Sequence Database, September 1982

A/Reference number: A00632
A/Accession: A00632

A/Molecule type: genomic RNA

A/Residues: 1-526 <SCH>

A/Cross-references: UNIPROT:P00526; UNIPROT:O92806; UNIPARC:UPI000002BA63

A/Note: as a result of base variations, residues 242 and 288 may be replaced by Thr and R/Weil, J.C.; Ghysdael, J.; Vogt, P.K.; Smart, J.E.

Nature 291, 675-677, 1981

A/Title: Homologous tyrosine phosphorylation sites in transformation-specific gene products

A/Reference number: A38019; MUID:81220979; PMID:6264320

A/Contents: annotation; phosphorylation site

C/Genetics: src
C/Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C/Keywords: ATP; autophosphorylation; blocked amino end; lipidprotein; myristylation; and
F/148-245/Domain: SH2 homology <SH2>
F/265-523/Domain: protein kinase homology <KIN>

F/273-281/Region: protein kinase ATP-binding motif
F/2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F/295/Active site: lys #status predicted
F/416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 86.1%; Score 2463; DB 1; Length 526;
Best Local Similarity 90.1%; Pred. No. 1,66-116;
Matches 472; Conservative 13; Mismatches 31; Indels 8; Gaps 2;

```
QY 1 MGSNKSFKPDASQRRRLSEENVHAGAFPPASQTSKPSADGHRGSAAPFPAAEP 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MGSNKSFKPDSPQRRLSEPDSTH--HGSPASQTDDETAAPDAHPNPSRSFGTVATEP 58
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 KLGGFNSSDTVMSPQAGALAGGVTFVALVYDESRETDLSFKGERLQIVNNTKVD 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 59 KLFWGFNTSDTVSPQAGALAGGVTFVALVYDESRETDLSFKGERLQIVNNTKVD 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 VREGDWMIAHSLSTGQGYIPSNVVA PSDSIQAEEMWFGKITRRESRLILNAENPGTF 180
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 115 --EGDWMIAHSLTTGQGYIPSNVVA PSDSIQAEEMWFGKITRRESRLILNAENPGTF 172
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 181 LVRESETTKAGYCLSVDFPNAGKLVNKHKKRLDSGFFYITSRTQFNSIQQLVAYYSK 240
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 173 LVKSEETTKAGYCLSVDFPNAGKLVNKHKKRYLYLGSGFYITSRTQFNSIQQLVAYYSK 232
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 241 HADGLCHRLTTVCPTSPQOTQGLAKDAMEIPRESRLIEVLGQCCFGEVMMGTNNTTV 300
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 233 HADGLCHRLANVCPTSPQOTQGLAKDAMEIPRESRLIEVLGQCCFGEVMMGTNNTTV 292
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 301 AIKTLKPGTMSPEAFLOEAQVMKKLRHEKLVQVAVVSEBPIYLVTEYNNKSLIDFLKG 360
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 293 AIKTLKPGTMSPEAFLOEAQVMKKLRHEKLVQVAVVSEBPIYLVTEYNNKSLIDFLKG 352
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 361 ETGKYTLRLPOLVMSAQIASGMAYVERMYVHRDLRAANILVGENLVCKVADFGIARLIE 420
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 353 EMGKYTLRLPOLVMAAQIASGMAYVERMYVHRDLRAANILVGENLVCKVADFGIARLIE 412
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 421 DNEYTARQAGKFPKWTAPAPALYGRFTIKSDWVSFEILLTELTKRVPVPGVNNREVL 480
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 413 DNEYTARQAGKFPKWTAPAPALYGRFTIKSDWVSFEILLTELTKRVPVPGVNNREVL 472
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 481 DVERGYRMPCPPECESLHDLMOQCWKRPESRPTEYLOAFL 524
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 473 DVERGYRMPCPPECESLHDLMOQCWKRPESRPTEYLOAFL 516
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

RESULT 12

S26420 protein-tyrosine kinase (EC 2.7.1.112) src - Rous sarcoma virus

C/Species: Rous sarcoma virus
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Oct-2004
C/Accession: S26420; S20676

R/Kashuba, V.I.; Rynditch, A.V.; Dostalova, V.; Hlozaneck, I.; Zubak, S.V.; Kavanan, V.M.

submitted to the EMBL Data Library, September 1992

A/Description: Molecular cloning and DNA sequence analysis of duck-adapted variant of Rous

A/Reference number: S26417
A/Accession: S26420

A/Molecule type: preliminary

A/Residues: 1-526 <KAS>

A/Cross-references: UNIPROT:Q07461; UNIPARC:UPI000010512B; EMBL:X68524; NID:961903; PIDN

submitted to the EMBL Data Library, March 1990

A/Reference number: S20676
A/Accession: S20676

A/Molecule type: DNA

A/Residues: 1-526 <KAS>
A/Cross-references: UNIPARC:UPI000010512B; EMBL:X51861; NID:961896; PIDN:CAA36154.1; PID
C/Genetics: src
C/Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C/Keywords: ATP; autophosphorylation; blocked amino end; lipidprotein; myristylation; phos

A:Residues: 1-532 <STE>
A:Cross-references: UNIPROT:Q91851; UNIPARC:UPI0000172581; GB:M24704; GB:J04822; NID:g21
R:Steele, R.E.; Choen, R.; Rai, B.B.A.; Winokur, S.T.; Unger, T.P.
Oncogene 7, 2345-2350, 1992
A>Title: Structural organization of a src gene from xenopus laevis.
A:Reference number: 151564; MUID:93064714; PMID:1437158
A:Accession: 151564
A:Status: translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-113 <ST2>
A:Cross-references: UNIPARC:UPI00000PD97A; GB:M33646; NID:G214808; PIDN:AAA49963.1; PID:
C:Genetics:
A:Insertions: 80/1
C:Superfamily: protein kinase homology; SH2 homology; SH3 homology
C:Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
F:87-136/Domain: SH3 homology <SH3>
F:147-244/Domain: SH2 homology <SH2>
F:264-522/Domain: protein kinase homology <KIN>
F:272-280/Region: protein kinase ATP-binding motif
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:294/Active site: Lys #status predicted
F:415,526/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 85.44; Score 2442.5; DB 1; Length 532;
Best Local Similarity 85.54; Pred. No. 1,7e-115;
Matches 467; Conservative 27; Mismatches 33; Indels 19; Gaps 4;

QY 1 MGSNKSXPXASQRRRLSEPSENVHAGAPFAPSQTSPKASDGHGSPSAF-----VP 55
DB 1 MGATSKPRGGRPRSLDIVEGSHQPFSTLSASQTENK--SLDSHRPAPQPFQGCNDLT 58
QY 56 PAAPKPLFGFNSDVTYTSPOKAGALAGVTFVALYDYSRTETDLSFKKGERLQIVNN 115
DB 59 P-----FGINSDITTSPOKGTPLAGVTFVALYDYSRTETDLSFKKGERLQIVNN 112
QY 116 TRKVDVREGDWMVLAHSLSTGQTGYIPSNVAPSDSIQAEWYFGKITRRSERLLAEN 175
DB 113 T-----EGDMLKRLSSSGQTGYIPSNVAPSDSIQAEWYFGKITRRSERLLLLEN 166
QY 176 PRGTFVRESSETTKGAYCLSVSPFNAGKLVNKHVKIRKLDSDGGFYITSRTOFNSLOLV 235
DB 167 PRGTFVRESSETTKGAYCLSVSPFNAGKLVNKHVKIRKLDSDGGFYITSRTOFNSLOLV 226
QY 236 AYSKADGICHRLLTYCPTSKPOTQGLADAMEIPRESLRLEVKLQGGCGEYVMGTNN 295
DB 227 AYSKADGICHRLLTYCPTSKPOTQGLADAMEIPRESLRLEVKLQGGCGEYVMGTNN 286
QY 296 GTTRVAILKTLKPGTMSPEAFLOEAQVMKKLRHEKLVQLYAVVSEEPYIYITEVMKGSLL 355
DB 287 GTTRVAILKTLKPGTMSPEAFLOEAQVMKKLRHEKLVQLYAVVSEEPYIYITEVMKGSLL 346
QY 356 DFLKGETGKYLRLPOLVDMASQIASGMAVVERMNVYVRDLRAANIIVGENLVCKVADFG 415
DB 347 DFLKGETGKYLRLPOLVDMASQIASGMAVVERMNVYVRDLRAANIIVGENLVCKVADFG 406
QY 416 ARLIDNEYTARQAKFPITWTAPEALYGRFTIKSDVMSFGIILLTELTKGRVPYGMV 475
DB 407 ARLIDNEYTARQAKFPITWTAPEALYGRFTIKSDVMSFGIILLTELTKGRVPYGMV 466
QY 476 NREVLDOVERGYMPCPECPESLHDLMOQCKRKEPERPTFEYLAFLDYFTSTPEY 535
DB 467 NREVLDOVERGYMPCPECPESLHDLMOQCKRKEPERPTFEYLAFLDYFTSTPEY 526
QY 536 QPGENTL 541
DB 527 QPGDNL 532

RESULT 15
S52313
protein-tyrosine kinase (EC 2.7.1.112) src - Rous sarcoma virus
C:Species: Rous sarcoma virus
C:Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 05-Oct-2004

C:Accession: S52313
R:Tyosyan, A.; Yatsula, B.; Shlurman, M.; Molnova, E.; Kaverina, I.; Musackina, E.; Leeb,
submitted to the EMBL Data Library, January 1995
A:Description: Two new isoforms of v-src oncogene isolated from low and high metastatic f
A:Reference number: S52313
A:Accession: S52313
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-545 <RT>
A:Cross-references: UNIPROT:Q86362; UNIPARC:UPI0000105D06; EMBL:X84074; NID:9663083; PIDN:
C:Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology,
C:Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; phos
F:108-157/Domain: SH3 homology <SH3>
F:168-265/Domain: SH2 homology <SH2>
F:285-543/Domain: protein kinase homology <KIN>
F:293-301/Region: protein kinase ATP-binding motif
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:315/Active site: Lys #status predicted
F:436/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 85.04; Score 2431; DB 2; Length 545;
Best Local Similarity 86.84; Pred. No. 6.6e-115;
Matches 472; Conservative 15; Mismatches 29; Indels 28; Gaps 4;

QY 1 MGSNKSXPXASQRRRLSEPSENVHAGAPFAPSQTSPK-----PAS----- 42
DB 1 MGSNKSXPXASQRRRLSEPSENVHAGAPFAPSQTSPK-----PAS----- 58
QY 43 --ADGHRPSAFAFPAPAPKPLFGFNSDVTYTSPOKAGALAGVTFVALYDYSRTET 100
DB 59 AAPTDRHTPRSRSGTYANERKPLFGDPFTSDVTYTSPOKAGALAGVTFVALYDYSRTET 118
QY 101 DLSFKGERLQIVNNTRKVDVREGDWMVLAHSLSTGQTGYIPSNVAPSDSIQAEWYFGK 160
DB 119 DLSFKGERLQIVNNTRKVDVREGDWMVLAHSLSTGQTGYIPSNVAPSDSIQAEWYFGK 172
QY 161 ITRRESRLLNENPRGTFVRESSETTKGAYCLSVSPFNAGKLVNKHVKIRKLDSDGGF 220
DB 173 ITRRESRLLNENPRGTFVRESSETTKGAYCLSVSPFNAGKLVNKHVKIRKLDSDGGF 232
QY 221 YITSRTQFNSLOLVVAYSHADGICHRLLTYCPTSKPOTQGLADAMEIPRESLRLEVK 280
DB 233 YITSRTQFNSLOLVVAYSHADGICHRLLTYCPTSKPOTQGLADAMEIPRESLRLEVK 292
QY 281 LGGCGFGEYVMGTWNGTTRVAILKTLKPGTMSPEAFLOEAQVMKKLRHEKLVQLYAVVSE 340
DB 293 LGGCGFGEYVMGTWNGTTRVAILKTLKPGTMSPEAFLOEAQVMKKLRHEKLVQLYAVVSE 352
QY 341 PIYIVTEVMKGSLLDPLKGETGKYLRLPOLVDMASQIASGMAVVERMNVYVRDLRAANI 400
DB 353 PIYIVTEVMKGSLLDPLKGETGKYLRLPOLVDMASQIASGMAVVERMNVYVRDLRAANI 412
QY 401 LVGENLVCKVADFGIARLIDNEYTARQAKFPITWTAPEALYGRFTIKSDVMSFGIILL 460
DB 413 LVGENLVCKVADFGIARLIDNEYTARQAKFPITWTAPEALYGRFTIKSDVMSFGIILL 472
QY 461 TELTKGRVPYPMGNVREVLDOVERGYMPCPECPESLHDLMOQCKRKEPERPTFEYL 520
DB 473 TELTKGRVPYPMGNVREVLDOVERGYMPCPECPESLHDLMOQCKRKEPERPTFEYL 532
QY 521 QAFU 524
DB 533 QAFU 536

Search completed: June 5, 2006, 17:16:39
Job time : 23.7202 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 5, 2006, 17:01:48 ; Search time 155.049 Seconds
(without alignments) 3227.587 Million cell updates/sec

Title: US-10-691-079-3

Perfect score: 2859

Sequence: 1 MGSNKSXPKXASQRRSLRP.....AFLEDYFTSTPEYQVPENL 541

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2854	99.8	540	1 SRC_MOUSE	P05480 mus musculus
2	2854	99.8	541	2 Q2M414_MOUSE	Q2M414 mus musculus
3	2837.5	99.2	542	2 Q9J310_RAT	Q9J310 rattus norv
4	2830.5	98.7	542	2 Q76P87_HUMAN	Q76P87 homo sapien
5	2812	98.4	535	2 Q80XU2_MOUSE	Q80XU2 mus musculus
6	2795	97.8	535	2 Q3UXD6_MOUSE	Q3UXD6 mus musculus
7	2773.5	97.0	535	1 SRC_HUMAN	P12931 homo sapien
8	2772.5	97.0	535	1 SRC_RAT	Q9WU99 rattus norv
9	2707.5	94.7	523	2 Q45QJ2_RAT	Q45QJ2 rattus norv
10	2643	92.4	532	1 SRC_CHICK	P00523 gallus gall
11	2598	90.9	586	1 SRC_AVIS2	P15054 avian sarco
12	2591	90.6	567	1 SRC_AVIS	P14084 avian sarco
13	2590	90.6	587	2 Q64817_GRETR	Q64817 avian sarco
14	2576	90.1	536	1 SRC_AVIS1	P14085 avian sarco
15	2510	87.8	525	1 SRC_AVISR	P00525 avian sarco
16	2510	87.8	525	1 SRC_RSUSA	P00524 avian sarco
17	2479	86.7	526	2 Q60567_GRETR	Q60567 rous sarcom
18	2468	86.3	525	1 SRC_RSUSA	P25020 rous sarcom
19	2468	86.3	537	2 Q7ZX73_XENLA	Q7ZX73 xenopus lae
20	2467	86.3	526	2 Q64994_GRETR	Q64994 rous sarcom
21	2465.5	86.2	526	2 Q5MA59_XENTR	Q5MA59 xenopus tro
22	2465	86.2	526	2 Q93080_GRETR	Q93080 rous sarcom
23	2463.5	86.2	523	2 Q85477_GRETR	Q85477 rous sarcom
24	2463.5	86.2	535	2 Q92957_RSUSA	Q92957 rous sarcom
25	2463	86.1	526	2 Q92806_GRETR	Q92806 rous sarcom
26	2462	86.1	525	1 SRC_RSUSA	P63185 rous sarcom
27	2458	86.0	525	1 SRC_RSVP	P00526 rous sarcom
28	2452	85.8	526	2 Q64993_RSUSA	Q64993 rous sarcom
29	2448	85.6	526	2 Q07461_GRETR	Q07461 rous sarcom
30	2443.5	85.5	532	2 Q2TAR1_XENLA	Q2TAR1 xenopus lae
31	2439.5	85.3	531	1 SRC2_XENLA	P13116 xenopus lae

ALIGNMENTS

```

RESULT 1
SRC_MOUSE STANDARD; PRT; 540 AA.
ID SRC_MOUSE
AC P05480;
DT 01-NOV-1988, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1995, sequence version 2.
DT 07-MAR-2006, entry version 65.
DE Neuronal proto-oncogene tyrosine-protein kinase Src (BC 2.7.1.112)
DE (p60-Src) (c-Src) (pp60c-src).
GN Name=Src;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [MENA].
RC STRAIN=BALB/c;
RX MEDLINE=87263406; PubMed=2440106;
RA Martinez R., Mathey-Prevot B., Bernards A., Baltimore D.;
RT "Neuronal pp60c-src contains a six-amino acid insertion relative to
RT its non-neuronal counterpart.";
RL Science 237:411-415(1987).
[2]
RP INTERACTION WITH DDEF1/ASAP1.
RX MEDLINE=99038209; PubMed=9819391;
RA Brown M.T., Andrade J., Radhakrishna H., Donaldson J.G., Cooper J.A.,
RA Randazzo P.A.;
RT "ASAP1, a phospholipid-dependent arf GTPase-activating protein that
RT associates with and is phosphorylated by Src.";
RL Mol. Cell. Biol. 18:7038-7051(1998).
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC tyrosine phosphate.
CC -1- INTERACTION: Interacts with DDEF1/ASAP1 via its SH3 domain.
CC -1- SUBUNIT: Interacts with DDEF1/ASAP1 via its SH3 domain.
CC P07141:Ce11; NDEXP-2; IntAct=EBI-296680; EBI-777188;
CC -1- PTM: Phosphorylated on Tyr-534 by c-Src kinase (CSK). The
CC phosphorylated form is termed pp60c-src. The phosphorylated tail
CC interacts with the SH2 domain thereby repressing kinase activity
CC (by similarity).
CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
CC subfamily.
CC -1- SIMILARITY: Contains 1 SH2 domain.
CC -1- SIMILARITY: Contains 1 SH3 domain.
-----
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EMBL: M17031; AAA40135.1; -; mRNA.
DR PIR; A43610; A43610.
DR HSSP; P12931; 1A09.
DR SMR; P05480; 85-540.
DR IntAct; P05480; -.
DR Ensembl; ENSMUSG00000027646; Mus musculus.

```

FT	MGI; MG1;98397; Src.
DR	GGO; GGO:0005515; F:protein binding; IPI.
DR	GGI; GGO:00044713; F:protein-tyrosine kinase activity; IMP.
DR	GGI; GGO:00064468; F:protein amino acid phosphorylation; IDA.
DR	InterPro; IPRO00719; Prot_kinase.
DR	InterPro; IPRO02290; Ser_thr_pkinase.
DR	InterPro; IPRO00980; SH2.
DR	InterPro; IPRO01452; SH3.
DR	InterPro; IPRO01245; Tyr_pkinase.
DR	InterPro; IPRO08266; Tyr_pkinase_AS.
DR	Pfam; PF07714; Kinase_Tyr_1.
DR	Pfam; PF00017; SH2_1.
DR	Pfam; PF00018; SH3_1; 1.
DR	PRINTS; PR00401; SH2DOMAIN.
DR	PRINTS; PR00452; SH3DOMAIN.
DR	PRINTS; PR00109; TYRKINASE.
DR	ProDom; PD000001; Prot_kinase; 1.
DR	ProDom; PD000093; SH2; 1.
DR	ProDom; PD000066; SH3; 1.
DR	SMART; SMO0252; SH2; 1.
DR	SMART; SMO0326; SH3; 1.
DR	SMART; SMO0219; TyrcKc; 1.
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR	PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR	PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR	PROSITE; PS50001; SH2; 1.
DR	PROSITE; PS50002; SH3; 1.
KW	ATP-binding; Kinase; Lipoprotein; Myristate; Nucleotide-Binding;
KW	Phosphorylation; Proto-oncogene; SH2 domain; SH3 domain; Transferase;
KM	Tyrosine-protein kinase.
FT	INIT_MET 0 0
FT	CHAIN 1 540
FT	
FT	
FT	
FT	DOMAIN 82 149
FT	DOMAIN 155 252
FT	DOMAIN 274 527
FT	NP_BIND 280 288
FT	ACT_SITE 393 393
FT	BINDING 302 302
FT	MOD_RES 423 423
FT	
FT	
FT	MOD_RES 534 534
FT	LIPID 1 1
QO	SEQUENCE 540 AA; 60487 MW; 42BA0EEB5D752AA CRC64; N-myristoyl glycine (By similarity). N-myristoyl glycine (By similarity).

Query Match	99.8%	Score 2854	DB 1	Length 540
Best Local Similarity	100.0%	Pred. NO. 2.5e-180		
Matches 540	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	2	GSNKSKEPDASQRRRSLEPSENVHAGAGAFPASQTPSKPASADGHRGSAAFVPPAAEPK	61	
Db	1	GSNKSKEPDASQRRRSLEPSENVHAGAGAFPASQTPSKPASADGHRGSAAFVPPAAEPK	60	
QY	62	LFQGFNSSDTYSQQRAGALAGVTFPALYDYBSRTETDLSFKKGERLQIVNTRKQDV	121	
Db	61	LFQGFNSSDTYSQQRAGALAGVTFPALYDYBSRTETDLSFKKGERLQIVNTRKQDV	120	
QY	122	REGGMWLAHLSSTQOTGYIPSNVYAPSPSIQAEEMYFEKTRIRRESERLILNAENRGTEL	181	
Db	121	REGGMWLAHLSSTQOTGYIPSNVYAPSPSIQAEEMYFEKTRIRRESERLILNAENRGTEL	180	
QY	182	VRESEETTKGACLSVSPDFDNAGKLVNKKYKTRKLDGSGFYTTSRQFNSLQOLVAYYSKH	241	
Db	181	VRESEETTKGACLSVSPDFDNAGKLVNKKYKTRKLDGSGFYTTSRQFNSLQOLVAYYSKH	240	
QY	242	ADGLCHRLTVVCPYTSKQPTQGLADAMEIIPRESLRLEVLQGGCGEYVMGTWNGTTTVA	301	
Db	241	ADGLCHRLTVVCPYTSKQPTQGLADAMEIIPRESLRLEVLQGGCGEYVMGTWNGTTTVA	300	
QY	302	IKTLKPTMSEAPALQEAQVWKKLRHEKLVOLYAVVSEPIYIYEVNKKSLDLDFLGE	361	
Db	301	IKTLKPTMSEAPALQEAQVWKKLRHEKLVOLYAVVSEPIYIYEVNKKSLDLDFLGE	360	

Qy	362	GGKLRLEPOLVDMSQIASGMAVYERNNYVHRDLDAANNLVGENLVCKVADGGLARLIED	421
Db	361	TGKLRLEPOLVDMSQIASGMAVYERNNYVHRDLDAANNLVGENLVCKVADGGLARLIED	420
Qy	422	NEYTAROGAKFPFKMTAPEALVYGRFTTKSDVMSFGILLTETLTJTKGRVVPYPGMVRNEVL	481
Db	421	NEYTAROGAKFPFKMTAPEALVYGRFTTKSDVMSFGILLTETLTJTKGRVVPYPGMVRNEVL	480
Qy	482	QVERGYRNPCEPCECESLHDLMCQWRKEPERPFTEYLQALVEDYFTSTPEQYOGENVL	541
Db	481	QVERGYRNPCEPCECESLHDLMCQWRKEPERPFTEYLQALVEDYFTSTPEQYOGENVL	540

ID	Q2M414_MOUSE	PRELIMINARY;	PRT;	541 AA.
AC	Q2M414;			
DT	21-FEB-2006,	integrated into UniProtKB/TrEMBL.		
DT	21-FEB-2006,	sequence version 1.		
DT	21-FEB-2006,	entry version 1.		
DE	Src.			
GN	Name=Src;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;			
OC	Muroidea; Muridae; Murinae; Mus.			
OX	NCBI_TaxId=10090;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	STRAIN=CAST/Eij; TISSUE=Brain;			
RA	Farber C.R., Corva P.M., Medrano J.F.;			
RT	"Characterization of quantitative trait loci influencing growth and			
RT	adiposity using congenic mouse strains."			
RL	Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.			
CC	-----			
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms			
CC	Distributed under the Creative Commons Attribution License			
CC	-----			
DR	EMBL; AY902331; AAX0616.1; -; Genomic DNA.			
DR	SEQUENCE 541 AA; 60645 MW; 0534AF027783BCF CRC64;			

Query Match	Similarity	Score	DB 2	Length	541;
Best Local	99.8%	Pred. No.2.5e-180;			
Matches	540;	Conservative	0;	Mismatches	1;
				Indels	0;
				Gaps	0
QY	1	MGSNKSKPKDASQRRRLSPSENVHGAGAPASQTPSPKSPASADGHRGPSAAFPVPAAP	60		
Db	1	MGSNKSKPKDASQRRRLSPSENVHGAGAPASQTPSPKSPASADGHRGPSAAFPVPAAP	60		
QY	61	KLREGFNSSDVTYSPQAPGALAGVTTTVALYDYSKRETTDLSFKKGEPLQIVNNTRKD	120		
Db	61	KLREGFNSSDVTYSPQAPGALAGVTTTVALYDYSKRETTDLSFKKGEPLQIVNNTRKD	120		
QY	121	VREEDMWLAHSLSGQGTGYIPSNVYAPSDSIQAEEMYFGKITRRESERLLNAENPRGTF	180		
Db	121	VREEDMWLAHSLSGQGTGYIPSNVYAPSDSIQAEEMYFGKITRRESERLLNAENPRGTF	180		
QY	181	LVRESETTKGAYCLSVSDFDNAGKLVNKHYYIKIRKIDSGGFYITSTFQNSLOOLVAYYSK	240		
Db	181	LVRESETTKGAYCLSVSDFDNAGKLVNKHYYIKIRKIDSGGFYITSTFQNSLOOLVAYYSK	240		
QY	241	HADGCHRLTVCPCTSPKPTQGLAKDAWEIPRESRLRVKDGQGFGEVMGTNGTTFV	300		
Db	241	HADGCHRLTVCPCTSPKPTQGLAKDAWEIPRESRLRVKDGQGFGEVMGTNGTTFV	300		
QY	301	AIKTLKPGTMSPEAFLOEAQVMKCLRHEKLVOLVAVVSEEPYIYITEYNNKSLDPLFG	360		
Db	301	AIKTLKPGTMSPEAFLOEAQVMKCLRHEKLVOLVAVVSEEPYIYITEYNNKSLDPLFG	360		
QY	361	ETGKTLRLPOLVDMSAQISGMAVYERNNYVHRDLRAANILVGENLVCKVADFGRLARLE	420		
Db	361	ETGKTLRLPOLVDMSAQISGMAVYERNNYVHRDLRAANILVGENLVCKVADFGRLARLE	420		

QY 421 DNEYTAROGAKPPIKWTAPPAALYGRFTIKSDVMSFGILLTETTTKGRVVPYGVNREV 480
DB 421 DNEYTAROGAKPPIKWTAPPAALYGRFTIKSDVMSFGILLTETTTKGRVVPYGVNREV 480
QY 481 DQVERGRMRCPPECESLHDLMCQCRKEPERPTEYLQAFLEDFSTTEPOYQGEN 540
DB 481 DQVERGRMRCPPECESLHDLMCQCRKEPERPTEYLQAFLEDFSTTEPOYQGEN 540
QY 541 L 541
DB 541 L 541
RESULT 3
Q9J10_RAT PRELIMINARY; PRT; 542 AA.
AC Q9J10; integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DT 01-OCT-2000, entry version 1.
DE Neuronal C-SRC tyrosine-specific protein kinase.
GN Name=Src;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21148003; PubMed=1124956; DOI=10.1016/S0028-3908(00)00185-4;
RA Linden A., Storevik M., Lakso M., Haapasaalo A., Lee D., Winklin J.M.,
RA Sei Y., Castren E., Wong G.
RT "Increased expression of neuronal Src and tyrosine phosphorylation of
RT NMDA receptors in rat brain after systemic treatment with MK-801." ,
RL Neuropharmacology 40:469-481(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Linden A.-M., Storevik M., Lakso M., Wong G., Castren E.,
RA Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL; AF157016; AAF80335.1; -; mRNA.
CC HSSP; P12931; 1043.
CC SRK; Q9J10; 87-542.
CC Ensembl; ENSRNOG0000009495; Rattus norvegicus.
DR RCD; 620795; Src.
DR GO; GO:0016301; F:kinase activity; TAS.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IDA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_Chr_kinase.
DR InterPro; IPR009880; SH2.
DR InterPro; IPR001452; SH3.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR Pfam; PF00714; PK2ase_Tyr; 1.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH3; 1.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRINTS; PR00452; SH2DOMAIN.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR ProDom; PD000093; SH2; 1.
DR ProDom; PD000065; SH3; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 1.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS50001; SH2; 1.

DR PROSITE; PS50002; SH3; 1.
KM Kinase.
SQ SEQUENCE 542 AA; 60727 MM; 6AC21D6DD66B039 CRC64;
Query Match 99.2%; Score 2837.5; DB 2; Length 542;
Best Local Similarity 99.3%; Pred. No. 3.1e-179;
Matches 538; Conservative 2; Mismatches 1; Indels 1; Gaps 1;
QY 1 MGSNKSXPKASQRRRLSEFSENVHAGAGAPASQTSKSPASAGCHGPSAAFP-PAE 59
DB 1 MGSNKSXPKASQRRRLSEFSENVHAGAGAPASQTSKSPASAGCHGPSAAFP-PAE 60
QY PKLFGFNSSDPTVTSPPRAGLAGVTFVALDYESTETDLSFFKGGRLQIVNTRKV 119
DB PKLFGFNSSDPTVTSPPRAGLAGVTFVALDYESTETDLSFFKGGRLQIVNTRKV 120
QY 120 DVREGDWMLAHSLSGTQGYI PSNYVAPSDSIQAEWYFGKITRSESRLLINENPRT 179
DB 121 DVREGDWMLAHSLSGTQGYI PSNYVAPSDSIQAEWYFGKITRSESRLLINENPRT 180
QY 180 FLVRESSTTGAYCLSYSDPDNAKGLAVKIKIRKLDSCGFYITSRQFNSLQQLVAYYS 239
DB 181 FLVRESSTTGAYCLSYSDPDNAKGLAVKIKIRKLDSCGFYITSRQFNSLQQLVAYYS 240
QY 240 KHADELCHRLTTVCPTSKPOTQGLAKDAWEIPRESLBLEVLGGCGEVMGTWGTTR 299
DB 241 KHADELCHRLTTVCPTSKPOTQGLAKDAWEIPRESLBLEVLGGCGEVMGTWGTTR 300
QY 300 VAIKTLKPGTMSPEAFLOEAVMCKLRHEKLVQLYAVVSEPIYIVTEYNKGSLLDFLK 359
DB 301 VAIKTLKPGTMSPEAFLOEAVMCKLRHEKLVQLYAVVSEPIYIVTEYNKGSLLDFLK 360
QY 360 GETGKYLRPLQYVMSAQISGMAVERMNVHDLPAANTLVGBNLVCKADGLARLI 419
DB 361 GETGKYLRPLQYVMSAQISGMAVERMNVHDLPAANTLVGBNLVCKADGLARLI 420
QY 420 EDNEYTAROGAKPPIKWTAPPAALYGRFTIKSDVMSFGILLTETTTKGRVVPYGVNREV 479
DB 421 EDNEYTAROGAKPPIKWTAPPAALYGRFTIKSDVMSFGILLTETTTKGRVVPYGVNREV 480
QY 480 LDQVERGRMRCPPECESLHDLMCQCRKEPERPTEYLQAFLEDFSTTEPOYQGE 539
DB 481 LDQVERGRMRCPPECESLHDLMCQCRKEPERPTEYLQAFLEDFSTTEPOYQGE 540
QY 540 NL 541
DB 541 NL 542
RESULT 4
Q76P87_HUMAN PRELIMINARY; PRT; 542 AA.
ID Q76P87; integrated into UniProtKB/TrEMBL.
AC Q76P87;
DT 05-JUL-2004, sequence version 1.
DT 05-JUL-2004, entry version 12.
DE OTHUMP00000030931.
GN Name=SRC; ORFNames=RP5-823N20.1-006;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Wallis J.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
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CC Distributed under the Creative Commons Attribution-NonDerivs License
CC EMBL; AL133293; CAC10573.1; -; genomic_DNA.
DR HSSP; P12931; 1A09.

DR SMR; Q76P87; 87-542.
 DR Ensembl; ENSG00000197122; Homo sapiens.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_Thr_kinase.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR008266; Tyr_kinase_AS.
 DR Pfam; PF00017; Pkinase_Tyr; 1.
 DR Pfam; PF00018; SH2; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR ProDom; PD000093; SH2; 1.
 DR ProDom; PD000066; SH3; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00219; Tyrc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 DR SQUENCE 542 AA; 60589 MW; C12D30FBDC5FF6B CRC64;

Query Match 98.7%; Score 2820.5; DB 2; Length 542;
 Best Local Similarity 98.7%; Pred. No. 4.1e-178;

Matches 535; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 1 MGSNKSFPKQASQRRSLSPSENVHGA-GGAFPASQTPSPKPSADGHRGSAAFVPPAAE 59
 DB 1 MGSNKSFPKQASQRRSLSPSENVHGA-GGAFPASQTPSPKPSADGHRGSAAFVPPAAE 60
 QY 60 PKLFGGNSDVTYSPRAALAGVTTVALDYESTRTDLSFKKGERLQIVNTRKY 119
 DB 61 PKLFGGNSDVTYSPRAALAGVTTVALDYESTRTDLSFKKGERLQIVNTRKY 120
 QY 120 DVAEGDWMLAHSSTGQTGYIPSNVYAPSDISQAEEYFPKTRRESERLLLAENRGT 179
 DB 121 DVAEGDWMLAHSSTGQTGYIPSNVYAPSDISQAEEYFPKTRRESERLLLAENRGT 180
 QY 180 FLVRESSTTGAYCLSVSDPDNAKGLNVKHKIRKLDGSGFYITSRTOFNSLQOLVAYYS 239
 DB 181 FLVRESSTTGAYCLSVSDPDNAKGLNVKHKIRKLDGSGFYITSRTOFNSLQOLVAYYS 240
 QY 240 KAADGLCHRLTYTCPSKPTQGLADAWMEIPRESLRLVYKLGQGGCEGVWMTGCTTR 239
 DB 241 KAADGLCHRLTYTCPSKPTQGLADAWMEIPRESLRLVYKLGQGGCEGVWMTGCTTR 300
 QY 300 VALKTLKPGMSDEAFLOEAOVWKGLRHEKLVOLYAVVSEPTIYIVENWKKSLDLDFLK 359
 DB 301 VALKTLKPGMSDEAFLOEAOVWKGLRHEKLVOLYAVVSEPTIYIVENWKKSLDLDFLK 360
 QY 360 GETGKTLRLPOLVDMSQIASGMAVYERNVYHRDLAANILVGENLVCKVADFGIARLI 419
 DB 361 GETGKTLRLPOLVDMSQIASGMAVYERNVYHRDLAANILVGENLVCKVADFGIARLI 420
 QY 420 EDNEYTARQCAKPIPKTAPBAALYGRFTIKSDVMSGILLTBLTTKGRVPIYGMVNRV 479
 DB 421 EDNEYTARQCAKPIPKTAPBAALYGRFTIKSDVMSGILLTBLTTKGRVPIYGMVNRV 480
 QY 480 LDQVERGYRMPCEPCESLHDLCCQWRKEPERPFEYLQALFLEYFTSTEPQVQGE 539
 DB 481 LDQVERGYRMPCEPCESLHDLCCQWRKEPERPFEYLQALFLEYFTSTEPQVQGE 540
 QY 540 NL 541
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DB 541 NL 542
 RESULT 5
 ID Q80XU2_MOUSE PRELIMINARY; PRT; 535 AA.
 AC Q80XU2;
 DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
 DT 01-JUN-2003, sequence version 1.
 DT 07-FEB-2006, entry version 18.
 DE Rous sarcoma oncogene, isoform 2.
 OS Name=Src;
 GN Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N; TISSUE=salivary gland;
 RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richard S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Blakeley R.A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Skalska D.E.,
 RA Schenker A., Schein J.E., Jones S.J.M., Maira M.A.;
 RT "generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N; TISSUE=salivary gland;
 RG NIH MGC Project;
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
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 CC
 CC EMBL; BC039953; AAH39953.1; -; mRNA.
 DR HSSP; P12931; 1043.
 DR SMR; Q80XU2; 86-535.
 DR Ensembl; ENSMUSG00000027646; Mus musculus.
 DR MGI; MGI:98397; Src.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR GO; GO:0004714; F:protein serine/threonine kinase activity; RCA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IMP.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IDA.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_Thr_kinase.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR008266; Tyr_kinase_AS.
 DR Pfam; PF00017; Pkinase_Tyr; 1.
 DR Pfam; PF00018; SH2; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR ProDom; PD000093; SH2; 1.

RA Nagashima T., Nimata K., Okido T., Pavan W.J., Petree G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Kamachandani M.,
RA Ravasi T., Reed J.C., Reed U.J., Reid Y., Ring B.Z., Ringwald M.,
RA Sadelain A., Schneider C., Sempke C.A., Setou M., Shmada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita K.,
RA Vercario R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wysshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavalon M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazune N., Sato K.,
RA Shitaki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hasehizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sasaki K., Sasaki D., Shibata K., Shinagawa A.,
RA Yamanishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y. ;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs." ;
RL Nature 420:563-573(2002).
[5]
RP NCLECTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Placenta;
RC MEDLINE=1085660; PubMed=1121781; DOI=10.1038/35055500;
RX Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Aachi T., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,
RA Saito T., Okazaki Y., Gotojori T., Bono H., Kaekawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gless C., King B., Kochwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirral L.M., Staudli F., Suzuki R., Tomita M., Wagner L., Mashio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Balarelli R., Barh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gaetclinch S., Hill D., Hofmann M., Hume D.A., Kamlya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli T., Momberees P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya F., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-Oka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
RA Wysshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Konteuki S.,
RA Hayashizaki Y. ;
RT "Functional annotation of a full-length mouse cDNA collection." ;
RL Nature 409:685-690(2001).
[6]
RP NCLECTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Placenta;
RC MEDLINE=20459374; PubMed=11042159; DOI=10.1101/gr.145100;
RX Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y. ;
RT "Normalization and substructure of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes." ;
RL Genome Res. 10:1617-1630(2000).
[7]
RP NCLECTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Placenta;
RC MEDLINE=20530913; PubMed=11076661; DOI=10.1101/gr.153600;
RX Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama Y., Nishi K., Kitsuai T., Teshiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kasahagi K.,
RA Fujitake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y. ;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer." ;
RL Genome Res. 10:1757-1771(2000).
[8]
RP NCLECTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Placenta;
RA Arakawa T., Carninci P., Fukuda S., Hasehizume W., Hayashida K.,
RA Hori F., Iida Y., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA Nishiyori H., Nomura K., Ohno M., Sakazune N., Sano H., Sasaki D.,
RA Shibata K., Shitaki T., Tagami Y., Tagami Y., Waki K., Watanishi A.,
RA Morimatsu M., Hayashizaki Y. ;

CC	Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
CC	-----
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC	Distributed under the Creative Commons Attribution-NoDerivs license
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DR	EMBL AK146056; BAE36865.1; -, mRNA.
DR	MGI:98397; Src.
DR	GO GO:0005515; F:protein binding; IPI.
DR	GO GO:0004674; F:protein serine/threonine kinase activity; RCA.
DR	GO GO:0004713; F:protein-tyrosine kinase activity; IMP.
DR	GO GO:0006468; P:protein amino acid phosphorylation; IDA.
DR	InterPro: IPRO00719; Prot_kinase.
DR	InterPro: IPRO02290; Ser_Thr_kinase.
DR	InterPro: IPRO00980; SH2.
DR	InterPro: IPRO01452; SH3.
DR	InterPro: IPRO01245; Tyr_kinase.
DR	InterPro: IPRO08266; Tyr_kinase_AS.
DR	Pfam: PF07714; Pkinase_Tyr. 1.
DR	Pfam: PF00017; SH2; 1.
DR	Pfam: PF00018; SH3_1; 1.
DR	PRINTS: PR00401; SH2DOMAIN.
DR	PRINTS: PR00452; SH3DOMAIN.
DR	PRINTS: PR00109; TYRKINASE.
DR	ProdDom: PD000001; Prot_kinase; 1.
DR	ProdDom: PD000093; SH2; 1.
DR	ProdDom: PD000066; SH3; 1.
DR	SMART: SMO0252; SH2; 1.
DR	SMART: SMO0326; SH3; 1.
DR	SMART: SMO0219; TyrcKc; 1.
DR	PROSITE: PS00107; PROTEIN KINASE ATP; 1.
DR	PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR	PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR	PROSITE: PS50001; SH2; 1.
DR	PROSITE: PS50002; SH3; 1.
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Matches 531, Conservative 0; Mismatches 4; Indels 6; Gaps 1,	
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117	--EGDWMLAHSLSTGCGTGYIPSNVAVPDSIQAEEMTFGKITRRESERLLIENPRCTF 174
181	LVRSEETTKGAYCYLSVSDFDNAKGLNVHYKIRKLDSGGFFITRTOPNSILOOVAAYSK 240
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 Db 535 L 535

RESULT 7
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 AC P12931; Q86VB9; Q9H5A8;
 DT 01-OCT-1989, integrated into UniProtKB/Swiss-Prot.
 DT 01-NOV-1995, sequence version 2.
 DT 07-MAR-2006, entry version 79.
 DE Proto-oncogene tyrosine-protein kinase Src (BC 2.7.1.112) (p60-Src)
 DE (c-Src) (p60c-src).
 GN Name=SRC; Synonyms=SRC1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OC NCBI_TaxID=9606;
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 NP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RP MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
 RX Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavridis G., Almeida J.P., Babbage A.K., Bagguley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Cordy N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
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 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Leveasleth M.H., Leverisha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConachie L.J., McIay K., McMurtry A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
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 RA Rice C.M., Rose M.T., Scott C.E., Sehra H.K., Showkhen R., Sims S.,
 RA Stuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.B.,
 RA Swan R.M., Symcote N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Williams S.A.,
 RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilmings L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.,
 RT "The DNA sequence and comparative analysis of human chromosome 20.",
 RL Nature 414:865-871(2001).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
 RC TISSUE=Lung, and Skin;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.J., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loughran N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Besek S.A., McKernan P.C., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Holik S.W.,
 RA Villalón D.R., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Rodriguez A.C., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.",
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE OF 1-184 (ISOFORM 1).
 RX MEDLINE=87257903; PubMed=3299057;
 RA Tanaka A., Gibbs C.P., Arthur R.R., Anderson S.K., Kung H.-J.,
 RA Fujita D.J.,
 RT "DNA sequence encoding the amino-terminal region of the human c-src
 RT protein: implications of sequence divergence among src-type kinase
 RT oncogenes.",
 RL Mol. Cell. Biol. 7:1978-1983(1987).
 RN [4]
 RP NUCLEOTIDE SEQUENCE OF 185-535 (ISOFORM 1).
 RX MEDLINE=85213483; PubMed=2582238;
 RA Anderson S.K., Gibbs C.P., Tanaka A., Kung H.-J., Fujita D.J.,
 RT "Human cellular src gene: nucleotide sequence and derived amino acid
 RT sequence of the region coding for the carboxy-terminal two-thirds of
 RT p60c-src.",
 RL Mol. Cell. Biol. 5:1122-1129(1985).
 RN [5]
 RP NUCLEOTIDE SEQUENCE OF 97-138 (ISOFORM 2).
 RX MEDLINE=90040822; PubMed=2681803;
 RA Payer J.M., Bolen J.B.,
 RT "Neuron-specific splicing of C-SRC RNA in human brain.",
 RL J. Neurosci. Res. 24:89-96(1989).
 RN [6]
 RP NUCLEOTIDE SEQUENCE OF 375-535 (ISOFORM 1).
 RX MEDLINE=85187981; PubMed=2581127;
 RA Parker R.C., Mardon G., Lebo R.V., Varnus H.E., Bishop J.M.,
 RT "Isolation of duplicated human c-src genes located on chromosomes 1
 RT and 20.",
 RL Mol. Cell. Biol. 5:831-838(1985).
 RN [7]
 RP ALTERNATIVE SPLICING.
 RX PubMed=1691439;
 RA Payer J.M., Bolen J.B.,
 RT "Identification of a novel neuronal C-SRC exon expressed in human
 RT brain.",
 RL Mol. Cell. Biol. 10:2035-2040(1990).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 85-535.
 RX MEDLINE=97117105; PubMed=9024657; DOI=10.1038/385595a0;
 RA Xu W., Harrison S.C., Eck M.J.,
 RT "Three-dimensional structure of the tyrosine kinase c-Src.",
 RL Nature 385:595-602(1997).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 144-248.
 RX MEDLINE=97317069; PubMed=9174343; DOI=10.1021/b1970019n;
 RA Charlifson P.S., Shevchuk L.M., Rocque W., Hummel C.W., Jordan S.R.,
 RA Mohr C., Pacofsky G.J., Peel M.R., Rodriguez M., Sternbach D.D.,
 RA Consler T.G.,
 RT "Peptide ligands of pp60(c-src) SH2 domains: a thermodynamic and
 RT structural study.",
 RL Biochemistry 36:6283-6293(1997).
 RN [10]
 RP STRUCTURE BY NMR OF 203-248.
 RX MEDLINE=95161382; PubMed=7532003;
 RA Xu R.X., Word J.M., Davis D.G., Rink M.J., Willard D.H. Jr.,
 RA Gampe R.T. Jr.,
 RT "Solution structure of the human pp60c-src SH2 domain complexed with a
 RT phosphorylated tyrosine pentapeptide.",
 RL Biochemistry 34:2107-2121(1995).
 CC -1- CATALYTIC ACTIVITY. ATP + a protein tyrosine = ADP + a protein
 CC tyrosine phosphate.
 CC -1- INTERACTION:
 CC Q6NVF1:Cent3 (xeno); NDExp=3; InAct=EBI-621482, EBI-621463;
 CC Q6Y6R3:IBK; NDExp=1; InAct=EBI-621482, EBI-81279;
 CC Q60749:Khdbs1 (xeno); NDExp=1; InAct=EBI-621482, EBI-519077;
 CC -1- ALTERNATIVE PRODUCTS:
 CC Evtent=Alternative splicing; Named isoforms=2;
 CC Name=1;

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CC      Ibold=P12931-1; Sequence=displayed;
CC      Name=2;
CC      Ibold=P12931-2; Sequence=VSP_012134;
CC      -1- P-TM: Phosphorylated on Tyr-529 by c-Src kinase (CSK). The
CC      phosphorylated form is termed pp60c-src. The phosphorylated tail
CC      interacts with the SH2 domain thereby repressing kinase activity.
CC      -1- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
CC      subfamily.
CC      -1- SIMILARITY: Contains 1 SH2 domain.
CC      -1- SIMILARITY: Contains 1 SH3 domain.
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NonDerivative License
CC      -----
DR      EMBL: A1133293; CAC34523.1; -; Genomic_DNA.
DR      EMBL: BC011566; AAH11566.1; -; mRNA.
DR      EMBL: BC051270; AAH51270.2; -; mRNA.
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DR      EMBL: X04000; CAA26485.1; JOINED; Genomic_DNA.
DR      PIR: A26891; TVHUSC.
DR      PDB: 1A07; X-ray; A/B=143-248.
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DR      PDB: 1HCT; NMR; B=143-248.
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QY      481 DOVERGYRMPCEPECESLHDMCQCRKPEPEEPFPEYLQAFLEDFPSTEPQYQYGEN 540
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QY      541 L 541
DB      535 L 535

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RESULT 8

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AC Q9WUD9;
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DT 30-MAY-2000, sequence version 2.
DT 07-MAR-2006, entry version 46.
DE Proto-oncogene tyrosine-protein kinase Src (EC 2.7.1.112) (p60-Src)
DE (c-Src) (pp60c-src).
GN Name=Src;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
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OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE [mRNA].
RC STRAIN=Sprague-Dawley; TISSUE=Testis;
RA Stockand J.D., Al-Khalili O., Spier B.J., Eaton D.C.;
RT "Rattus norvegicus proto-oncogene encoding tyrosine-protein kinase
RT pp60-c-src."
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC tyrosine phosphate.
CC -1- P-TM: Phosphorylated on Tyr-529 by c-Src kinase (CSK). The
CC phosphorylated form is termed pp60c-src. The phosphorylated tail
CC interacts with the SH2 domain thereby repressing kinase activity
CC (By similarity).
CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
CC subfamily.
CC -1- SIMILARITY: Contains 1 SH2 domain.
CC -1- SIMILARITY: Contains 1 SH3 domain.
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DR EMBL: AF130457; AAD24180.1; -; mRNA.
DR HSP: P12931.1A09.
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DR InterPro: IPR009880; SH2.
DR InterPro: IPR001452; SH3.
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DR PROSITE: PS50002; SH3; 1.
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PT FT 1 /Ftrid=PRO_0000088143.
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PT DOMAIN 150 247 SH3.
PT DOMAIN 269 522 Protein kinase.
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PT BINDING 297 297 ATP (By similarity).
PT MOD_RES 419 419 Phosphothreonine (by autocatalysis) (By
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PT MOD_RES 529 529 Phosphotyrosine (by CSK) (By similarity).
PT LIPID 1 1 N-myristoyl glycine (By similarity).
SQ SEQUENCE 535 AA; 59947 MW; AD083DD2357890BC CRC64;
Query Match 97.0%; Score 2772.5; DB 1; Length 535;
Best Local Similarity 97.6%; Pred. No. 6.1e-175;
Matches 528; Conservative 3; Mismatches 3; Indels 7; Gaps 2;
QY 2 GSNKSKPKDASORRRSRLEPSENVHAGCAFPASQTPSKPASADGHRGSAFVPP-AAEP 60
Db 1 GSNKSKRKDASORRRSRLEPSENVHAGCAFPASQTPSKPASADGHRGSAFVPPAAEP 60
QY 61 KLFQGFNSSTVTISPPQAGALAGVTTFVALVDYESTRTDLSFKKGERLQIVNTRKVD 120
Db 61 KLFQGFNSSTVTISPPQAGALAGVTTFVALVDYESTRTDLSFKKGERLQIVNNT--- 116
QY 121 VRGDMWLASLSTGQGYIPSNVVAPSDSQAEEMVFGKTRRESRLILNANPGTF 180
Db 121 VRGDMWLASLSTGQGYIPSNVVAAPDSQAEEMVFGKTRRESRLILNANPGTF 174
QY 117 --RDMWLASLSTGQGYIPSNVVAAPDSQAEEMVFGKTRRESRLILNANPGTF 174
QY 181 LVRESSTTKAYCLSVDPDAKGLANVHYKIRKLDGSGFYITSRTOFNSLQQLVAAYSK 240
Db 175 LVRESSTTKAYCLSVDPDAKGLANVHYKIRKLDGSGFYITSRTOFNSLQQLVAAYSK 234
QY 241 HADGLCHRLTTCVCTSPQTOGLAKDAWEIPRESLRLEVKLGQCQFGEVMGTNGTTRV 300
Db 235 HADGLCHRLTTCVCTSPQTOGLAKDAWEIPRESLRLEVKLGQCQFGEVMGTNGTTRV 294
QY 301 AIKTLKGTWSPFAFLQDAQVKKLRHEKLVQLVAVSEBPIYVTEPMNKGSLDLFLKG 360

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Db 295 AIKTLKGTWSPFAFLQDAQVKKLRHEKLVQLVAVSEBPIYVTEPMNKGSLDLFLKG 354
QY 361 ETGKYLRLPOLVMSAQIAGMAVVERMYVHRLRANILVGENNYCKVADPGLARLIE 420
Db 355 ETGKYLRLPOLVMSAQIAGMAVYDMMYVHRLRANILVGENNYCKVADPGLARLIE 414
QY 421 DNEYTAQGAKEPDKWAPAEALYGRFTIKSDVMSFGILLTELTTKGRVPPGAVNREVL 480
Db 415 DNEYTAQGAKEPDKWAPAEALYGRFTIKSDVMSFGILLTELTTKGRVPPGAVNREVL 474
QY 481 DVEGRYRMCPEPCPSLHDMQCWRKGBEERPTREYLAQFLADYFTSTEPQYQGEN 540
Db 475 DVEGRYRMCPEPCPSLHDMQCWRKGBEERPTREYLAQFLADYFTSTEPQYQGEN 534
QY 541 L 541
Db 535 L 535
RESULT 9
ID Q450J2_RAT PRELIMINARY; PRT; 523 AA.
AC Q450J2;
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Tyrosine protein kinase c-src (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SHR, and WKY.
RA Jackson E.K., Zhu C.;
RT "Genetic Similarity Between Spontaneously Hypertensive Rats and
RT Wistar-Kyoto Rats in the Coding Regions of Signal Transduction
RT Proteins."
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY. ATP + a protein tyrosine = ADP + a protein
CC tyrosine phosphate.
CC -!- SIMILARITY: Contains 1 SH3 domain.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
DR EMBL: DQ120510; AA223849.1; -; mRNA.
DR EMBL: DQ120509; AA223848.1; -; mRNA.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0000166; F:nucleotide binding; IEA.
DR GO: GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0007242; P:intracellular signaling cascade; IEA.
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_Chr_kinase.
DR InterPro: IPR000980; SH2.
DR InterPro: IPR001452; SH3.
DR InterPro: IPR001245; Tyr_kinase.
DR InterPro: IPR008266; Tyr_kinase_AS.
DR Pfam: PF07714; Pkinase_Tyr; 1.
DR Pfam: PF00017; SH2; 1.
DR Pfam: PF00018; SH3; 1.
DR PRINTS: PR00401; SH2DOMAIN.
DR PRINTS: PR00452; SH3DOMAIN.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Prot_kinase; 1.
DR ProDom: PD000093; SH2; 1.
DR ProDom: PD000066; SH3; 1.
DR SMART: SM00252; SH2; 1.
DR SMART: SM00326; SH3; 1.
DR SMART: SM00219; Tyrc; 1.

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DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 KW ATP-binding; Kinase; Nucleotide-binding; SH3 domain; Transferase;
 KW Tyrosine-protein kinase.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 523 AA; 58672 MW; 8D5DC2644FDF2C CRC64;
 Query Match 94.7%; Score 2707.5; DB 2; Length 523;
 Best Local Similarity 97.5%; Pred. No. 1.2e-170;
 Matches 516; Conservative 3; Mismatches 3; Indels 7; Gaps 2;
 QY 7 KPDASGRRRLSLSESENVHAGAFAPSQTPSKASADGHRGPAALVPP-AAEPKLFQG 65
 DB 1 KPXDASGRRRLSLSESENVHAGAFAPSQTPSKASADGHRGPAALVPPAAAEPKLFQG 60
 QY 66 FNSSDTVTSFORAGALAGVTTFFVALVDYESRTEPDSFPKGGRLQIVNNTTRKVDVREGD 125
 DB 61 FNSSDTVTSFORAGPLAGVTTFFVALVDYESRTEPDSFPKGGRLQIVNNT-----EGD 114
 QY 126 WMLAHSLSGTQGYIPENVYAPSDSIQAEEMWFGKTRRESERLLNAENPRGTFVRES 185
 DB 115 WMLAHSLSGTQGYIPENVYAPFDSIQAEEMWFGKTRRESERLLNAENPRGTFVRES 174
 QY 186 ETTKGAVCLSVSPDNAGKLVNHYKTRKLDSSGFYITSTQPSLQQLVAYISKADGL 245
 DB 175 ETTKGAVCLSVSPDNAGKLVNHYKTRKLDSSGFYITSTQPSLQQLVAYISKADGL 234
 QY 246 CHRLTVTCPTSKFOTQGLADAMEIPRESLRLEVKLGQGFGEVGMGTNGTRVAIKTL 305
 DB 235 CHRLTVTCPTSKFOTQGLADAMEIPRESLRLEVKLGQGFGEVGMGTNGTRVAIKTL 294
 QY 306 KPQTSPEAFLOEAQVWKLRHEKLVQLYAVSEEPYIYTEYNNKSLDPLKGETGY 365
 DB 295 KPQTSPEAFLOEAQVWKLRHEKLVQLYAVSEEPYIYTEYNNKSLDPLKGETGY 354
 QY 366 LRLPOLVDSNAQIASGMAIYERMYVNRDILRANILVGENLVCKVADFGILRLIEDNEYT 425
 DB 355 LRLPOLVDSNAQIASGMAIYERMYVNRDILRANILVGENLVCKVADFGILRLIEDNEYT 414
 QY 426 ARQGAEPFKMTAPEALYGRFTIKSVMSFGILLTLTKGRVPYGVNREVLDOVER 485
 DB 415 ARQGAEPFKMTAPEALYGRFTIKSVMSFGILLTLTKGRVPYGVNREVLDOVER 474
 QY 486 GYRMPCEPCEPSLHDMCCQMKRKEPERPTFEXLQAFLEDYFTSTEPQ 534
 DB 475 GYRMPCEPCEPSLHDMCCQMKRKEPERPTFEXLQAFLEDYFTSTEPQ 523
 RESULT 10
 SRC CHICK STANDARD; PRT; 532 AA.
 AC P00523; Q90992; Q91343; Q91343; Q92013; Q98915;
 DT 21-JUL-1986; Integrated into UniProtKB/Swiss-Prot.
 DT 15-JUL-1999; sequence version 3.
 DT 07-MAR-2006; entry version 78.
 DE Proto-oncogene tyrosine-protein kinase Src (EC 2.7.1.112) (p60-Src)
 DE (c-Src) (pp60c-src).
 GN Name=SRC;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxId=9031;
 RN [1]
 RP NUCLEOTIDE SEQUENCE (ISOFORM 1).
 RX MEDLINE=8315564; PubMed=6299580; DOI=10.1016/0092-8674(83)90073-9;
 RA Takeya T., Hanafusa H.;
 RT "Structure and sequence of the cellular gene homologous to the RSV src
 RT gene and the mechanism for generating the transforming virus.";

RL Cell 32:881-890(1983).
 RN [2]
 RP ERRATUM, AND SEQUENCE REVISION TO 525.
 RA Takeya T., Hanafusa H.;
 RL Cell 34:319-319(1983).
 RN [3]
 RP NUCLEOTIDE SEQUENCE (ISOFORM 2).
 RC TISSUE-Pectoralis muscle;
 RX MEDLINE=90318371; PubMed=2115117;
 RA Dorai T., Wang L.-H.;
 RT "An alternative non-tyrosine protein kinase product of the c-src gene
 RT in chicken skeletal muscle."
 RL Mol. Cell. Biol. 10:4068-4079(1990).
 RN [4]
 RP NUCLEOTIDE SEQUENCE (ISOFORM 1), AND PHOSPHORYLATION SITES TYR-415 AND
 RP TYR-435.
 RX MEDLINE=97008971; PubMed=8856081;
 RA Weiland A., Neubauer G., Courtneidge S.A., Mann M., Wierenga R.K.,
 RA Superti-Furga G.;
 RT "The purification and characterization of the catalytic domain of Src
 RT expressed in Schistosoma haematophyllum. Comparison of unphosphorylated
 RT and tyrosine phosphorylated species."
 RL Eur. J. Biochem. 240:756-764(1996).
 RN [5]
 RP NUCLEOTIDE SEQUENCE OF 1-6.
 RX MEDLINE=83059861; PubMed=6292480;
 RA Takeya T., Hanafusa H.;
 RT "DNA sequence of the viral and cellular src gene of chickens. II.
 RT Comparison of the src genes of two strains of Avian sarcoma virus and
 RT of the cellular homolog."
 RL J. Virol. 44:12-18(1982).
 RN [6]
 RP NUCLEOTIDE SEQUENCE OF 1-18 AND 484-533 (ISOFORM 1).
 RX MEDLINE=91304409; PubMed=1712905;
 RA Dorai T., Levy J.B., Kang L., Brugge J.S., Wang L.-H.;
 RT "Analysis of cDNAs of the proto-oncogene c-src: heterogeneity in 5'
 RT exon and possible mechanism for the genesis of the 3' end of v-src."
 RL Mol. Cell. Biol. 11:4165-4176(1991).
 RN [7]
 RP ATP-BINDING SITE.
 RX MEDLINE=84270751; PubMed=6431300;
 RA Kampe M.P., Taylor S.S., Sefton B.M.;
 RT "Direct evidence that oncogenic tyrosine kinases and cyclic AMP-
 RT dependent protein kinase have homologous ATP-binding sites."
 RL Nature 310:589-592(1984).
 RN [8]
 RP PHOSPHORYLATION.
 RX MEDLINE=86028181; PubMed=2996780; DOI=10.1016/0092-8674(85)90281-8;
 RA Gould K.L., Woodgett J.R., Cooper J.A., Buss J.E., Shalloway D.,
 RA Hunter T.;
 RT "Protein kinase C phosphorylates pp60src at a novel site."
 RL Cell 42:849-857(1985).
 RN [9]
 RP PHOSPHORYLATION SITE TYR-415.
 RX MEDLINE=82082387; PubMed=6273838;
 RA Smart J.E., Oppermann H., Czernilofsky A.P., Purchio A.F.,
 RA Erikson R.L., Bishop J.M.;
 RT "Characterization of sites for tyrosine phosphorylation in the
 RT transforming protein of Rous sarcoma virus (pp60v-src) and its normal
 RT cellular homolog (pp60c-src)."
 RL Proc. Natl. Acad. Sci. U.S.A. 78:6013-6017(1981).
 RN [10]
 RP PHOSPHORYLATION SITE TYR-526.
 RX MEDLINE=86151652; PubMed=2420005;
 RA Cooper J.A., Gould K.L., Cartwright C.A., Hunter T.;
 RT "Tyrosine 527 is phosphorylated in pp60c-src: implications for regulation."
 RL Science 231:1431-1434(1986).
 RN [11]
 RP PHOSPHORYLATION SITES THR-33; THR-45 AND SER-71.
 RX MEDLINE=89249341; PubMed=2470512; DOI=10.1016/0092-8674(89)90791-5;
 RA Shenoy S., Choi J.K., Bagrodia S., Copeland T.D., Maller J.L.,
 RA Shalloway D.;
 RT "Purified maturation promoting factor phosphorylates pp60c-src at the

RT sites phosphorylated during fibroblast mitosis." ;
 RL Cell 57:763-774(1989) .
 RN (12)
 RP X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 82-532.
 RX MEDLINE=98070614; PubMed=9405157; DOI=10.1006/jmb.1997.1426;
 RA Williams J.C., Weiland A., Gonfiant S., Thompson A.,
 RA Courtenay S.A., Superfi-Furga G., Wierenga R.K.,
 RT "The 2.35 A crystal structure of the inactivated form of chicken Src:
 RT a dynamic molecule with multiple regulatory interactions." ;
 RL J. Mol. Biol. 274:757-775(1997) .
 RN (13)
 RP STRUCTURE BY NMR OF 80-139.
 RX MEDLINE=92279385; PubMed=8504663; DOI=10.1016/0014-5793(93)81538-B;
 RA Yu H., Rosen M.K., Schreiber S.L.,
 RT "H and 15N assignments and secondary structure of the Src SH3
 RT domain." ;
 RL FEBS Lett. 324:87-92(1993) .
 CC -1- FUNCTION: Unknown.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
 CC tyrosine phosphate.
 CC -1- ENZYME REGULATION: Becomes activated when its major tyrosine
 CC phosphorylation site is not phosphorylated. It can also be
 CC activated by point mutations as well as by truncations at the C-
 CC terminal end or by other mutations.
 CC -1- SUBUNIT: pp60c-src forms a complex with polyoma virus middle T
 CC antigen.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P00523-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P00523-2; Sequence=VSP_011844, VSP_011845;
 CC Note=Membrane-bound;
 CC -1- TISSUE SPECIFICITY: Expressed to high levels, and with a high
 CC degree of kinase activity, in certain fully differentiated cells
 CC such as neurons, platelets and macrophages. Isoform 1 is widely
 CC expressed. Isoform 2 is expressed only in the muscle.
 CC -1- PTM: Phosphorylated on Tyr-526 by C-Src kinase (CSK). The
 CC phosphorylated form is termed pp60c-src. The phosphorylated tail
 CC interacts with the SH2 domain thereby repressing kinase activity
 CC (by similarity) .
 CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
 CC subfamily.
 CC -1- SIMILARITY: Contains 1 SH2 domain.
 CC -1- SIMILARITY: Contains 1 SH3 domain.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NonDerivs license
 CC -----
 DR EMBL: J00402; CAA23596.1; -; Genomic DNA.
 DR EMBL: J00908; -; NOT ANNOTATED CDS; Genomic DNA.
 DR EMBL: M57290; AAA49078.1; -; mRNA.
 DR EMBL: S43604; AAD13831.1; -; mRNA.
 DR EMBL: S43616; AAD13835.1; -; mRNA.
 DR EMBL: S43587; AAD13830.1; -; mRNA.
 DR EMBL: S43609; AAD13832.1; -; mRNA.
 DR EMBL: S43614; AAD13834.1; -; mRNA.
 DR EMBL: S43579; AAB19353.2; -; mRNA.
 DR PIR: A00630; TVCHS.
 DR PDB: 1FIW; X-ray; A=144-246.
 DR PDB: 1FZF; X-ray; A=144-246.
 DR PDB: 1NLO; NMR; C=80-139.
 DR PDB: 1NLP; NMR; C=80-139.
 DR PDB: 1P13; X-ray; A/B=144-245.
 DR PDB: 1PRL; NMR; C=76-139.
 DR PDB: 1PRM; NMR; C=76-139.
 DR PDB: 1RLP; NMR; C=76-139.
 DR PDB: 1RLQ; NMR; C=76-139.
 DR PDB: 1SRL; NMR; @=76-139.
 DR PDB: 1SRM; NMR; @=76-139.
 DR PDB: 2PTK; X-ray; @=-.
 DR Ensemble; ENSGALG00000003855; Gallus gallus.
 DR Linkhub; P00523; -.

DR	InterPro:	IPR000719;	Prot_kinase.
DR	InterPro:	IPR002290;	Sec_thr_kinase.
DR	InterPro:	IPR00980;	SH2.
DR	InterPro:	IPR001452;	SH3.
DR	InterPro:	IPR001245;	Tyr_kinase.
DR	InterPro:	IPR008266;	Tyr_kinase_AS.
DR	Pfam:	PF07714;	Kinase_Tyr_1.
DR	Pfam:	PF00017;	SH2; 1.
DR	Pfam:	PF00018;	SH3_1; 1.
DR	PRINTS:	PR00401;	SH2DOMAIN.
DR	PRINTS:	PR00452;	SH3DOMAIN.
DR	PRINTS:	PR00109;	TYRKINASE.
DR	ProDom:	PD000001;	prot_kinase; 1.
DR	ProDom:	PD000093;	SH2; 1.
DR	ProDom:	PD000066;	SH3; 1.
DR	SMART:	SM00252;	SH2; 1.
DR	SMART:	SM00326;	SH3; 1.
DR	SMART:	SM00219;	TyrcK; 1.
DR	PROSITE:	PS00107;	PROTEIN_KINASE_ATP; 1.
DR	PROSITE:	PS50011;	PROTEIN_KINASE_DOM; 1.
DR	PROSITE:	PS00109;	PROTEIN_KINASE_TYR; 1.
DR	PROSITE:	PS50001;	SH2; 1.
DR	PROSITE:	PS50002;	SH3; 1.
KM	3D-structure, Alternative splicing; ATP-binding; Kinase; Lipoprotein; Myristate; Nucleotide-binding; Phosphorylation; Proto-oncogene; SH2 domain; SH3 domain; Tyrosine-protein kinase.		
FT	INIT MET	0	By similarity.
FT	CHAIN	1	Proto-oncogene tyrosine-protein kinase Src.
FT		532	/FTID=PRO_0000088144.
FT	DOMAIN	80	SH3.
FT	DOMAIN	147	SH2.
FT	DOMAIN	266	Protein kinase.
FT	NP BIND	272	ATP (By similarity).
FT	ACT_SITE	385	Proton acceptor (By similarity).
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Query Match			
Best Local Similarity 92.4%; Score 2643; DB 1; Length 532;			
Matches 503; Conservative 12; Mismatches 17; Indels 8; Gaps 2			
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DB	1	GSSKKRPDPSPQRRLSLPPDSSTH--HGGFSPASQPKNKAADPTNTPSRSFETVAITEPK	58
QY	62	LFGGNSSSDTYSPPRAGLAGGVTFVALYYESRTETDLSFFKIGSERLOIVNTRKVDV	121
DB	59	LFGNTSIDTYSPPRAGLAGGVTFVALYYESTRETDLDFKIGGERIOIVNNT-----	113
QY	122	REGDWMLAHSLSTGGTGYYIPSNNYVASPSDIOAEWYFGKITRESERLLLNENPGTEL	181
DB	114	-EGDWMLAHSLITGGTGYYIPSNYVASPSIOAEWYFGKITRESERLLLNENPNRGTEL	172
QY	182	VRESSTTGAYKCLSYSPFDNAKGLNVKIKIRKLDSGGYITISRFQFNLSLQOLVAAYSCH	241
QY	173	VRESSTTGAYCCLSYSDPDNAKGLNVKHVKIRKLDSGGFYITISKRFQFSSLQOLVAAYSCH	232
DB	242	ADGLCHRILTVCCPTSKPOTOGIAXDAWEIPIRESLTLEVLGGCGCFGEVMWGTMNGTTRYA	301
QY	223	ADGLCHRILTVCCPTSKPOTOGIAXDAWEIPIRESLTLEVLGGCGCFGEVMWGTMNGTTRYA	292
DB	302	IKTLPGTMSPEAFQLQBAOVMMKLEHEKLVOLVAVVSEBPIYIVTEYNMKGSILDFLKG	361
QY	293	IKTLPGTMSPEAFQLQBAOVMMKLEHEKLVOLVAVVSEBPIYIVTEYNMKGSILDFLKG	352
QY	362	TGKYTRLPOLYDMSAQAISGAUYVERMYVVRHDLPAAINVGENLVCKYADGLARLIID	421
DB	353	MGYTRLPOLYDMAQAISGAUYVERMYVVRHDLPAAINVGENLVCKYADGLARLIID	412
QY	422	NEYTAQAKFPFKTATAPALYGFFTLKSDVMSGILLTTLTKGRVVPQANREVLD	481
DB	413	NEYTAQAKFPFKTATAPALYGFFTLKSDVMSGILLTTLTKGRVVPQANREVLD	472
QY	482	QVERVYRNAPCEPCESLHDLMCQWRKEPERPFVEYLQALFEDYFTSTDEPOYGENTL	541

Db 473 OVERGYRMPCEPCPSLHDMCQKRCOPBEERPTFEYLQAFLEDTYSTRPEQPCENTL 532

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RESULT 11
SRC_AVIS2 ID SRC_AVIS2 STANDARD; PRT; 586 AA.
AC P15054;
DT 01-APR-1990, integrated into UniProtKB/Swiss-Prot.
DT 30-APR-2005, sequence version 2.
DT 07-MAR-2006, entry version 64.
DE Tyrosine-protein kinase transforming protein Src (EC 2.7.1.112) (p60-
DE Src) (v-Src) (pp60v-src).
GN Name=v-Src;
OS Avian sarcoma virus (strain PR2257).
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Alpharetrovirus; unclassified Alpharetrovirus.
OX NCBI_TaxID=11879;
[1]
RP NUCLEOTIDE SEQUENCE [GENOMIC RNA].
RX MEDLINE=89094972; PubMed=2463376;
RA Geryk J., Dezezele P., Barlier J.V., Svoboda J., Nehyba J., Karakoz I.,
RA Rynditch A.V., Yatsula B.A., Calothy G.;
RT "Transduction of the cellular src gene and 3' adjacent sequences in
RT avian sarcoma virus PR2257."
RL J. Virol. 63:481-492(1989).
[2]
RP NUCLEOTIDE SEQUENCE [GENOMIC RNA].
RA Yatsula B.A., Geryk J., Svoboda J., Rynditch A.V., Calothy G.,
RA Dezezele P.;
RL Submitted (APR-1992) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: This phosphoprotein, required for both the initiation
CC and the maintenance of neoplastic transformation, is a protein
CC kinase that catalyzes the phosphorylation of tyrosine residues in
CC vitro.
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC tyrosine phosphate.
CC -!- PTM: The phosphorylated form is termed pp60v-src.
CC -!- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
CC subfamily.
CC -!- SIMILARITY: Contains 1 SH2 domain.
CC -!- SIMILARITY: Contains 1 SH3 domain.
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CC
EMBL: M21526; AAA42583.1; -; Genomic_RNA.
EMBL: X51863; CA436156.1; -; Genomic_RNA.
DR PIR; A30174; TVFVPR.
DR HSSP; P00523; 2PTK.
DR SMR; P15054; 83-524.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001452; SH3.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR Pfam; PF07714; PKinase_Tyr; 1.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH3; 1; 1.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRINTS; PR00452; SH3DOMAIN.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR ProDom; PD000093; SH2; 1.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00001; SH2; 1.

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DR PROSITE; PS00002; SH3; 1.
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KW Oncogene; Phosphorylation; SH2 domain; SH3 domain; Transferrase;
KW Tyrosine-protein kinase.
FT INIT_MET 0
FT CHAIN 1 586
FT By similarity.
FT Tyrosine-protein kinase transforming
FT protein Src.
FT /Pfam=PRO_0000088148.
FT SH2.
FT SH3.
FT DOMAIN 80 141
FT 147 244
FT 266 519
FT 272 280
FT 385 385
FT ACT_SITE 294 294
FT BINDING 294 294
FT MOD_RES 415 415
FT Phosphotyrosine (by autocatalysis) (By
FT similarity).
FT N-myristoyl glycine (by host) (By
FT similarity).
FT LIPID 1 1
FT SEQUENCE 586 AA; 65670 MW; 76520EF485B5CD02 CRC64;
Query Match 90.9%; Score 2598; DB 1; Length 586;
Best Local Similarity 93.0%; Pred. No. 2,5e-163;
Matches 495; Conservative 12; Mismatches 17; Indels 8; Gaps 2;
QY 2 GSNKSKPKDASQRRRLSESENVHGAGAPASQTPSKASADGHRGPAAPVPAAPK 61
DB 1 GSKSKPKDPSQRRRLSEPPDSTH--HGCFPASPQTKTAAPDTHKTPSRSPQVATERR 58
QY 62 LFGFNSDPTVTSPPORAGIAGVTFVALYDESFTETDLSFKKGERLQIVNTRKDV 121
DB 59 LFGFPTSTVTSPPORAGIAGVTFVALYDESFTETDLSFKKGERLQIVNTRKDV 113
QY 122 REGDMLASLSNGQGVYPSNVVAPSDISOAEWFEFGITRESRLLNENPGTF 181
DB 114 -EGDMLASLSLTGGQGVYPSNVVAPSDISOAEWFEFGITRESRLLNENPGTF 172
QY 182 VRESSTTKAYCISVDFPNAGLNVKHYKIKLDSGFGYITSRTQFNSLQQLVAYSGH 241
DB 173 VRESSTTKAYCISVDFPNAGLNVKHYKIKLDSGFGYITSRTQFNSLQQLVAYSGH 232
QY 242 ADGLCHRLTTCVPTSKPTQGLAKDAMEIPRSRLRLEVKLGQCGFGEVWGVTTRVA 301
DB 233 ADGLCHRLTTCVPTSKPTQGLAKDAMEIPRSRLRLEVKLGQCGFGEVWGVTTRVA 292
QY 302 ITLKRGTSPPAFLOEAVMKLRHEKLVQYAVVSEEPITYVTEYMKSLDPLKGB 361
DB 293 ITLKRGTSPPAFLOEAVMKLRHEKLVQYAVVSEEPITYVTEYMKSLDPLKGB 352
QY 362 TGKYLRLPOLVMSAQIASGMAYVERMYVHDLRAANILVGENLVCKYADFGALRIED 421
DB 353 MGKTLRLPOLVMSAQIASGMAYVERMYVHDLRAANILVGENLVCKYADFGALRIED 412
QY 422 NEYTAQGAFFPKWTAPAAALYGRFTIKSDVMSFGILLTELTTKGRVYPGQVNEVID 481
DB 413 NEYTAQGAFFPKWTAPAAALYGRFTIKSDVMSFGILLTELTTKGRVYPGQVNEVID 472
QY 482 OVERGYRMPCEPCPSLHDMCQKRCOPBEERPTFEYLQAFLEDTYSTRPEQPCENTL 533
DB 473 OVERGYRMPCEPCPSLHDMCQKRCOPBEERPTFEYLQAFLEDTYSTRPEQPCENTL 524
RESULT 12
SRC_AVIS2 ID SRC_AVIS2 STANDARD; PRT; 567 AA.
AC P14084;
DT 01-JAN-1990, integrated into UniProtKB/Swiss-Prot.
DT 30-APR-2005, sequence version 2.
DT 07-MAR-2006, entry version 60.
DE Tyrosine-protein kinase transforming protein Src (EC 2.7.1.112) (p60-
DE Src) (v-Src) (pp60v-src).
GN Name=v-Src;
OS Avian sarcoma virus (strain S1).
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;

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CC Alpharetrovirus; unclassified Alpharetrovirus.
OK NCBI_TaxID=11881;
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=87064539; Pubmed=3097513;
RA Ikawa S., Hagino-Yamagishi K., Kawai S., Yamamoto T., Toyoshima K.;
RT "Activation of the cellular src gene by transducing retrovirus.";
RL Mol. Cell Biol. 6:2420-2428(1986).
CC CC
CC -1 FUNCTION: This phosphoprotein, required for both the initiation
CC and the maintenance of neoplastic transformation, is a protein
CC kinase that catalyzes the phosphorylation of tyrosine residues in
CC vitro.
CC -1 CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC tyrosine phosphate.
CC -1 PTM: The phosphorylated form is termed pp60v-src.
CC -1 SIMILARITY: Belongs to the Tyr protein kinase family. SRC
CC subfamily.
CC -1 SIMILARITY: Contains 1 SH2 domain.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs license
CC -----
DR PIR: A25375; TVPVSL.
DR HSSP; P00523; ZPTK.
DR SMR; P14084; 83-524.
DR InterPro; IPR000719; Prot_Kinase.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR InterPro; IPR001452; SH2.
DR InterPro; IPR001452; SH3.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR Pfam; PF07714; Pkinase_Tyr; 1.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH3; 1; 1.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRINTS; PR00452; SH3DOMAIN.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_Kinase; 1.
DR ProDom; PD000093; SH2; 1.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 1.
DR SMART; SM00219; TyrcK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00001; SH2; 1.
DR PROSITE; PS50002; SH3; 1.
KW ATP-binding; Kinase; Lipoprotein; Myristate; Nucleotide-Binding;
KW Oncogene; Phosphorylation; SH2 domain; SH3 domain; Transferase;
KW Tyrosine-protein kinase.
KV Tyrosine-protein kinase.
FT INIT_MET 0
FT CHAIN 1 567
FT FT
FT DOMAIN 80 141
FT DOMAIN 147 244
FT DOMAIN 266 519
FT NP_BIND 272 280
FT ACT_SITE 385 385
FT BINDING 294 294
FT MOD_RES 415 415
FT LIPID 1
FT SEQUENCE 567 AA; 63501 MW; EA4FCC3B195A098D CRC64;
N-myristoyl glycine (by host).
By similarity.
Tyrosine-protein kinase transforming
protein Src.
/FTId=PRO_0000088150.
SH3.
SH2.
Protein kinase.
ATP (By similarity).
Proton acceptor (By similarity).
ATP (By similarity).
Phosphotyrosine (by autocatalysis) (By
similarity).

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DR DB GSSKSKPDPQGRARRSLRPPDSTH--HGCFPASQTNPNTKAAPDTNHTPKRSFCVTATEPK 58
OY 62 LFGFNSSDVTYSPOPAGALACGVTTFVALIYYESRTETDLSPKKERLQIVANNTKADV 121
DB 59 LFGFNTSDVTYSPOPAGALACGVTTFVALIYYESRTETDLSPKKERLQIVANN----- 113
OY 122 RRGDMWLASHLSTGGTGYIPSNYYVA PSDSIQAEBWFGKITRESERLLINANPRGTFL 101
DB 114 -EGDWMLASHLTTGGTGYPISNYVAPSDSIQAEBWFGKITRESERLLINPENPGTFL 172
OY 182 VRESFTKGAYCLSYDFDNANGKLNVKHAKIRKLDSGCGFYITSRTQPSNLQQLVAAYSKEH 241
DB 173 VRESFTKGAYCLSYDFDNANGKLNVKHAKIRKLDSGCGFYITSRTQPSNLQQLVAAYSKEH 222
OY 242 ADGLCHRLITTVCPSTKPOTQGLAKDAWEIPRESLRLEVLGGCCFGEVMWGVTNGTTRVA 301
DB 223 ADGLCHRLITTVCPSTKPOTQGLAKDAWEIPRESLRLEVLGGCCFGEVMWGVTNGTTRVA 292
OY 302 IKTLKPGTMSPPAFIOEAVWMKKLHEKLVOLYAVSEERIYYEYWNMGSLDDPLKGE 361
DB 293 IKTLKPGTMSPPAFIOEAVWMKKLHEKLVRIYAAVSEERIYYEYWNMGSLDDPLKGE 352
OY 362 TGKYURLPOLVMSAOIASGMAYVERMNYVRHDDLRAANTILVGNELCVKADFGLARLIED 421
DB 353 MGKYLRLPOLVDMAQAIASGMAYVERMNYVRHDDLRAANTILVGNELCVKADFGLARLIED 412
OY 422 NEYTAROGAKFPDIKWTAPEPALYGRFTIKSDVMSFGILLTELTTKRPVPYGVWNRRELD 481
DB 413 NEYTAROGAKFPDIKWTAPEPALYGRFTIKSDVMSFGILLTELTTKRPVPYGVWNRRELD 472
OY 482 QVERGRMPCEPCESHLHLMCOCRKRPERRPTFEYLQAFLEDYFTSTEP 533
DB 473 QVERGRMPCEPCESHLHLMCOCRKMDPERPTEYLOAFLEDYFTSTEP 524

RESULT 13
O64817_9RETNR PRELIMINARY; PRT; 587 AA.
ID O64817; AC O64817; DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 28.
DE Protein-tyrosine kinase.
GN Name=src; OS Avian sarcoma virus.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Alpharetrovirus; unclassified Alpharetrovirus.
OX NCBI_TaxId=11876; [1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=PR257/16; RC MEDLINE=95016532; PubMed=7931166;
RX Yaculea B.A., Geryk J., Svoboda J., Rynditch A.V., Calochy G.,
RA Dezelle P.; "Evolution and origin of virus PR257, a recent c-src transducing
RT virus"; J. Gen. Virol. 75:2777-2781(1994).
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CC
DR EMBL, L21974; AAC37877.1; -; Genomic_DNA.
DR HSMB, P00523; 2PTRK.
DR SMK, O64817; 84-525.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006466; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001452; SH3.
DR InterPro; IPR001245; Tyr_kinase.
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DR InterPro; IPR008266; Tyr_pkinase_AS.
 DR Pfam; PF07714; Pkinase_Tyr; 1.
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 DR Pfam; PF00018; SH3; 1; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00452; SH3DOMAIN.
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 DR ProDom; PD000001; Prot_kinase; 1.
 DR ProDom; PD000093; SH2; 1.
 DR ProDom; PD000066; SH3; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00219; TYRKC; 1.
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 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 DR Kinase; Tyrosine-protein kinase.
 KW SEQUENCE 587 AA; 65779 MW; BAAC3FA44234F02 CRC64;
 Query Match 90.6%; Score 2590; DB 2; Length 587;
 Best Local Similarity 92.7%; Pred. No. 8.4e-163;
 Matches 494; Conservative 12; Mismatches 19; Indels 8; Gaps 2;

QY 1 MGSNKSAPKQASQRRRLSEPNVHGAGAFPAQSPKSPADSGHGRGSAAPVPAAP 60
 DB 1 MGSNKSAPKQPSQRRRLSEPNVHGAGAFPAQSPKSPADSGHGRGSAAPVPAAP 58
 QY 61 KLFGEFNSDPTVTSPPQAGALAGGVTFVALYDYESTRTDLSFKGERLQIVNTRKVD 120
 DB 59 KLFGEFNTSDPTVTSPPQAGALAGGVTFVALYDYESTRTDLSFKGERLQIVNTRKVD 114
 QY 121 VRGSDWLAHSLSTGCGCYIPSNVVASDSIOAEWTFGKITRRESRLILNAENPGTF 180
 DB 115 --BGDWLAHSLSTGCGCYIPSNVVASDSIOAEWTFGKITRRESRLILNAENPGTF 172
 QY 181 LVASEETTKAYCLSYSPFNAGKLVKIRKLDGSGGYTSRQFNSLQQLVAYYSK 240
 DB 173 LVASEETTKAYCLSYSPFNAGKLVKIRKLDGSGGYTSRQFNSLQQLVAYYSK 232
 QY 241 HADGLCHRLTTCVPTSPKQTOGLAKDAWEIPRESLRLEVLGCGCFGEVMGWTNGTRV 300
 DB 233 HADGLCHRLTTCVPTSPKQTOGLAKDAWEIPRESLRLEVLGCGCFGEVMGWTNGTRV 292
 QY 301 AITLTKPGTMSPAAPLOEAQVMKLRHEKLVOLYAVVSEPIYIVTEYNAKSLDPLKG 360
 DB 293 AITLTKPGTMSPAAPLOEAQVMKLRHEKLVOLYAVVSEPIYIVTEYNAKSLDPLKG 352
 QY 361 ETGKYRLPOLVMSAQISGMAYVERMNVVHDLRAANTLVGENLVCKVADFGRLRLIE 420
 DB 353 ETGKYRLPOLVMSAQISGMAYVERMNVVHDLRAANTLVGENLVCKVADFGRLRLIE 412
 QY 421 DNEYTARQAGKFPKIKTAPAPALYGRFTIKSDVMSFGILLTELTTKGRVYPGVNVREVL 480
 DB 413 DNEYTARQAGKFPKIKTAPAPALYGRFTIKSDVMSFGILLTELTTKGRVYPGVNVREVL 472
 QY 481 DQVERGYRNPCEPCESLHDLGCGCKRKEPERPFEYIQAFLDYFTSTEP 533
 DB 473 DQVERGYRNPCEPCESLHDLGCGCKRKEPERPFEYIQAFLDYFTSTEP 525

RESULT 14
 SRC_AVIST STANDARD; PRT; 556 AA.
 AC P14085;
 DT 01-JUN-1990, integrated into UniProtKB/Swiss-Prot.
 DT 30-AUG-2005, sequence version 2.
 DT 07-MAR-2006, entry version 60.
 DE Tyrosine-protein kinase transforming protein Src (BC 2.7.1.112) (p60-Src) (v-Src) (pp60v-src).
 GN Name=v-Src;
 OS Avian sarcoma virus (strain S2).

CC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
 CC Alpharetrovirus; unclassified Alpharetrovirus.
 CC NCBI_TaxID=11882;
 RN [1]
 RX NCLECTIDE SEQUENCE.
 RX MEDLINE=87064539; PubMed=3097513;
 RA Ikawa S., Hagiino-Yamagishi K., Kawai S., Yamamoto T., Toyoshima K.;
 RT "Activation of the cellular src gene by transducing retrovirus.";
 RL Mol. Cell. Biol. 6:2420-2428(1986).
 CC -1- FUNCTION: This phosphoprotein, required for both the initiation
 CC and the maintenance of neoplastic transformation, is a protein
 CC kinase that catalyzes the phosphorylation of tyrosine residues in
 CC vitro.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
 CC tyrosine phosphate.
 CC -1- PTM: The phosphorylated form is termed p60v-src.
 CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
 CC subfamily.
 CC -1- SIMILARITY: Contains 1 SH2 domain.
 CC -1- SIMILARITY: Contains 1 SH3 domain.
 CC
 CC -----
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DR PIR; B25375; TVFV82.
 DR HSSP; P00523; 2PTK.
 DR SMR; P14085; 83-532.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
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 DR InterPro; IPR001452; SH3.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR InterPro; IPR008266; Tyr_pkinase_AS.
 DR Pfam; PF07714; Pkinase_Tyr; 1.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR ProDom; PD000093; SH2; 1.
 DR ProDom; PD000066; SH3; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00219; TYRKC; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 KW ATP-binding; Kinase; Lipoprotein; Myristate; Nucleotide-binding;
 KW Oncogene; Phosphorylation; SH2 domain; SH3 domain; Transferase;
 KW Tyrosine-protein kinase.
 FT INIT MET 0
 FT CHAIN 1 556
 FT
 FT DOMAIN 80 141
 FT DOMAIN 147 244
 FT DOMAIN 266 519
 FT NE BIND 272 280
 FT ACT SITE 284 385
 FT BINDING 294 294
 FT MOD_RES 415 415
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 FT LIPID 1 1
 FT
 SO SEQUENCE 556 AA; 62452 MW; 0F7A904CA3FEA9CC CRC64;
 Query Match 90.1%; Score 2576; DB 1; Length 556;
 Best Local Similarity 88.7%; Pred. No. 6.5e-162;
 Matches 494; Conservative 16; Mismatches 21; Indels 26; Gaps 3;

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QY 2 GSNKSKPKDASOBRRSLSESENVHAGAGAPASOTPSKPSASADGHRGSAFVPAPEPK 61
DB 1 GSSKSKPKDPSQRRRSLEPPDSTH--HGFPASOTPEKTAAPDHRTPSSFGTVATEPK 58
QY 62 LFGSPNSDPVTSQBPAGALAGGVTTFVALYDYSESRTETDLSFKKGRLOQIVNNTKRYDV 121
DB 59 LFGSPNSDPVTSQBPAGALAGGVTTFVALYDYSESRTETDLSFKKGRLOQIVNNT 113
QY 122 REGDWMLHSLSTGQGYIPSNVAPSDSIQAEWYFGKITTRESEKLLIENPRTGTF 181
DB 114 -EGDWMVLSHSLTGTGTGYIPSNVAPSDSIQAEWYFGKITTRESEKLLIENPRTGTF 172
QY 182 VRESEKTKGAYCISVSPDNAGKINVKHYIKRKIDSGFPYITSTORNSIQOLVAYYSKH 241
DB 173 VRESEKTKGAYCISVSPDNAGKINVKHYIKRKIDSGFPYITSTORNSIQOLVAYYSKH 232
QY 242 ADGLCHRLTYVCPSTKSPQTOGLAKDAWEIPRESRLRLVKKLQGGCFGVMWGTNGTTRVA 301
DB 233 ADGLCHRLTYVCPSTKSPQTOGLAKDAWEIPRESRLRLVKKLQGGCFGVMWGTNGTTRVA 292
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DB 293 IKTLKPGTMSPEAFLOAQVWKLRHKKLVQLYAVASEEPIYIVTEYMNKSLIDFLKGE 352
QY 362 TGKYLRLPOLVDMASQIASCMAVYERNNVYARDLRAANILVGENLNCVKADFGIARLIED 421
DB 353 MGKYLRLPOLVDMASQIASCMAVYERNNVYARDLRAANILVGENLNCVKADFGIARLIED 412
QY 422 NEXTAROGAKFPIKMTAPEALYGRFTIKSDVMSFGILLTELTKGRVPYPCGMVNRVLD 481
DB 413 NEXTAROGAKFPIKMTAPEALYGRFTIKSDVMSFGILLTELTKGRVPYPCGMVNRVLD 472
QY 482 QVERGYMPCPEPCESLHDLMCQWKEPERPTEFYLOAFLEDYF----- 528
DB 473 QVERGYMPCPEPCESLHDLMCQWKEPERPTEFYLOAFLEDYGIILAWTPEWEDKQS 532
QY 529 -----TSTEPQYQGEN 540
DB 533 GPRGETASNKQERGED 549

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RA Feng S., Chen J.K., Yu H., Simon J.A., Schreiber S.L.;
RT "Two binding orientations for peptides to the Src SH3 domain:
RL development of a general model for SH3-ligand interactions.";
CC Science 266:1241-1247(1994).
CC -1- FUNCTION: This phosphoprotein, required for both the initiation
CC and the maintenance of neoplastic transformation, is a protein
CC kinase that catalyzes the phosphorylation of tyrosine residues in
CC vitro.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC tyrosine phosphate.
CC -1- PTM: The phosphorylated form is termed pp60v-src.
CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
CC subfamily.
CC -1- SIMILARITY: Contains 1 SH2 domain.
CC -1- SIMILARITY: Contains 1 SH3 domain.
CC -----
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CC -----
DB EMBL, K00928; AAA42565.1; -; Genomic_RNA.
DB PDB, 1QWE; NMR; A=80-139.
DB PDB, 1QWE; NMR; A=80-139.
DB SMR; P00525; 83-515.
DB LinkHub; P00525; -.
DB InterPro; IPR000719; Prot_kinase.
DB InterPro; IPR002290; Ser_Thr_kinase.
DB InterPro; IPR000980; SH2.
DB InterPro; IPR001452; SH3.
DB InterPro; IPR001245; Tyr_kinase.
DB InterPro; IPR008265; Tyr_kinase_AS.
DB Pfam; PR07714; Kinase_Tyr; 1.
DB Pfam; PR00017; SH2; 1.
DB Pfam; PR00018; SH3_1; 1.
DB PRINTS; PR00401; SH2DOMAIN.
DB PRINTS; PR00452; SH3DOMAIN.
DB PRINTS; PR00109; TYRKINASE.
DB ProDom; PD000001; Prot_kinase; 1.
DB ProDom; PD000093; SH2; 1.
DB ProDom; PD000066; SH3; 1.
DB SMART; SM00252; SH2; 1.
DB SMART; SM00326; SH3; 1.
DB SMART; SM00219; TyrKc; 1.
DB PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DB PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DB PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DB PROSITE; PS50001; SH2; 1.
DB PROSITE; PS50002; SH3; 1.
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KW Transferase; Tyrosine-protein kinase.
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FT CHAIN 1 525
FT Tyrosine-protein kinase transforming
FT protein Src.
FT /Ftrid=PRO_0000088147.
FT SH3.
FT DOMAIN 147 141
FT DOMAIN 147 244
FT DOMAIN 266 516
FT NP BIND 272 280
FT ACT SITE 385 385
FT BINDING 294 294
FT WOD_RES 415 415
FT LIPID 1 1
FT STRAND 85 87
FT STRAND 91 91
FT TURN 96 97
FT STRAND 98 98
FT STRAND 101 101
FT TURN 103 104
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FT STRAND 117 122
FT TURN 123 126
FT STRAND 127 132

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RESULT 15
SRC AVISR STANDARD; PRT; 525 AA.
ID SRC AVISR P00525;
AC P00525;
DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT 30-AUG-2005, sequence version 2.
DT 07-MAR-2006, entry version 72.
DE Tyrosine-protein kinase transforming protein Src (BC 2.7.1.112) (p60-
DE Src) (v-Src) (pp60v-src).
GN Name=v-Src;
OS Avian sarcoma virus (strain RASV1441).
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Alpharetrovirus; unclassified Alpharetrovirus.
OC NCBI_TaxID=11894;
OX [1]
RN NUCLEOTIDE SEQUENCE [GENOMIC RNA].
RP MEDLINE=83059858; PubMed=6292477;
RX Takeya T., Feldman R.A., Hanafusa H.;
RT "DNA sequence of the viral and cellular src gene of chickens. 1.
RT Complete nucleotide sequence of an EcoRI fragment of recovered avian
RT sarcoma virus which codes for gp37 and pp60src.";
RL J. Virol. 44:1-11(1982).

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RP PHOSPHORYLATION SITE TYR-415.
RX MEDLINE=81220979; PubMed=6264320;
RA Neil J.C., Gnyedael J., Vogt P.K., Smart J.E.;
RT "Homologous tyrosine phosphorylation sites in transformation-specific
RT gene products of distinct avian sarcoma viruses.";
RL Nature 291:675-677(1981).
RN [3]
RP STRUCTURE BY NMR OF 84-139.
RX MEDLINE=95063992; PubMed=7526465;

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FT HELIX 133 135
FT STRAND 136 138
SQ SEQUENCE 525 AA; 58747 MW; 0683903F8038E04C CRC64;

Query Match 87.8%; Score 2510; DB 1; Length 525;
Best Local Similarity 91.8%; Pred. No. 1,46-157;
Matches 480; Conservative 14; Mismatches 21; Indels 8; Gaps 2;

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   59 LFGGFNSDVTVSQFORAGALAGVTTFFVALYDYESRTETDLSFKKGERLQIVNTRKDV 121
   122 REGDWMLAHSLSTGQCYIPSNVYAPSDSIQAEWYFGKITRRESERLILNAENPRGTFL 181
   114 -EGDWMLAHSLTGTQCYIPSNVYAPSDSIQAEWYFGKITRRESERLILNPNPRGTFL 172
   182 VRESETTKGAYCISVSDPDNAKGLNVGHYKIRKLDGSGFYITSRTOPNSLQOLVAYYSK 241
   173 VRESETTKGAYCISVSDPDNAKGLNVGHYKIRKLDGSGFYITSRTOPNSLQOLVAYYSK 232
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   362 TGYLRLPOLVDMASQIASGMAYVERNNYVRDLRAANILVGENLVCKVADFGIARLIED 421
   353 MGKYLRLPOLVDMASQIASGMAYVERNNYVRDLRAANILVGENLVCKVADFGIARLIED 412
   422 NEXYTAQGAKEPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVYPGMVNRVLD 481
   413 NEXYTAQGAKEPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVYPGMONGEVLD 472
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   473 RVERGYRMPCPPCPESLHDLMLCCQWRKEPERPTEFYLOAFL 515
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Job time : 158.049 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 5, 2006, 17:15:49 ; Search time 31.0766 Seconds

(Without alignments)
1523.786 Million cell updates/sec

Title: US-10-691-079-3

Perfect score: 2859
Sequence: 1 MGSNKSXPKKASQRRSLRP.....AFLEDYRTSTPEYQPGENL 541Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

- 1: /EMC_Celerra_SIDS3/prodata/2/1aa/5.COMB.pep:*
- 2: /EMC_Celerra_SIDS3/prodata/2/1aa/6.COMB.pep:*
- 3: /EMC_Celerra_SIDS3/prodata/2/1aa/7.COMB.pep:*
- 4: /EMC_Celerra_SIDS3/prodata/2/1aa/H.COMB.pep:*
- 5: /EMC_Celerra_SIDS3/prodata/2/1aa/PCTUS.COMB.pep:*
- 6: /EMC_Celerra_SIDS3/prodata/2/1aa/RR.COMB.pep:*
- 7: /EMC_Celerra_SIDS3/prodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2778.5	97.2	536	1 US-07-820-011A-4	Sequence 4, Appl
2	2778.5	97.2	536	2 US-08-426-509A-13	Sequence 13, Appl
3	2778.5	97.2	536	2 US-08-232-545-13	Sequence 13, Appl
4	2778.5	97.2	536	2 US-09-444-711A-2	Sequence 2, Appl
5	2778.5	97.2	536	2 US-09-929-266-10	Sequence 10, Appl
6	2778.5	97.2	536	2 US-09-977-261-13	Sequence 13, Appl
7	2778.5	97.2	536	5 PCT-US93-00445-4	Sequence 4, Appl
8	2778.5	97.2	536	5 PCT-US93-05008-13	Sequence 13, Appl
9	2778.5	97.2	537	2 US-09-949-016-10282	Sequence 10282, A
10	2745.5	96.0	530	2 US-09-444-711A-4	Sequence 4, Appl
11	2645	92.5	533	1 US-07-820-011A-2	Sequence 3, Appl
12	2642	92.4	533	1 US-07-820-011A-2	Sequence 2, Appl
13	2642	92.4	533	5 PCT-US93-00445-2	Sequence 2, Appl
14	2111	73.8	543	2 US-08-426-509A-14	Sequence 14, Appl
15	2111	73.8	543	2 US-08-232-545-14	Sequence 14, Appl
16	2111	73.8	543	2 US-09-470-881-8	Sequence 8, Appl
17	2111	73.8	543	2 US-09-538-092-870	Sequence 870, App
18	2111	73.8	543	2 US-09-977-261-14	Sequence 14, Appl
19	2111	73.8	543	5 PCT-US95-05008-14	Sequence 14, Appl
20	2103	73.6	541	2 US-09-864-291-20	Sequence 20, Appl
21	1931.5	67.6	532	1 US-08-594-447-1	Sequence 1, Appl
22	1931.5	67.5	532	1 US-08-665-647-1	Sequence 1, Appl
23	1929.5	67.5	536	2 US-08-426-509A-12	Sequence 12, Appl
24	1929.5	67.5	536	2 US-08-232-545-12	Sequence 12, Appl
25	1929.5	67.5	536	2 US-09-977-261-12	Sequence 12, Appl
26	1929.5	67.5	536	5 PCT-US95-05008-12	Sequence 12, Appl

27	1928	67.4	537	2 US-08-426-509A-11	Sequence 11, Appl
28	1928	67.4	537	2 US-08-232-545-11	Sequence 11, Appl
29	1928	67.4	537	2 US-09-977-261-11	Sequence 11, Appl
30	1928	67.4	537	5 PCT-US95-05008-11	Sequence 11, Appl
31	1923	67.3	536	2 US-09-538-092-859	Sequence 859, App
32	1920	67.2	537	2 US-09-771-161A-212	Sequence 212, App
33	1920	67.2	537	2 US-09-771-161A-213	Sequence 213, App
34	1847.5	64.6	529	2 US-08-426-509A-15	Sequence 15, Appl
35	1847.5	64.6	529	2 US-08-232-545-15	Sequence 15, Appl
36	1847.5	64.6	529	2 US-09-538-092-885	Sequence 885, App
37	1847.5	64.6	529	2 US-09-977-261-15	Sequence 15, Appl
38	1847.5	64.6	529	5 PCT-US95-05008-15	Sequence 15, Appl
39	1744	61.0	485	2 US-10-094-749-2726	Sequence 2726, Ap
40	1520.5	53.2	573	2 US-09-949-016-10415	Sequence 10415, A
41	1520	53.2	505	2 US-08-426-509A-17	Sequence 17, Appl
42	1520	53.2	505	2 US-08-232-545-17	Sequence 17, Appl
43	1520	53.2	505	2 US-09-977-261-17	Sequence 17, Appl
44	1520	53.2	505	5 PCT-US95-05008-17	Sequence 17, Appl
45	1462.5	51.2	512	2 US-08-426-509A-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-07-820-011A-4
Sequence 4, Application US/07820011A
Patent No. 5336615
GENERAL INFORMATION:
APPLICANT: Bell, Leonard
APPLICANT: Madri, Joseph A.
APPLICANT: Warren, Stephen L.
APPLICANT: Luthinger, Daniel J.
TITLE OF INVENTION: Genetically Engineered
TITLE OF INVENTION: Endothelial Cells Exhibiting Enhanced
TITLE OF INVENTION: Migration
TITLE OF INVENTION: and Plasminogen Activator Activity
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maurice M. Klee
STREET: 1951 Burr Street
CITY: Fairfield
STATE: Connecticut
COUNTRY: USA
ZIP: 06430
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb storage
COMPUTER: IBM PC XT
OPERATING SYSTEM: PC-DOS/MS-DOS 2.10
SOFTWARE: Displaywrite 3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/820, 011A
FILING DATE: 19920106
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399
REFERENCE/DOCKET NUMBER: LB-101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255 1400
TELEFAX: (203) 254 1101
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 536 amino acids
TYPE: AMINO ACID
TOPOLOGY: Linear
MOLECULE TYPE: Protein
HYPOTHETICAL: No
FRAGMENT TYPE: Complete Sequence
ORIGINAL SOURCE:
ORGANISM: Homo sapien
PUBLICATION INFORMATION:
AUTHORS: Anderson, Stephen K.

/ AUTHORS: Gibbs, Carol P.
 / AUTHORS: Tanaka, Akio
 / AUTHORS: Kung, Heing-jien
 / AUTHORS: Fujita, Donald J.
 / TITLE: Human Cellular src Gene:
 / TITLE: Nucleotide Sequence and Derived Amino
 / TITLE: Acid Sequence of the Region Coding for
 / TITLE: the Carboxy-Terminal Two-Thirds of
 / TITLE: pp60c-src
 / JOURNAL: Molecular and Cellular Biology
 / VOLUME: 5
 / ISSUE: 5
 / PAGES: 1122-1129
 / DATE: May, 1985
 / PUBLICATION INFORMATION:
 / AUTHORS: Tanaka, Akio
 / AUTHORS: Gibbs, Carol P.
 / AUTHORS: Arthur, Richard R.
 / AUTHORS: Anderson, Stephen K.
 / AUTHORS: Kung, Heing-jien
 / AUTHORS: Fujita, Donald J.
 / TITLE: DNA Sequence Encoding the
 / TITLE: Amino-Terminal Region of the Human c-src
 / TITLE: Protein: Implications of Sequence
 / TITLE: Divergence among src-Type Kinase
 / TITLE: Oncogenes
 / JOURNAL: Molecular and Cellular Biology
 / VOLUME: 7
 / ISSUE: 5
 / PAGES: 1978-1983
 / DATE: May, 1987
 / US-07-820-011A-4

Query Match 97.2%; Score 2778.5; DB 1; Length 536;
 Best Local Similarity 97.6%; Pred. No. 2.6e-214;
 Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;

QY 1 MGSNKSXPDAOSRRSLSPSENVHGA-GGAPASOTPSKPSADGHRPSAFAVPPAAE 59
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 DB 61 PKLFGFNSDVTSPORAGALAGVTFVALYDYESRTETDLSFKKGERLQIVNNT--- 117
 QY 120 DVREGDWMLAHSLSTGQTYIPSNVYAPSDSIQAEEMYPGKITRRESERLLNAENPRGT 179
 DB 118 ---EGDWMLAHSLSTGQTYIPSNVYAPSDSIQAEEMYPGKITRRESERLLNAENPRGT 174
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 DB 175 FLVRESEITTKGAYCISVSPFDNAKGLNVKHYKIRKLDGSGFYITSTRQFNSLQOLVAYYS 234
 QY 240 KKAADGLCHRLTTCPTSKPTQGLAKDAWEIPRESRLRLEVKLGQCGFGEVWMTNGTTR 299
 DB 235 KKAADGLCHRLTTCPTSKPTQGLAKDAWEIPRESRLRLEVKLGQCGFGEVWMTNGTTR 294
 QY 300 VALKITLKEGTMSPEALQEAQVWKKLRHEKLVOLYAVVSEEPYIYTEYNNKSLLDPLK 359
 DB 295 VALKITLKEGTMSPEALQEAQVWKKLRHEKLVOLYAVVSEEPYIYTEYNNKSLLDPLK 354
 QY 360 GETGKTLRLPOLVDMSAOIASGMAVYERMYVARDIRANILVGENLVCAVDFGLARLI 419
 DB 355 GETGKTLRLPOLVDMSAOIASGMAVYERMYVARDIRANILVGENLVCAVDFGLARLI 414
 QY 420 EDNEYTAROGAKPEPKMTAPEALYGRFTIKSDVMSFGILLTELTKGRVYPGMVNRREV 479
 DB 415 EDNEYTAROGAKPEPKMTAPEALYGRFTIKSDVMSFGILLTELTKGRVYPGMVNRREV 474
 QY 480 LDOVERGYMPCEPPECPSLHDLMLCCQWKKEPERFTFYLQAFLEDYFTSTPEYQOPGE 539
 DB 475 LDOVERGYMPCEPPECPSLHDLMLCCQWKKEPERFTFYLQAFLEDYFTSTPEYQOPGE 534

QY 540 NL 541
 DB 535 NL 536

RESULT 2
 US-08-426-509A-13
 / Sequence 13, Application US/08426509A
 / Patent No. 6326469
 / GENERAL INFORMATION:
 / APPLICANT: Ullrich, Axel
 / APPLICANT: Glehizky, Mikhail
 / APPLICANT: Sures, Imran G.
 / TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN
 / TITLE OF INVENTION: TYROSINE KINASES
 / NUMBER OF SEQUENCES: 21
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Pennie & Edmonds
 / STREET: 1155 Avenue of the Americas
 / CITY: New York,
 / STATE: NY
 / COUNTRY: USA
 / ZIP: 10036-2711
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Diskette
 / COMPUTER: IBM Compatible
 / OPERATING SYSTEM: DOS
 / SOFTWARE: FastSeq Version 2.0
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/426,509A
 / FILING DATE: 21-APR-1995
 / CLASSIFICATION: 435
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: 08/232,545
 / FILING DATE:
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Coruzzi, Laura A
 / REGISTRATION NUMBER: 30,742
 / REFERENCE/DOCKET NUMBER: 7683-0074-999
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: 212-790-9090
 / TELEFAX: 212-869-9741
 / TELEX: 66141 PENNIE
 / INFORMATION FOR SEQ ID NO: 13:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 536 amino acids
 / TYPE: amino acid
 / STRANDEDNESS: unknown
 / TOPOLOGY: unknown
 / MOLECULE TYPE: No. 6326469e
 / US-08-426-509A-13

Query Match 97.2%; Score 2778.5; DB 2; Length 536;
 Best Local Similarity 97.6%; Pred. No. 2.6e-214;
 Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;

QY 1 MGSNKSXPDAOSRRSLSPSENVHGA-GGAPASOTPSKPSADGHRPSAFAVPPAAE 59
 DB 1 MGSNKSXPDAOSRRSLSPSENVHGA-GGAPASOTPSKPSADGHRPSAFAVPPAAE 60
 QY 60 PKLFGFNSDVTSPORAGALAGVTFVALYDYESRTETDLSFKKGERLQIVNTRKY 119
 DB 61 PKLFGFNSDVTSPORAGALAGVTFVALYDYESRTETDLSFKKGERLQIVNNT--- 117
 QY 120 DVREGDWMLAHSLSTGQTYIPSNVYAPSDSIQAEEMYPGKITRRESERLLNAENPRGT 179
 DB 118 ---EGDWMLAHSLSTGQTYIPSNVYAPSDSIQAEEMYPGKITRRESERLLNAENPRGT 174
 QY 180 FLVRESEITTKGAYCISVSPFDNAKGLNVKHYKIRKLDGSGFYITSTRQFNSLQOLVAYYS 239
 DB 175 FLVRESEITTKGAYCISVSPFDNAKGLNVKHYKIRKLDGSGFYITSTRQFNSLQOLVAYYS 234
 QY 240 KKAADGLCHRLTTCPTSKPTQGLAKDAWEIPRESRLRLEVKLGQCGFGEVWMTNGTTR 299

Db 235 KHAADGLCHRLTTCVPTSKPQTQGLAKDAMEIPRESLBLEVLCGGCGCEGVMWGTMGTTR 294
Qy 300 VAIKTLKPGTMSPEAFLOEAQVMKKLRHEKLVOLYAVVSEBPIYIVTEYNNKSGLLDPLK 359
Db 295 VAIKTLKPGTMSPEAFLOEAQVMKKLRHEKLVOLYAVVSEBPIYIVTEYNNKSGLLDPLK 354
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Db 355 GETGKYLRPLQVLVMSAQIASGMAYVERMNYVHRDLPAANTLVGENLVCKVADFGLARLI 414
Qy 420 EDNEYTAROGAKFPITKMTAPEALYGRFTIKSDVMSFGILLTELTTGKRVYPCGMVNRV 479
Db 415 EDNEYTAROGAKFPITKMTAPEALYGRFTIKSDVMSFGILLTELTTGKRVYPCGMVNRV 474
Qy 480 LDQYERGTRMPCPEPCESLHDLQCQCKRKEBERPTEFYLAQLEDFYFTSTEPQYQGE 539
Db 475 LDQYERGTRMPCPEPCESLHDLQCQCKRKEBERPTEFYLAQLEDFYFTSTEPQYQGE 534
Qy 540 NL 541
Db 535 NL 536
RESULT 3
US-08-232-545-13
; Sequence 13, Application US/08232545
; Patent No. 6506578
; GENERAL INFORMATION:
; APPLICANT: Ullrich, Axel
; APPLICANT: Gishizsky, Mikhail
; APPLICANT: Sures, Iman G.
; TITLE OF INVENTION: No. 6506578e1 Megakaryocytic Protein Tyrosine
; TITLE OF INVENTION: Kinases
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Penile & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,545
; FILING DATE: 22-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Cortuzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7683-050
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)790-9090
; TELEFAX: (212)869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 536 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-232-545-13

Query Match 97.2%; Score 2778.5; DB 2; Length 536;
Best Local Similarity 97.6%; Pred. No. 2.6e-214;
Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;

Qy 1 MGSNKSXPKQASQRRRLSEPSENVHGA-GGAFPASQTPSPKPSADGHRGSPAAAFVPPAAE 59

Db 1 MGSNKSXPKQASQRRRLSEPSENVHGA-GGAFPASQTPSPKPSADGHRGSPAAAFVPPAAE 60
Qy 60 PKLFGFNSSDVTYTPQAGALAGVTTFFVALYDSERTETDLSFKKGERLQIVNTRKV 119
Db 61 PKLFGFNSSDVTYTPQAGALAGVTTFFVALYDSERTETDLSFKKGERLQIVNTRKV 117
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Db 118 ---BGDWWLAHSLSTGQGTGTPSNYVAPSPDSIQAEENYFGKLTRESEBRLLNENPCT 174
Qy 180 FLVASETTGAYCLASDSDPNAGLWKKYKIKLDSGGFYTSRTQFNSLQOLVAYYS 239
Db 175 FLVASETTGAYCLASDSDPNAGLWKKYKIKLDSGGFYTSRTQFNSLQOLVAYYS 234
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Db 235 KHAADGLCHRLTTCVPTSKPQTQGLAKDAMEIPRESLBLEVLCGGCGCEGVMWGTMGTTR 294
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Db 295 VAIKTLKPGTMSPEAFLOEAQVMKKLRHEKLVOLYAVVSEBPIYIVTEYNNKSGLLDPLK 354
Qy 360 GETGKYLRPLQVLVMSAQIASGMAYVERMNYVHRDLPAANTLVGENLVCKVADFGLARLI 419
Db 355 GETGKYLRPLQVLVMSAQIASGMAYVERMNYVHRDLPAANTLVGENLVCKVADFGLARLI 414
Qy 420 EDNEYTAROGAKFPITKMTAPEALYGRFTIKSDVMSFGILLTELTTGKRVYPCGMVNRV 479
Db 415 EDNEYTAROGAKFPITKMTAPEALYGRFTIKSDVMSFGILLTELTTGKRVYPCGMVNRV 474
Qy 480 LDQYERGTRMPCPEPCESLHDLQCQCKRKEBERPTEFYLAQLEDFYFTSTEPQYQGE 539
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Qy 540 NL 541
Db 535 NL 536
RESULT 4
US-09-444-711A-2
; Sequence 2, Application US/09444711A
; Patent No. 6764633
; GENERAL INFORMATION:
; APPLICANT: Yeatman, Timothy J.
; APPLICANT: Itby, Rosalyn B.
; TITLE OF INVENTION: Mutated SRC Oncogene Composition and Methods
; FILE REFERENCE: USF-1136
; CURRENT APPLICATION NUMBER: US/09/444,711A
; CURRENT FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)_(536)
; OTHER INFORMATION: amino acid sequence of non-receptor tyrosine kinase encoded
; OTHER INFORMATION: by the normal c-Src coding region
US-09-444-711A-2

Query Match 97.2%; Score 2778.5; DB 2; Length 536;
Best Local Similarity 97.6%; Pred. No. 2.6e-214;
Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;

Qy 1 MGSNKSXPKQASQRRRLSEPSENVHGA-GGAFPASQTPSPKPSADGHRGSPAAAFVPPAAE 59

Db 1 MGSNKSXPKQASQRRRLSEPSENVHGA-GGAFPASQTPSPKPSADGHRGSPAAAFVPPAAE 60

Qy 119

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Db 61 PKLFGFNSSDVTYTSQORAGPLAGGVTTFVALYDYSRTETDLSFKKGERLQIVNNT --- 117
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Db 118 ---EGDWMHLAHSISTGQTGYIPSNVYAPSDSIQAEWYFGKTRRESERLLNAENPRGT 174
Qy 180 FLVRESEETTKGAYCLASVSDPDNAKGLNVGHYKIRKLDGSGFYITSTRTOFNSLQOLVAYYS 239
Db 175 FLVRESEETTKGAYCLASVSDPDNAKGLNVGHYKIRKLDGSGFYITSTRTOFNSLQOLVAYYS 234
Qy 240 KHAADGLCHRLITVTCPTSKPQTQGLANDAMEIPRESLRLEVKLGQCGFGEVWMTGNQTTT 299
Db 235 KHAADGLCHRLITVTCPTSKPQTQGLANDAMEIPRESLRLEVKLGQCGFGEVWMTGNQTTT 294
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Qy 360 GETGKTLRLPOLVDMASQIASGMAYVERMYVHRDLRAANILVGENLVCKVADFGIARLI 419
Db 355 GETGKTLRLPOLVDMASQIASGMAYVERMYVHRDLRAANILVGENLVCKVADFGIARLI 414
Qy 420 EDNEYTAROGAKFPIMKTAPBAALYGRFTIKSDVMSFGILLTELTTKGRVPPGMVNRREV 479
Db 415 EDNEYTAROGAKFPIMKTAPBAALYGRFTIKSDVMSFGILLTELTTKGRVPPGMVNRREV 474
Qy 480 LDQVERGYMPCBPCEPESLHDLCCQWKKEPBERPFEYLOAFLEDYTSTBPQYOPGB 539
Db 475 LDQVERGYMPCBPCEPESLHDLCCQWKKEPBERPFEYLOAFLEDYTSTBPQYOPGB 534
Qy 540 NL 541
Db 535 NL 536
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RESULT 5
US-09-929-266-10
; Sequence 10, Application US/09929266
; Patent No. 6824981
; GENERAL INFORMATION:
; APPLICANT: Brian T. Chait
; APPLICANT: Darin R. Lacieme
; APPLICANT: Paul M. Lizardi
; APPLICANT: Eric S. Kershner
; APPLICANT: Jon S. Morrow
; APPLICANT: Matthew E. Roth
; APPLICANT: Kevin J. McConnell
; TITLE OF INVENTION: ULTRA-SENSITIVE DETECTION SYSTEMS
; FILE REFERENCE: 01173.000302
; CURRENT APPLICATION NUMBER: US/09/929,266
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/224,939
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/283,498
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FaalSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-929-266-10
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Query Match 97.2%; Score 2778.5; DB 2; Length 536;
Best Local Similarity 97.6%; Pred. No. 2.6e-214;
Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;
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Db 235 KHAADGLCHRLITVTCPTSKPQTQGLANDAMEIPRESLRLEVKLGQCGFGEVWMTGNQTTT 294
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Db 295 VAIKTLKPGTMSPEAFLOEAQVWKLRHEKLVOLYAVVSEBPIYIYTEYMSKSLDPLK 354
Qy 360 GETGKTLRLPOLVDMASQIASGMAYVERMYVHRDLRAANILVGENLVCKVADFGIARLI 419
Db 355 GETGKTLRLPOLVDMASQIASGMAYVERMYVHRDLRAANILVGENLVCKVADFGIARLI 414
Qy 420 EDNEYTAROGAKFPIMKTAPBAALYGRFTIKSDVMSFGILLTELTTKGRVPPGMVNRREV 479
Db 415 EDNEYTAROGAKFPIMKTAPBAALYGRFTIKSDVMSFGILLTELTTKGRVPPGMVNRREV 474
Qy 480 LDQVERGYMPCBPCEPESLHDLCCQWKKEPBERPFEYLOAFLEDYTSTBPQYOPGB 539
Db 475 LDQVERGYMPCBPCEPESLHDLCCQWKKEPBERPFEYLOAFLEDYTSTBPQYOPGB 534
Qy 540 NL 541
Db 535 NL 536
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RESULT 6
US-09-977-261-13
; Sequence 13, Application US/09977261
; Patent No. 6908984
; GENERAL INFORMATION:
; APPLICANT: ULIRICH, AXEL
; APPLICANT: GISHIZKY, MIKHAIL
; APPLICANT: SURES, IRMINGARD
; TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES
; FILE REFERENCE: 038602/1259
; CURRENT APPLICATION NUMBER: US/09/977,261
; PRIOR FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 08/232,545
; PRIOR FILING DATE: 1994-04-22
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-977-261-13
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Query Match 97.2%; Score 2778.5; DB 2; Length 536;
Best Local Similarity 97.6%; Pred. No. 2.6e-214;
Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;
Qy 1 MGSNKSXPDAQORRRSLSEPSENVHGA-GGAPPASQTPSKPASADGHRGSAAFVPPAAE 59
Db 1 MGSNKSXPDAQORRRSLSEPSENVHGA-GGAPPASQTPSKPASADGHRGSAAFVPPAAE 60
Qy 60 PKLFGFNSSDVTYTSQORAGALAGVTTFVALYDYSRTETDLSFKKGERLQIVNNTKRV 119
Db 61 PKLFGFNSSDVTYTSQORAGPLAGGVTTFVALYDYSRTETDLSFKKGERLQIVNNT --- 117
Qy 120 DVREGDWMHLAHSISTGQTGYIPSNVYAPSDSIQAEWYFGKTRRESERLLNAENPRGT 179
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Db 118 ---BGDMWLAHSLSTGQGYIIPSNYVAPSDSIQAEWYFGKITRRESERLLLNENRGCT 174
QY 180 FLVRESETTGAYCLSVSDPDNAKGLVVKYIKRLDSGCFYITSRTQFNSLQOLVAYYS 239
Db 175 FLVRESETTGAYCLSVSDPDNAKGLVVKYIKRLDSGCFYITSRTQFNSLQOLVAYYS 234
QY 240 KHAADGLCHRLITTVCTPSTKPTQGLAKDAMEIPRESLLEVLAGGCGGCEGVMGTMNGTTR 299
Db 235 KHAADGLCHRLITTVCTPSTKPTQGLAKDAMEIPRESLLEVLAGGCGGCEGVMGTMNGTTR 294
QY 300 VAIKTLKPGTMSPEAFIOEAQVMKGLRHEKLVOLYAVVSEEPYITVEYNNKGSLLDPLK 359
Db 295 VAIKTLKPGTMSPEAFIOEAQVMKGLRHEKLVOLYAVVSEEPYITVEYNNKGSLLDPLK 354
QY 360 GETGKYLRPLQVLVDMASQIASGMAVVERMNVYHRDLRAANILVGENIVCKVADGLARLI 419
Db 355 GETGKYLRPLQVLVDMASQIASGMAVVERMNVYHRDLRAANILVGENIVCKVADGLARLI 414
QY 420 EDNEYTARQGAKEPKIKWTAPALYGRFTIKSDVMSFGILLTTLTGKRVYPGMNVREV 479
Db 415 EDNEYTARQGAKEPKIKWTAPALYGRFTIKSDVMSFGILLTTLTGKRVYPGMNVREV 474
QY 480 LDQVERGYRMPCEPCESLHDLMCQCKRKEPERPTEFYLAFLDYFTSTBPQYQPG 539
Db 475 LDQVERGYRMPCEPCESLHDLMCQCKRKEPERPTEFYLAFLDYFTSTBPQYQPG 534
QY 540 NL 541
Db 535 NL 536

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RESULT 7
PCT-US93-00445-4
; Sequence 4, Application PC/TUS9300445
; GENERAL INFORMATION:
; APPLICANT: Bell, Leonard
; APPLICANT: Madri, Joseph A.
; APPLICANT: Warren, Stephen L.
; APPLICANT: Luthinger, Daniel J.
; TITLE OF INVENTION: Genetically Engineered
; TITLE OF INVENTION: Endothelial Cells
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Maurice M. Klee
; STREET: 1951 Burr Street
; CITY: Fairfield
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06430
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 760 Kb storage
; COMPUTER: DELL 486/50
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: Displaywrite 3
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/00445
; FILING DATE: 19930105
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/820, 011
; FILING DATE: 06-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Klee, Maurice M.
; REGISTRATION NUMBER: 30,399
; REFERENCE/DOCKET NUMBER: ALX-101PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203) 253 1400
; TELEFAX: (203) 254 1101
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 536 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: Linear

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; MOLECULE TYPE: Protein
; HYPOTHETICAL: No
; FRAGMENT TYPE: Complete Sequence
; ORIGINAL SOURCE:
; ORGANISM: Homo sapien
; PUBLICATION INFORMATION:
; AUTHORS: Anderson, Stephen K.
; AUTHORS: Gibbs, Carol P.
; AUTHORS: Tanaka, Akio
; AUTHORS: Kung, Hsing-Jien
; TITLE: Human Cellular src Gene:
; TITLE: Nucleotide Sequence and Derived Amino
; TITLE: Acid Sequence of the Region Coding for
; TITLE: the Carboxy-Terminal Two-Thirds of
; JOURNAL: Molecular and Cellular Biology
; VOLUME: 5
; ISSUE: 5
; PAGES: 1122-1129
; DATE: May, 1985
; PUBLICATION INFORMATION:
; AUTHORS: Tanaka, Akio
; AUTHORS: Gibbs, Carol P.
; AUTHORS: Arthur, Richard R.
; AUTHORS: Anderson, Stephen K.
; AUTHORS: Kung, Hsing-Jien
; TITLE: DNA Sequence Encoding the
; TITLE: Amino-Terminal Region of the Human c-src
; TITLE: Protein: Implications of Sequence
; TITLE: Divergence among src-Type Kinase
; TITLE: Oncogenes
; JOURNAL: Molecular and Cellular Biology
; VOLUME: 7
; ISSUE: 5
; PAGES: 1978-1983
; DATE: May, 1987
; PCT-US93-00445-4

Query Match 97.2%; Score 2778.5; DB 5; Length 536;
Best Local Similarity 97.6%; Pred. No. 2.6e-214;
Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;

QY 1 MGSNKSXPXKASQRRSLSPSENVHGA-GGAFPASQTPSKRPASADGHRGSAFVPPAAE 59
Db 1 MGSNKSXPXKASQRRSLSPSENVHGA-GGAFPASQTPSKRPASADGHRGSAFVPPAAE 60
QY 60 PKLFGFNSSDYTVSPQAGALAGVTTFVALYDYESTETDLSFKGGERLQIYNNTRKV 119
Db 61 PKLFGFNSSDYTVSPQAGALAGVTTFVALYDYESTETDLSFKGGERLQIYNNTRKV 117
QY 120 DVREGDMWLAHSLSTGQGYIIPSNYVAPSDSIQAEWYFGKITRRESERLLLNENRGCT 179
Db 118 ---BGDMWLAHSLSTGQGYIIPSNYVAPSDSIQAEWYFGKITRRESERLLLNENRGCT 174
QY 180 FLVRESETTGAYCLSVSDPDNAKGLVVKYIKRLDSGCFYITSRTQFNSLQOLVAYYS 239
Db 175 FLVRESETTGAYCLSVSDPDNAKGLVVKYIKRLDSGCFYITSRTQFNSLQOLVAYYS 234
QY 240 KHAADGLCHRLITTVCTPSTKPTQGLAKDAMEIPRESLLEVLAGGCGGCEGVMGTMNGTTR 299
Db 235 KHAADGLCHRLITTVCTPSTKPTQGLAKDAMEIPRESLLEVLAGGCGGCEGVMGTMNGTTR 294
QY 300 VAIKTLKPGTMSPEAFIOEAQVMKGLRHEKLVOLYAVVSEEPYITVEYNNKGSLLDPLK 359
Db 295 VAIKTLKPGTMSPEAFIOEAQVMKGLRHEKLVOLYAVVSEEPYITVEYNNKGSLLDPLK 354
QY 360 GETGKYLRPLQVLVDMASQIASGMAVVERMNVYHRDLRAANILVGENIVCKVADGLARLI 419
Db 355 GETGKYLRPLQVLVDMASQIASGMAVVERMNVYHRDLRAANILVGENIVCKVADGLARLI 414
QY 420 EDNEYTARQGAKEPKIKWTAPALYGRFTIKSDVMSFGILLTTLTGKRVYPGMNVREV 479

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Db 415 EDNEYTARQAKPPIKMTAPEALYGRFTIKSDVMSFGILITELTTKGRVPGVMNREV 474
Qy 480 LDQVGRGYMPCPECPESLHDLMCQCKRKEPBERPTEFYLOAFLEDYFTSTEPQOPGE 539
Db 475 LDQVGRGYMPCPECPESLHDLMCQCKRKEPBERPTEFYLOAFLEDYFTSTEPQOPGE 534
Qy 540 NL 541
Db 535 NL 536

RESULT 8
PCT-US95-05008-13
Sequence 13, Application PC/TUS9505008
GENERAL INFORMATION:
APPLICANT: Sugen, Inc.
APPLICANT: 515 Galveston Drive
APPLICANT: Redwood City, California 94063-4720
APPLICANT: United States of America
APPLICANT: Miesgenachafen E.V.
APPLICANT: Hofgarten Str. 2
APPLICANT: Munchen 80539
APPLICANT: Germany
TITLE OF INVENTION: Novel Megakaryocytic Protein Tyrosine
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Penile & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05008
FILING DATE: 24-APR-1995
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/232,545
FILING DATE: 22-APR-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-074
TELEPHONE: (212)790-9090
TELEFAX: (212)869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 536 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
PCT-US95-05008-13

Query Match 97.2%; Score 2778.5; DB 5; Length 536;
Best Local Similarity 97.6%; Pred. No. 2.6e-214;
Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;

Qy 1 MGSNKSXPDAQORRSLSPESENVHGA-GGAFPASQTPSPKASADGHRGSAAFVPPAAE 59
Db 1 MGSNKSXPDAQORRSLSPESENVHGA-GGAFPASQTPSPKASADGHRGSAAFVPPAAE 60
Qy 60 PKLFGGFNSSDVTYTSQRAAGALAGVTTFTVALYDYESRTETDLSFKKGERLQIVNTRKY 119

Db 61 PKLFGGFNSSDVTYTSQRAAGALAGVTTFTVALYDYESRTETDLSFKKGERLQIVNTRKY 117
Qy 120 DVREGDWMLAHSLSTQGTGYIPSNVYAPSDSIQAEWYTGKITTRESSELLNAENPRGT 179
Db 118 ---EGDWMLAHSLSTQGTGYIPSNVYAPSDSIQAEWYTGKITTRESSELLNAENPRGT 174
Qy 180 FLVRESETTKGAAYCQVSPFDNAKGLNAGHYKIRKLDGSGFYITSTRTOFNSLQQLVAAYYS 239
Db 175 FLVRESETTKGAAYCQVSPFDNAKGLNAGHYKIRKLDGSGFYITSTRTOFNSLQQLVAAYYS 234
Qy 240 KHAADGLCHRLITTCPTSKPQTOGLADAMEIPRESRLREVKLGQCGFGEVWMTNGTTR 299
Db 235 KHAADGLCHRLITTCPTSKPQTOGLADAMEIPRESRLREVKLGQCGFGEVWMTNGTTR 294
Qy 300 VAIKTLKPGTMSPEALQEAQVMKKLRHEKLVOLYAVSEBPYIYTEWNGKSLDPLK 359
Db 295 VAIKTLKPGTMSPEALQEAQVMKKLRHEKLVOLYAVSEBPYIYTEWNGKSLDPLK 354
Qy 360 GETGKYLRLPOLVDMSAOLASGMAVYERMYVHRDLRAANILVGENLVCKVADFGIARLI 419
Db 355 GETGKYLRLPOLVDMSAOLASGMAVYERMYVHRDLRAANILVGENLVCKVADFGIARLI 414
Qy 420 EDNEYTARQAKPPIKMTAPEALYGRFTIKSDVMSFGILITELTTKGRVPGVMNREV 479
Db 415 EDNEYTARQAKPPIKMTAPEALYGRFTIKSDVMSFGILITELTTKGRVPGVMNREV 474
Qy 480 LDQVGRGYMPCPECPESLHDLMCQCKRKEPBERPTEFYLOAFLEDYFTSTEPQOPGE 539
Db 475 LDQVGRGYMPCPECPESLHDLMCQCKRKEPBERPTEFYLOAFLEDYFTSTEPQOPGE 534
Qy 540 NL 541
Db 535 NL 536

RESULT 9
US-09-949-016-10282
Sequence 10282, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10282
LENGTH: 537
TYPE: PRT
ORGANISM: Human
US-09-949-016-10282

Query Match 97.2%; Score 2778.5; DB 2; Length 537;
Best Local Similarity 97.6%; Pred. No. 2.6e-214;
Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;

Qy 1 MGSNKSXPDAQORRSLSPESENVHGA-GGAFPASQTPSPKASADGHRGSAAFVPPAAE 59
Db 2 MGSNKSXPDAQORRSLSPESENVHGA-GGAFPASQTPSPKASADGHRGSAAFVPPAAE 61
Qy 60 PKLFGGFNSSDVTYTSQRAAGALAGVTTFTVALYDYESRTETDLSFKKGERLQIVNTRKY 119
Db 62 PKLFGGFNSSDVTYTSQRAAGALAGVTTFTVALYDYESRTETDLSFKKGERLQIVNTRKY 118

Qy	301	AIKTLKPGTMSDEAFIOEIQWKKLRHEKLVOLYAVVSEEPITYIVTEYVMKGSLLDPFKG	3660
Db	293	AIKTLKPGTMSDEAFIOEIQWKKLRHEKLVOLYAVVSEEPITYIVTEYVMKGSLLDPFKG	3529
Qy	361	ETGKTLRLPQLVDMSAQISGMAVYVERMYVHRDLPAANILVGENLVCKVADFGLARLIE	4200
Db	353	EWGKTLRLPQLVDMAAQISGMAVYVERMYVHRDLPAANILVGENLVCKVADFGLARLIE	4122
Qy	421	DNEYTAROGAKFPIKWTAPAEALYGRFTTKSDVMSFGILLTELTTTGKRVVYPCGMVNRVL	4800
Db	413	DNEYTAROGAKFPIKWTAPAEALYGRFTTKSDVMSFGILLTELTTTGKRVVYPCGMVNRVL	4722
Qy	481	DOVERGYRMPCEPCECSLHDLIMCQCRKBPBEERPTFEYLQAFLEBDYFTSTEPQYQGEN	5400
Db	473	DOVERGYRMPCEPCECSLHDLIMCQCRMRDPEERPTFEYLQAFLEBDYFTSTEPQYQGEN	5322
Qy	541 L 541		
Db	533 L 533		

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US-07-820-011a-2
: Sequence 2, Application US/07820011A
: Patent No. 5336615
: GENERAL INFORMATION:
: APPLICANT: Bell, Leonard
: APPLICANT: Madril, Joseph A.
: APPLICANT: Warren, Stephen L.
: APPLICANT: Luthringer, Daniel J.
: TITLE OF INVENTION: Genetically Engineered
: TITLE OF INVENTION: Endothelial Cells Exhibiting Enhanced
: TITLE OF INVENTION: Migration
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Maurice M. Klee
: STREET: 1951 Burr Street
: CITY: Fairfield
: STATE: Connecticut
: COUNTRY: USA
: ZIP: 06430
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 5.25 inch, 360 Kb storage
: COMPUTER: IBM PC XT
: OPERATING SYSTEM: PC-DOS/MS-DOS 2.10
: SOFTWARE: Displaywrite 3
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/820,011A
: FILING DATE: 19920106
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Klee, Maurice M.
: REGISTRATION NUMBER: 30,399
: REFERENCE/DOCKET NUMBER: LB-101
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (203) 255 1400
: TELEFAX: (203) 254 1101
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 533 amino acids
: TYPE: AMINO ACID
: TOPOLOGY: Linear
: MOLECULE TYPE: Protein
: HYPOTHEICAL: No
: FRAGMENT TYPE: Complete Sequence
: ORIGINAL SOURCE:
: ORGANISM: Gallus, gallus
: PUBLICATION INFORMATION:
: AUTHORS: Takeya, Tatsuo
: AUTHORS: Hanafusa, Hidesaburo
: TITLE: Structure and Sequence of the

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;
 ; TITLE: Cellular Gene Homologous to the RSV src
 ; TITLE: Gene and the Mechanism for Generating the
 ; TITLE: Transforming Virus
 ; JOURNAL: Cell
 ; VOLUME: 32
 ; PAGES: 881-890
 ; DATE: March, 1983
 ; US-07-8320-011A-2

Query Match	92.4%;	Score 2642;	DB 1;	Length 533;
Best Local Similarity	92.8%;	Pred. No. 2.3e-203;		
Matches 502;	Conservative 14;	Mismatches 17;	Indels 8;	Gaps 2;

Oy		MSGNKKPDXAQRRRSLLEPSNNVYAGGAPPAQOTSPKPSAAQHGGSPAALFVPRAEP	60
Dd	1	MSSSKSPKDPBQRRRSLEPPDSTH--HGPPAQOTPKTNAAPTHTTPSRSGYATERP	58
Oy		KLFGFNSSDYTSBPQRAGALAGVTTFVALYDRESRTEDLSFKKEBRLOIVNNTKYD	120
Dd	59	KLFGFNSTDYTPSPQRAGALAGVTTFVALYDRESRTEDLSFKKEBRLOIVNNT----	114
Oy	121	VREGDWMLAHSLSTGOTGYIPSNVYABSDSIOAEEMVFCKITRRESRLILMANPRGT	180
Dd	115	--EGDWMLAHSLTTGOTGYIPSNVYABSDSIOAEEMVFCKITRRESERLLINPENRGTE	172
Oy	181	LVAESRTTKGAACLSVDPEDNAKGLNVGHYIKRLDGSGFFITSRIQFNSLOOLVAYYSK	240
Dd	173	LVAESRTTKGAACLSVDPEDNAKGLNVGHYIKRLDGSGFFITSRIQFNSLOOLVAYYSK	232
Oy	241	HADGICHLRTTYCPTSPKQTQGLADAMEIPRESLRLEVKLGCGCFGEVMKGTMNGITRY	300
Dd	233	HADGICHLRTTYCPTSPKQTQGLADAMEIPRESLRLEVKLGCGCFGEVMKGTMNGITRY	292
Oy	301	AITTLKPETMSSEBALQBAQVMKCLRHEKLVQLYAVVSEBPIIYVIEYNMKSLLDFLKG	360
Dd	293	AITTLKPETMSSEBALQBAQVMKCLRHEKLVQLYAVVSEBPIIYVIEYNMKSLLDFLKG	352
Oy	361	ENGKYLRLQVLVDMSAOIASGMAYVERNNVYHRDLRAANILVBENLVCKRADGSLARLE	420
Dd	353	ENGKYLRLQVLVDMAAOIASGMAYVERNNVYHRDLRAANILVBENLVCKRADGSLARLE	412
Oy	421	DNEYTAROGAKPEPKMTAPEALYGRFTIKSDVWSFGILLTELTTKGRVYPGVAVREYL	480
Dd	413	DNEYTRROGAKPEPKMTAPEALYGRFTIKSDVWSFGILLTELTTKGRVYPGVAVREYL	472
Oy	481	DVERGYRNPCPECPESLIHLMQCQMKREEBERPTEYILOAFLEDYFTISDEPOYGGEN	540
Dd	473	DVERGYRNPCPECPESLIHLMQCQMRDDEBERPTEYILOAFLEDYFTISDEPOYGGEN	532
Oy	541	L 541	
Dd	533	L 533	

```

1 RESULT 13
2 PCT-US93-00445-2
3
4 Sequence 2, Application PC/TUS9300445
5
6 GENERAL INFORMATION:
7
8 APPLICANT: Bell, Leonard
9
10 APPLICANT: Madril, Joseph A.
11
12 APPLICANT: Warren, Stephen L.
13
14 APPLICANT: Luthringer, Daniel J.
15
16 TITLE OF INVENTION: Genetically Engineered
17
18 TITLE OF INVENTION: Endothelial Cells
19
20 NUMBER OF SEQUENCES: 4
21
22 CORRESPONDENCE ADDRESS:
23
24 ADDRESSEE: Maurice M. Klee
25
26 STREET: 1951 Burr Street
27
28 CITY: Fairfield
29
30 STATE: Connecticut
31
32 COUNTRY: USA
33
34 ZIP: 06430
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36 COMPUTER READABLE FORM:
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MEDIUM TYPE: 3.5 inch, 760 kb storage
 COMPUTER: DELL 486/50
 OPERATING SYSTEM: DOS 5.0
 SOFTWARE: Displaywrite 3
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US93/00445
 FILING DATE: 19930105
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/820,011
 FILING DATE: 06-JAN-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Klee, Maurice M.
 REGISTRATION NUMBER: 30,399
 REFERENCE/DOCKET NUMBER: ALX-101PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (203) 255 1400
 TELEFAX: (203) 254 1101
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 533 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 MOLECULE TYPE: Protein
 HYPOTHETICAL: NO
 FRAGMENT TYPE: Complete Sequence
 ORIGINAL SOURCE:
 ORGANISM: Gallus gallus
 PUBLICATION INFORMATION:
 AUTHORS: Takeya, Tatsuo
 TITLES: Hanafusa, Hidesaburo
 TITLE: Structure and Sequence of the
 TITLE: Cellular Gene Homologous to the RSV arc
 TITLE: Gene and the Mechanism for Generating the
 TITLE: Transforming Virus
 JOURNAL: Cell
 VOLUME: 32
 PAGES: 881-890
 DATE: March, 1983

Query Match	92.4%	Score 2642	DB 5	Length 533
Best Local Similarity	92.8%	Pred. No. 2.3e-203		
Matches 502	Conservative 14	Mismatches 17	Indels 8	Gaps 2
QY	1	MGNSKSRPKDASQRRRSLEPSENVHAGGAFPAQSPSPKSPASADGHRGSPAIFYPAAP	60	
Db	1	MGSSKSRPKDQSRRRSLEPPDSTH--HGCFPAQTPPKTKAAPDTHRPSPSGTVATEP	58	
QY	61	KLREGFSSDPVTVSPQRAAGALAGVTTTVALYDYSRRETDLSFKKGRLOIVNTRKVD	120	
Db	59	KLFGFPTSDPVTVSPQRAAGALAGVTTTVALYDYSRRETDLSFKKGRLOIVNNT---	114	
QY	121	VREGDWMLAHSLSTGQGTGYPNSNYAPSDSIQAEWYFGKITRRESERLLNNAENPGTF	180	
Db	115	--EEDWMLAHSLTTGQGTGYPNSNYAPSDSIQAEWYFGKITRRESERLLNNAENPGTF	172	
QY	181	LVRESEFTTGKAYCUSVSDFDNAKGLNVKHYIKRKIDSGGFIYTSFTQFNSLQOLVAAYYSK	240	
Db	173	LVRESEFTTGKAYCUSVSDFDNAKGLNVKHYIKRKIDSGGFIYTSFTQFSSLQOLVAAYYSK	232	
QY	241	HADGLCHRLTTCVCTSPKQTOGLAKDAWEIPRESRLREVKLGQGGQFGVWMTGTVGRV	300	
Db	233	HADGLCHRLTTCVCTSPKQTOGLAKDAWEIPRESRLREVKLGQGGQFGVWMTGTVGRV	292	
QY	301	AIKTLKPGTMSPEAFLOEAQYWKLLRHKLVOLVYAVSEEPYIYITEYMNKSLDLPFKG	360	
Db	293	AIKTLKPGTMSPEAFLOEAQYWKLLRHKLVOLVYAVSEEPYIYITEYMNKSLDLPFKG	352	
QY	361	ETGTYLRLPOLVDMSAQIASGMAYYERNNYVHRDLRANILVGENLVCKVADFGLARILE	420	
Db	353	EMGTYLRLPOLVDMAAQIASGMAYYERNNYVHRDLRANILVGENLVCKVADFGLARILE	412	

Oy	421	DNETARQGAFTPIKMTA	PEALYGRFTIKSDVMSFGILLT	LTTKGRPPYGMVREYL	480
Db	413	DNETARQGAFTPIKMTA	PEALYGRFTIKSDVMSFGILLT	LTTKGRPPYGMVREYL	472
Oy	481	DQVRGYMPCPECBESLHDL	MCQCKRKEPBERPTFETYLQAF	LDEYFTSTBEYOXGEN	540
Db	473	DQVRGYMPCPECBESLHDL	MCQCKRDPBERPTFETYLQAF	LDEYFTSTBEYOGEN	532
Oy	541	L	541		
Db	533	L	533		

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1      RESULT 14
2      US-08-426-509A-14
3      Sequence 14, Application US/08426509A
4      Patent No. 6326469
5      GENERAL INFORMATION:
6      APPLICANT: Ullrich,, Axel
7      APPLICANT: Gishizsky,, Mikhail
8      APPLICANT: Sures,, Irman G.
9      TITLE OF INVENTION: NOVEL MEKKAPOCYTIC PROTEIN
10     TITLE OF INVENTION: TYROSINE KINASES
11     NUMBER OF INVENTION: 21
12     NUMBER OF SEQUENCES: 21
13     CORRESPONDENCE ADDRESS:
14     ADDRESSEE: Pennie & Edmonds
15     STREET: 1155 Avenue of the Americas
16     CITY: New York,
17     STATE: NY
18     COUNTRY: USA
19     ZIP: 10036-2711
20     COMPUTER READABLE FORM:
21     MEDIUM TYPE: Diskette
22     COMPUTER: IBM Compatible
23     OPERATING SYSTEM: DOS
24     SOFTWARE: FastSeq Version 2.0
25     CURRENT APPLICATION DATA:
26     APPLICATION NUMBER: US/08/426,509A
27     FILING DATE: 21-APR-1995
28     CLASSIFICATION: 435
29     PRIOR APPLICATION DATA:
30     APPLICATION NUMBER: 08/232,545
31     FILING DATE:
32     ATTORNEY/AGENT INFORMATION:
33     NAME: Coruzzi, Laura A
34     REGISTRATION NUMBER: 30,742
35     REFERENCE/DOCKET NUMBER: 7683-0074-999
36     TELECOMMUNICATION INFORMATION:
37     TELEPHONE: 212-790-9090
38     TELEFAX: 212-869-9741
39     TELETYPE: 66141 PENNIE
40     INFORMATION FOR SEQ ID NO: 14:
41     SEQUENCE CHARACTERISTICS:
42     LENGTH: 543 amino acids
43     TYPE: amino acid
44     STRANDEDNESS: unknown
45     TOPOLOGY: unknown
46     MOLECULE TYPE: No. 6326469e
47     US-08-426-509A-14

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Query Match Similarity	73.8%;	Score 211;	DB 2;	Length 543;
Best Local Similarity	72.8%;	Pred. No. 8.8e-161;		
Matches	405;	Conservative	49;	Mismatches 74; Indels 28; Gaps 4

QY	1	MGSNKS	K-----PKASQRRRLSLEPENHGAAGAEPA	SGQSPKPSADGHR-----	47
				:::	
DB	1	MGLCKSKENKSPALKYRPENTPEPSTSVSHG	GAFTTYS	PCPPSSAKTANV	FFSLSM
QY	48	--GSAAFVPPAAE	PKLFGFNSSDVTYS	PORAGALAGVTT	FVALYDYSRTETDLS
DB	61	PFGGSSGVT	-----FGASSSPSV	PSYPALVGTGVT	IFVALYDYEARTE
QY	106	KGERLQIVNTRK	QVDREGDMWLAHSL	STGQTGY	PSNVVADSDSIQAEEMVFGK
					TRRE
					165

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Db      114 KGERFQIINN-----EGDWEARSATGKNGITPSNYYVAPADSIOAEWYFGKMGKRD 167
Qy      166 SERLLLAENPRGTFIVRESEETTKGAYCISVSPDNAGLNVKHYKIRKLDGSGFYITSR 225
        168 AERLLINPGNQRIQIFLVRESEETTKGAYSLIRDMDEIRGDNVVKHYKIRKLDNGGYITTR 227
Qy      226 TQNSIQOLVAAYYSKADGICHRLTTCPTSKPQTQGLADAMEIPRESIRLEVKLGQGC 265
        228 AQPDTIQKLVKHYTHADGICHRLTTCPTVKPQTQGLADAMEIPRESIRLEVKLGQGC 287
Qy      286 FGEVMMGTWNGTTRVAIKTLKPGTMSPEAFLOEAQVMKLRHEKLVOLYAVVSEBPIYIV 345
        288 FGEVMMGTWNGTTRVAIKTLKPGTMSPEAFLOEAQVMKLRHEKLVOLYAVVSEBPIYIV 347
Qy      346 TEYMNKGSLLDPLKSGTGYLRPLQVDMASQAISGMAVYERNYVHRDLRAANIIVGEN 405
        348 TEYMNKGSLLDPLKSGTGYLRPLQVDMASQAISGMAVYERNYVHRDLRAANIIVGEN 407
Qy      406 LVCKKADFGIARLIENDEYTAQAGAKPIKMTAPEALYGRFTIKSDVMSFGILLTELTT 465
        408 LVCKKADFGIARLIENDEYTAQAGAKPIKMTAPEALYGRFTIKSDVMSFGILLTELVT 467
Qy      466 KGRVYPGMVNRREVLQVERGYRMPCCPCCPSLHDLMCQWKREPERPTFEYLQAFLE 525
        468 KGRVYPGMVNRREVLQVERGYRMPCCPCCPSLHDLMCQWKREPERPTFEYLQAFLE 527
Qy      526 DYTSTTEPOYQGENL 541
        528 DYTSTTEPOYQGENL 543
Db

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RESULT 15
US-08-232-545-14
Sequence 14, Application US/08232545
Patent No. 6506578
GENERAL INFORMATION:

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APPLICANT: Ulrich, Axel
APPLICANT: Glisheky, Mikhail
APPLICANT: Sures, Iman G.
TITLE OF INVENTION: No. 6506578e1 Megakaryocytic Protein Tyrosine
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,545
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-050
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
TELEFAX: (212)869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 543 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown

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MOLECULE TYPE: protein
US-08-232-545-14

Query Match 73.8%; Score 2111; DB 2; Length 543;
Best Local Similarity 72.8%; Pred. No. 8.8e-161;
Matches 405; Conservative 49; Mismatches 74; Indels 28; Gaps 4;

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Qy      1 MGSNKRK----PDAQQRRLSEPSNENHAGAGAPFASQPSKAPADGHR----- 47
        1 MGIKSKENKSPAIKRYRPENTPEPVSTSVHYGAEPITVSPCSSSAKGAIVNPFSSLSMT 60
Db      48 --GPSAFAVPPAEPKLFGEFNSDVTSTSPQAGALAGAGTTEVALVDYDESRTETLSFK 105
        61 PFGSSGVTP-----FGASSSFVSVSSSYRAGLTGVTITVALVDYDEARTETLSFK 113
Qy      106 KGERLOIVNTRKVDVBEQDMLAHSLSGQGTGYIPSNYVAPDSIOAEWYFGKTRRE 165
        114 KGERFQIINN-----EGDWEARSATGKNGITPSNYYVAPADSIOAEWYFGKMGKRD 167
Qy      166 SERLLLAENPRGTFIVRESEETTKGAYCISVSPDNAGLNVKHYKIRKLDGSGFYITSR 225
        168 AERLLINPGNQRIQIFLVRESEETTKGAYSLIRDMDEIRGDNVVKHYKIRKLDNGGYITTR 227
Qy      226 TQNSIQOLVAAYYSKADGICHRLTTCPTSKPQTQGLADAMEIPRESIRLEVKLGQGC 285
        228 AQPDTIQKLVKHYTHADGICHRLTTCPTVKPQTQGLADAMEIPRESIRLEVKLGQGC 287
Db      286 FGEVMMGTWNGTTRVAIKTLKPGTMSPEAFLOEAQVMKLRHEKLVOLYAVVSEBPIYIV 345
        288 FGEVMMGTWNGTTRVAIKTLKPGTMSPEAFLOEAQVMKLRHEKLVOLYAVVSEBPIYIV 347
Qy      346 TEYMNKGSLLDPLKSGTGYLRPLQVDMASQAISGMAVYERNYVHRDLRAANIIVGEN 405
        348 TEYMNKGSLLDPLKSGTGYLRPLQVDMASQAISGMAVYERNYVHRDLRAANIIVGEN 407
Qy      406 LVCKKADFGIARLIENDEYTAQAGAKPIKMTAPEALYGRFTIKSDVMSFGILLTELTT 465
        408 LVCKKADFGIARLIENDEYTAQAGAKPIKMTAPEALYGRFTIKSDVMSFGILLTELVT 467
Qy      466 KGRVYPGMVNRREVLQVERGYRMPCCPCCPSLHDLMCQWKREPERPTFEYLQAFLE 525
        468 KGRVYPGMVNRREVLQVERGYRMPCCPCCPSLHDLMCQWKREPERPTFEYLQAFLE 527
Qy      526 DYTSTTEPOYQGENL 541
        528 DYTSTTEPOYQGENL 543
Db

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Search completed: June 5, 2006, 17:18:17
Job time : 32.0766 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 5, 2006, 17:37:14 ; Search time 108.267 Seconds
(without alignments)
2314.645 Million cell updates/sec

Title: US-10-691-079-3

Perfect score: 2859

Sequence: 1 MGSNKSXPDAASQRRSLRP.....AFLEDYRTSTPEYQPGENL 541

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA Main:*
- 1: /EMC_Ceitera_SIDS3/prodata/2/pubppa/US07_PUBCOMB.pap:*
 - 2: /EMC_Ceitera_SIDS3/prodata/2/pubppa/US08_PUBCOMB.pap:*
 - 3: /EMC_Ceitera_SIDS3/prodata/2/pubppa/US09_PUBCOMB.pap:*
 - 4: /EMC_Ceitera_SIDS3/prodata/2/pubppa/US10_PUBCOMB.pap:*
 - 5: /EMC_Ceitera_SIDS3/prodata/2/pubppa/US10B_PUBCOMB.pap:*
 - 6: /EMC_Ceitera_SIDS3/prodata/2/pubppa/US11_PUBCOMB.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2859	100.0	541	US-10-691-079-3	Sequence 3, Appli
2	2837.5	99.2	542	US-10-732-923-13447	Sequence 13447, A
3	2820.5	98.7	542	US-10-691-079-1	Sequence 1, Appli
4	2778.5	97.2	536	US-09-977-260-13	Sequence 13, Appl
5	2778.5	97.2	536	US-09-929-266-10	Sequence 10, Appl
6	2778.5	97.2	536	US-09-977-261-13	Sequence 13, Appl
7	2778.5	97.2	536	US-10-691-079-2	Sequence 2, Appli
8	2778.5	97.2	536	US-10-887-588-2	Sequence 2, Appli
9	2778.5	97.2	536	US-10-487-641-2	Sequence 2, Appli
10	2778.5	97.2	536	US-10-825-568-10	Sequence 10, Appl
11	2778.5	97.2	536	US-10-821-231C-1	Sequence 1, Appli
12	2778.5	97.2	536	US-10-469-469-273	Sequence 273, App
13	2778.5	97.2	536	US-11-233-510-24	Sequence 24, Appl
14	2773.5	97.0	535	US-10-394-322A-56	Sequence 56, Appl
15	2773.5	97.0	535	US-10-814-109-4	Sequence 4, Appli
16	2745.5	96.0	530	US-10-887-588-4	Sequence 4, Appli
17	2711.5	94.8	530	US-10-330-773-749	Sequence 749, App
18	2648	92.6	533	US-10-276-633-1	Sequence 1, Appli
19	2648	92.6	533	US-10-732-923-13652	Sequence 13652, A
20	2645	92.5	533	US-10-732-923-13654	Sequence 13654, A
21	2645	92.5	533	US-11-230-995-3	Sequence 3, Appli
22	2643	92.4	533	US-10-732-923-13650	Sequence 13650, A
23	2623	91.7	533	US-10-276-633-2	Sequence 2, Appli
24	2603	91.0	587	US-10-732-923-13472	Sequence 13472, A
25	2596	90.8	568	US-10-732-923-13474	Sequence 13474, A
26	2590	90.6	587	US-10-732-923-13469	Sequence 13469, A
27	2581	90.3	557	US-10-732-923-13475	Sequence 13475, A

28	2515	88.0	526	US-10-732-923-13499	Sequence 13499, A
29	2498	87.4	526	US-10-732-923-13484	Sequence 13484, A
30	2498	87.4	772	US-10-732-923-13485	Sequence 13485, A
31	2479	86.7	526	US-10-732-923-13483	Sequence 13483, A
32	2473	86.5	526	US-10-732-923-13497	Sequence 13497, A
33	2468	86.3	537	US-10-732-923-13636	Sequence 13636, A
34	2467	86.3	526	US-10-732-923-13493	Sequence 13493, A
35	2467	86.3	526	US-10-732-923-13498	Sequence 13498, A
36	2466	86.3	526	US-10-732-923-13489	Sequence 13489, A
37	2465	86.2	526	US-10-732-923-13486	Sequence 13486, A
38	2463.5	86.2	523	US-10-732-923-13488	Sequence 13488, A
39	2463.5	86.2	535	US-10-732-923-13495	Sequence 13495, A
40	2463	86.1	526	US-10-732-923-13491	Sequence 13491, A
41	2452	85.8	526	US-10-732-923-13487	Sequence 13487, A
42	2448	85.6	526	US-10-732-923-13487	Sequence 13487, A
43	2444.5	85.5	532	US-10-732-923-13633	Sequence 13633, A
44	2442.5	85.4	532	US-10-732-923-13635	Sequence 13635, A
45	2439.5	85.3	532	US-10-732-923-13637	Sequence 13637, A

ALIGNMENTS

RESULT 1
US-10-691-079-3

Sequence 3, Application US/10691079

Publication No. US20040176313A1

GENERAL INFORMATION:

APPLICANT: AVENTIS PHARMA S.A.

TITLE OF INVENTION: Inhibitors of SRC kinase for use in Alzheimer's disease

FILE REFERENCE: PRAV002/00930

CURRENT APPLICATION NUMBER: US/10/691,079

CURRENT FILING DATE: 2003-10-22

NUMBER OF SEQ ID NOS: 5

SOFTWARE: Patentin version 3.1

SEQ ID NO 3

LENGTH: 541

TYPE: PRT

ORGANISM: Murinae gen. sp.

US-10-691-079-3

Query Match 100.0%; Score 2859; DB 4; Length 541;
Best Local Similarity 100.0%; Pred. No. 4e-177;
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MGSNKSXPDAASQRRSLRPSENVHAGAFPAASQTPSPKPSADGHRGSAFVPPAEP	60
DB	1	MGSNKSXPDAASQRRSLRPSENVHAGAFPAASQTPSPKPSADGHRGSAFVPPAEP	60
QY	61	KLFGGNSPTVTSPQRAAGAGCTTFFVALLYBESRTETDLSFKGGERLQIVNTRKVD	120
DB	61	KLFGGNSPTVTSPQRAAGAGCTTFFVALLYBESRTETDLSFKGGERLQIVNTRKVD	120
QY	121	VREGDWMALSLSTGQGYIPSNVVAPSDSIOABEWFGKITRRESRLILMNEPRGTF	180
DB	121	VREGDWMALSLSTGQGYIPSNVVAPSDSIOABEWFGKITRRESRLILMNEPRGTF	180
QY	181	LVESEETTKAAYCISVSPDNAGLVKHKIRKLDSGGEFYITSRTQFNSLQOLVAYYSK	240
DB	181	LVESEETTKAAYCISVSPDNAGLVKHKIRKLDSGGEFYITSRTQFNSLQOLVAYYSK	240
QY	241	HADGLCHRLTTCVPTSPKQTOGLAKDAWEIPRSLRLVETLGGCGCFEVMWNGTTRV	300
DB	241	HADGLCHRLTTCVPTSPKQTOGLAKDAWEIPRSLRLVETLGGCGCFEVMWNGTTRV	300
QY	301	AITTKRGTMSPAPLOEAOVMKKLRHEKLVOLYAVVSEEPITYVREYMGSLDPLKG	360
DB	301	AITTKRGTMSPAPLOEAOVMKKLRHEKLVOLYAVVSEEPITYVREYMGSLDPLKG	360
QY	361	ETGKYRLPOLVDMASQIASGMAVVERMNVVHRDLRAANILVGBNLCVKVADFGLABIE	420
DB	361	ETGKYRLPOLVDMASQIASGMAVVERMNVVHRDLRAANILVGBNLCVKVADFGLABIE	420

QY 421 DNEVTAQAGAKFPKMTAPBAALYGRFTIKSDVMSFGILLTELTKGRVVPGMVNRVL 480
 DB 421 DNEVTAQAGAKFPKMTAPBAALYGRFTIKSDVMSFGILLTELTKGRVVPGMVNRVL 480
 QY 481 DQVERGYRMPCCPECPESLHDLMCQWRKEBERPTEFYLAFLDYFTSTEPQYQGEN 540
 DB 481 DQVERGYRMPCCPECPESLHDLMCQWRKEBERPTEFYLAFLDYFTSTEPQYQGEN 540
 QY 541 L 541
 DB 541 L 541
 RESULT 2
 US-10-732-923-13447
 ; Sequence 13447, Application US/10732923
 ; Publication No. US20050108791A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Edgerton, Michael D
 ; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
 ; FILE REFERENCE: 38-15(52796)C
 ; CURRENT APPLICATION NUMBER: US/10/732,923
 ; CURRENT FILING DATE: 2003-12-10
 ; PRIOR APPLICATION NUMBER: 10/310,154
 ; PRIOR FILING DATE: 2002-12-04
 ; NUMBER OF SEQ. ID NOS: 24149
 ; SEQ. ID NO 13447
 ; LENGTH: 542
 ; TYPE: PRT
 ; ORGANISM: Rattus norvegicus
 US-10-732-923-13447

Query Match 99.2%; Score 2837.5; DB 5; Length 542;
 Best Local Similarity 99.3%; Pred. No. 1e-175;
 Matches 538; Conservative 2; Mismatches 1; Indels 1; Gaps 1;
 QY 1 MGSNKSXPDAQRRRLSPSENVHAGAFAPASQTPSKDASADGHRGSAAFVPPAAE 59
 DB 1 MGSNKSXPDAQRRRLSPSENVHAGAFAPASQTPSKDASADGHRGSAAFVPPAAE 60
 QY 60 PKLFGFNSSDVTYSPQAGALAGVTTFVALYDYSRTETDLSFKKGERLQIVNNTKRV 119
 DB 61 PKLFGFNSSDVTYSPQAGALAGVTTFVALYDYSRTETDLSFKKGERLQIVNNTKRV 120
 QY 120 DVEEGMWLAHSISTGQTYIPSNVYAPSDSIQAEEMYPGKITRRSEBRLILNAENPRGT 179
 DB 121 DVEEGMWLAHSISTGQTYIPSNVYAPSDSIQAEEMYPGKITRRSEBRLILNAENPRGT 180
 QY 180 FLVRESETTGAYCLSVSPDNAGKLVNKHVKIRKLDGSGFYITSTRTOFNSLQQLVAYYS 239
 DB 181 FLVRESETTGAYCLSVSPDNAGKLVNKHVKIRKLDGSGFYITSTRTOFNSLQQLVAYYS 240
 QY 240 KHAHDLCHRLTTYCPSTKQTOGLADAMEIPRESLRLEVKLGQCGFGEVMMGTWGTTR 299
 DB 241 KHAHDLCHRLTTYCPSTKQTOGLADAMEIPRESLRLEVKLGQCGFGEVMMGTWGTTR 300
 QY 300 VALKTLPKGTMSPEAFLOBAQVWKLRHEKLVOLYAVVSEBPIYIVTEYMNKSLDPLK 359
 DB 301 VALKTLPKGTMSPEAFLOBAQVWKLRHEKLVOLYAVVSEBPIYIVTEYMNKSLDPLK 360
 QY 360 GETGKYLRLPOLVDMASQIASGMAVYERMYVHRDLRAANILVGENLVCKVADFGIARLI 419
 DB 361 GETGKYLRLPOLVDMASQIASGMAVYERMYVHRDLRAANILVGENLVCKVADFGIARLI 420
 QY 420 EDNEYTAQAGAKFPKMTAPBAALYGRFTIKSDVMSFGILLTELTKGRVVPGMVNRVL 479
 DB 421 EDNEYTAQAGAKFPKMTAPBAALYGRFTIKSDVMSFGILLTELTKGRVVPGMVNRVL 480
 QY 480 LDQVERGYRMPCCPECPESLHDLMCQWRKEBERPTEFYLAFLDYFTSTEPQYQGEN 539
 DB 481 LDQVERGYRMPCCPECPESLHDLMCQWRKEBERPTEFYLAFLDYFTSTEPQYQGEN 540
 QY 540 NL 541
 DB 540 NL 541

DB 541 NL 542
 RESULT 3
 US-10-691-079-1
 ; Sequence 1, Application US/10691079
 ; Publication No. US2004016313A1
 ; GENERAL INFORMATION:
 ; APPLICANT: AVENTIS PHARMA S.A.
 ; TITLE OF INVENTION: Inhibitors of SRC kinase for use in Alzheimer's disease
 ; FILE REFERENCE: FRAV2002/0030
 ; CURRENT APPLICATION NUMBER: US/10/691,079
 ; CURRENT FILING DATE: 2003-10-22
 ; NUMBER OF SEQ. ID NOS: 5
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ. ID NO 1
 ; LENGTH: 542
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-691-079-1

Query Match 98.7%; Score 2820.5; DB 4; Length 542;
 Best Local Similarity 98.7%; Pred. No. 1.3e-174;
 Matches 535; Conservative 3; Mismatches 3; Indels 1; Gaps 1;
 QY 1 MGSNKSXPDAQRRRLSPSENVHGA-GAPASQTPSKDASADGHRGSAAFVPPAAE 59
 DB 1 MGSNKSXPDAQRRRLSPSENVHAGAGAPASQTPSKDASADGHRGSAAFVPPAAE 60
 QY 60 PKLFGFNSSDVTYSPQAGALAGVTTFVALYDYSRTETDLSFKKGERLQIVNNTKRV 119
 DB 61 PKLFGFNSSDVTYSPQAGALAGVTTFVALYDYSRTETDLSFKKGERLQIVNNTKRV 120
 QY 120 DVEEGMWLAHSISTGQTYIPSNVYAPSDSIQAEEMYPGKITRRSEBRLILNAENPRGT 179
 DB 121 DVEEGMWLAHSISTGQTYIPSNVYAPSDSIQAEEMYPGKITRRSEBRLILNAENPRGT 180
 QY 180 FLVRESETTGAYCLSVSPDNAGKLVNKHVKIRKLDGSGFYITSTRTOFNSLQQLVAYYS 239
 DB 181 FLVRESETTGAYCLSVSPDNAGKLVNKHVKIRKLDGSGFYITSTRTOFNSLQQLVAYYS 240
 QY 240 KHAHDLCHRLTTYCPSTKQTOGLADAMEIPRESLRLEVKLGQCGFGEVMMGTWGTTR 299
 DB 241 KHAHDLCHRLTTYCPSTKQTOGLADAMEIPRESLRLEVKLGQCGFGEVMMGTWGTTR 300
 QY 300 VALKTLPKGTMSPEAFLOBAQVWKLRHEKLVOLYAVVSEBPIYIVTEYMNKSLDPLK 359
 DB 301 VALKTLPKGTMSPEAFLOBAQVWKLRHEKLVOLYAVVSEBPIYIVTEYMNKSLDPLK 360
 QY 360 GETGKYLRLPOLVDMASQIASGMAVYERMYVHRDLRAANILVGENLVCKVADFGIARLI 419
 DB 361 GETGKYLRLPOLVDMASQIASGMAVYERMYVHRDLRAANILVGENLVCKVADFGIARLI 420
 QY 420 EDNEYTAQAGAKFPKMTAPBAALYGRFTIKSDVMSFGILLTELTKGRVVPGMVNRVL 479
 DB 421 EDNEYTAQAGAKFPKMTAPBAALYGRFTIKSDVMSFGILLTELTKGRVVPGMVNRVL 480
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 DB 481 LDQVERGYRMPCCPECPESLHDLMCQWRKEBERPTEFYLAFLDYFTSTEPQYQGEN 540
 QY 540 NL 541
 DB 541 NL 542
 RESULT 4
 US-09-977-260-13
 ; Sequence 13, Application US/09977260
 ; Publication No. US20020192790A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ULLRICH, AXEL

APPLICANT: GISHIZKY, MIKHAIL
APPLICANT: SURES, IRMINGARD
TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES
FILE REFERENCE: 038602/1260
CURRENT APPLICATION NUMBER: US/09/977,260
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 08/232,545
PRIOR FILING DATE: 1994-04-22
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 536
TYPE: PRT
ORGANISM: Homo sapiens
US-09-977-260-13

Query Match 97.2%; Score 2778.5; DB 3; Length 536;
Best Local Similarity 97.6%; Pred. No. 6.6e-172;
Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;

QY 1 MGSNKSXPXKASQRRRLSEPSENVHGA-GGAFPASQTPSKPASADGHRGSAAFVPPAAE 59
DB 1 MGSNKSXPXKASQRRRLSEPSENVHGA-GGAFPASQTPSKPASADGHRGSAAFVPPAAE 60
QY 60 PKLFGFNSSDVTYSPQAGALAGVTTFVALDYESTRTDLSFKKGERLQIYNNTRKV 119
DB 61 PKLFGFNSSDVTYSPQAGALAGVTTFVALDYESTRTDLSFKKGERLQIYNNTRKV 117
QY 120 DVEBGDWMLHSLSTGQGYIPSNYVAPSDSIQAEYVFGKITRRESEBRLILNAENRGT 179
DB 118 ---EGDWMLHSLSTGQGYIPSNYVAPSDSIQAEYVFGKITRRESEBRLILNAENRGT 174
QY 180 FLVRESEETTGAYCLSVSDPDNAKGLNVKHYKIRKLDGSGFYITSRTOFNSLQQLVAYYS 239
DB 175 FLVRESEETTGAYCLSVSDPDNAKGLNVKHYKIRKLDGSGFYITSRTOFNSLQQLVAYYS 234
QY 240 KHADGLCHRLITTYCPTSKPOTQGLAKDAMEIPRESLRLVYLGCGCGEYVWGTMNGTTR 299
DB 235 KHADGLCHRLITTYCPTSKPOTQGLAKDAMEIPRESLRLVYLGCGCGEYVWGTMNGTTR 294
QY 300 VALKTLPKGTMSPEAFQEAQVWKLRHEKLVOLYAVVSEPIYIVTEYNNKSGSLDPLK 359
DB 295 VALKTLPKGTMSPEAFQEAQVWKLRHEKLVOLYAVVSEPIYIVTEYNNKSGSLDPLK 354
QY 360 GETGKYLRPLQVLDVMSAQIASGMAVYERMYVHRDLPAANILVGENLVCKVADFGRLRI 419
DB 355 GETGKYLRPLQVLDVMSAQIASGMAVYERMYVHRDLPAANILVGENLVCKVADFGRLRI 414
QY 420 EDNEYTRARQAKPPIKKTAPBAALYGRFTIKSDVMSFGILLTELTTGGRVPYPMVNRREV 479
DB 415 EDNEYTRARQAKPPIKKTAPBAALYGRFTIKSDVMSFGILLTELTTGGRVPYPMVNRREV 474
QY 480 LDVERGYRMPCEPCESLHDLWCOCWKREPERPFVEYLOAFLEBYFTSTEPQYQGE 539
DB 475 LDVERGYRMPCEPCESLHDLWCOCWKREPERPFVEYLOAFLEBYFTSTEPQYQGE 534
QY 540 NL 541
DB 535 NL 536

RESULT 5
US-09-929-266-10
Sequence 10, Application US/09929266
Publication No. US20030045694A1
GENERAL INFORMATION:
APPLICANT: Brian T. Chait
APPLICANT: Darin R. Latimer
APPLICANT: Paul M. Lizardi
APPLICANT: Eric R. Kershnar
APPLICANT: Jon S. Morrow
APPLICANT: Matthew B. Roth
APPLICANT: Martin J. Matthesich

APPLICANT: Kevin J. McConnell
APPLICANT: ULTRA-SENSITIVE DETECTION SYSTEMS
TITLE OF INVENTION: ULTRA-SENSITIVE DETECTION SYSTEMS
FILE REFERENCE: 01173.0003U2
CURRENT APPLICATION NUMBER: US/09/929,266
CURRENT FILING DATE: 2001-08-13
PRIOR APPLICATION NUMBER: 60/224,939
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/283,498
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 536
TYPE: PRT
ORGANISM: Homo sapiens
US-09-929-266-10

Query Match 97.2%; Score 2778.5; DB 3; Length 536;
Best Local Similarity 97.6%; Pred. No. 6.6e-172;
Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;

QY 1 MGSNKSXPXKASQRRRLSEPSENVHGA-GGAFPASQTPSKPASADGHRGSAAFVPPAAE 59
DB 1 MGSNKSXPXKASQRRRLSEPSENVHGA-GGAFPASQTPSKPASADGHRGSAAFVPPAAE 60
QY 60 PKLFGFNSSDVTYSPQAGALAGVTTFVALDYESTRTDLSFKKGERLQIYNNTRKV 119
DB 61 PKLFGFNSSDVTYSPQAGALAGVTTFVALDYESTRTDLSFKKGERLQIYNNTRKV 117
QY 120 DVEBGDWMLHSLSTGQGYIPSNYVAPSDSIQAEYVFGKITRRESEBRLILNAENRGT 179
DB 118 ---EGDWMLHSLSTGQGYIPSNYVAPSDSIQAEYVFGKITRRESEBRLILNAENRGT 174
QY 180 FLVRESEETTGAYCLSVSDPDNAKGLNVKHYKIRKLDGSGFYITSRTOFNSLQQLVAYYS 239
DB 175 FLVRESEETTGAYCLSVSDPDNAKGLNVKHYKIRKLDGSGFYITSRTOFNSLQQLVAYYS 234
QY 240 KHADGLCHRLITTYCPTSKPOTQGLAKDAMEIPRESLRLVYLGCGCGEYVWGTMNGTTR 299
DB 235 KHADGLCHRLITTYCPTSKPOTQGLAKDAMEIPRESLRLVYLGCGCGEYVWGTMNGTTR 294
QY 300 VALKTLPKGTMSPEAFQEAQVWKLRHEKLVOLYAVVSEPIYIVTEYNNKSGSLDPLK 359
DB 295 VALKTLPKGTMSPEAFQEAQVWKLRHEKLVOLYAVVSEPIYIVTEYNNKSGSLDPLK 354
QY 360 GETGKYLRPLQVLDVMSAQIASGMAVYERMYVHRDLPAANILVGENLVCKVADFGRLRI 419
DB 355 GETGKYLRPLQVLDVMSAQIASGMAVYERMYVHRDLPAANILVGENLVCKVADFGRLRI 414
QY 420 EDNEYTRARQAKPPIKKTAPBAALYGRFTIKSDVMSFGILLTELTTGGRVPYPMVNRREV 479
DB 415 EDNEYTRARQAKPPIKKTAPBAALYGRFTIKSDVMSFGILLTELTTGGRVPYPMVNRREV 474
QY 480 LDVERGYRMPCEPCESLHDLWCOCWKREPERPFVEYLOAFLEBYFTSTEPQYQGE 539
DB 475 LDVERGYRMPCEPCESLHDLWCOCWKREPERPFVEYLOAFLEBYFTSTEPQYQGE 534
QY 540 NL 541
DB 535 NL 536

RESULT 6
US-09-977-261-13
Sequence 13, Application US/09977261
Publication No. US20030054527A1
GENERAL INFORMATION:
APPLICANT: ULTRICH, AXEL
APPLICANT: GISHIZKY, MIKHAIL
APPLICANT: SURES, IRMINGARD
TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES
FILE REFERENCE: 038602/1259
CURRENT APPLICATION NUMBER: US/09/977,261

CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 08/232,545
PRIOR FILING DATE: 1994-04-22
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 536
TYPE: PRT
ORGANISM: Homo sapiens
US-09-977-261-13

Query Match 97.2%; Score 2778.5; DB 3; Length 536;
Best Local Similarity 97.6%; Pred. No. 6.6e-172;
Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;

QY 1 MGSNKSXPRDASQRRSLSEPSNVHGA-GGAFPASQTPSKPASADGHRPSAAPVPAAE 59
DB 1 MGSNKSXPRDASQRRSLSEPSNVHGA-GGAFPASQTPSKPASADGHRPSAAPVPAAE 60
QY 60 PKLFGFNSDVTYSPQRAGALAGVTTFVALYDYESRTETDLSFKKGERLQIVNNTKRY 119
DB 61 PKLFGFNSDVTYSPQRAGALAGVTTFVALYDYESRTETDLSFKKGERLQIVNNT--- 117
QY 120 DVREGDMWLAHSLSTGQTYIPSNVYAPSDSIQAEWYFGKTRRESEBLLNAENPRGT 179
DB 118 ---EGDMWLAHSLSTGQTYIPSNVYAPSDSIQAEWYFGKTRRESEBLLNAENPRGT 174
QY 180 FLVRESETTKGAAYCLSVSDFDNAKGLNVGKIRKLDSCGFYITSTRQFNSLQOLVAAYS 239
DB 175 FLVRESETTKGAAYCLSVSDFDNAKGLNVGKIRKLDSCGFYITSTRQFNSLQOLVAAYS 234
QY 240 KHADGICHLITVCPYSPKQTOGLAKDAWEIPRESLRLEVKLGOGCGFGEVMMGTWGTTR 299
DB 235 KHADGICHLITVCPYSPKQTOGLAKDAWEIPRESLRLEVKLGOGCGFGEVMMGTWGTTR 294
QY 300 VAIKTLKPGTMSPEAFLOEAQVWKKLRHEKLVQLYAVVSEEPYIYVTEYMNKSLDDFLK 359
DB 295 VAIKTLKPGTMSPEAFLOEAQVWKKLRHEKLVQLYAVVSEEPYIYVTEYMNKSLDDFLK 354
QY 360 GETGKYLRLPOLVDMSAQIASGMAYYERNVYHRDLRAANILVGENLVCKVADFGIARLI 419
DB 355 GETGKYLRLPOLVDMSAQIASGMAYYERNVYHRDLRAANILVGENLVCKVADFGIARLI 414
QY 420 EDNETYAROGAKPPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVYPGMYNREV 479
DB 415 EDNETYAROGAKPPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVYPGMYNREV 474
QY 480 LQOVERGYMPCPPECPSLHDMCQWKEBERPTFEYLQAFLEDYFTSTEPYQOPGE 539
DB 475 LQOVERGYMPCPPECPSLHDMCQWKEBERPTFEYLQAFLEDYFTSTEPYQOPGE 534
QY 540 NL 541
DB 535 NL 536

RESULT 7
US-10-691-079-2
Sequence 2, Application US/10691079
Publication No. US20040176313A1
GENERAL INFORMATION:
APPLICANT: AVENTIS PHARMA S.A.
TITLE OF INVENTION: Inhibitors of SRC kinase for use in Alzheimer's disease
FILE REFERENCE: FRAV2002/0030
CURRENT APPLICATION NUMBER: US/10/691,079
CURRENT FILING DATE: 2003-10-22
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 536
TYPE: PRT
ORGANISM: Homo sapiens
US-10-691-079-2

Query Match 97.2%; Score 2778.5; DB 4; Length 536;
Best Local Similarity 97.6%; Pred. No. 6.6e-172;
Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;

QY 1 MGSNKSXPRDASQRRSLSEPSNVHGA-GGAFPASQTPSKPASADGHRPSAAPVPAAE 59
DB 1 MGSNKSXPRDASQRRSLSEPSNVHGA-GGAFPASQTPSKPASADGHRPSAAPVPAAE 60
QY 60 PKLFGFNSDVTYSPQRAGALAGVTTFVALYDYESRTETDLSFKKGERLQIVNNTKRY 119
DB 61 PKLFGFNSDVTYSPQRAGALAGVTTFVALYDYESRTETDLSFKKGERLQIVNNT--- 117
QY 120 DVREGDMWLAHSLSTGQTYIPSNVYAPSDSIQAEWYFGKTRRESEBLLNAENPRGT 179
DB 118 ---EGDMWLAHSLSTGQTYIPSNVYAPSDSIQAEWYFGKTRRESEBLLNAENPRGT 174
QY 180 FLVRESETTKGAAYCLSVSDFDNAKGLNVGKIRKLDSCGFYITSTRQFNSLQOLVAAYS 239
DB 175 FLVRESETTKGAAYCLSVSDFDNAKGLNVGKIRKLDSCGFYITSTRQFNSLQOLVAAYS 234
QY 240 KHADGICHLITVCPYSPKQTOGLAKDAWEIPRESLRLEVKLGOGCGFGEVMMGTWGTTR 299
DB 235 KHADGICHLITVCPYSPKQTOGLAKDAWEIPRESLRLEVKLGOGCGFGEVMMGTWGTTR 294
QY 300 VAIKTLKPGTMSPEAFLOEAQVWKKLRHEKLVQLYAVVSEEPYIYVTEYMNKSLDDFLK 359
DB 295 VAIKTLKPGTMSPEAFLOEAQVWKKLRHEKLVQLYAVVSEEPYIYVTEYMNKSLDDFLK 354
QY 360 GETGKYLRLPOLVDMSAQIASGMAYYERNVYHRDLRAANILVGENLVCKVADFGIARLI 419
DB 355 GETGKYLRLPOLVDMSAQIASGMAYYERNVYHRDLRAANILVGENLVCKVADFGIARLI 414
QY 420 EDNETYAROGAKPPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVYPGMYNREV 479
DB 415 EDNETYAROGAKPPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVYPGMYNREV 474
QY 480 LQOVERGYMPCPPECPSLHDMCQWKEBERPTFEYLQAFLEDYFTSTEPYQOPGE 539
DB 475 LQOVERGYMPCPPECPSLHDMCQWKEBERPTFEYLQAFLEDYFTSTEPYQOPGE 534
QY 540 NL 541
DB 535 NL 536

RESULT 8
US-10-887-588-2
Sequence 2, Application US/10887588
Publication No. US20040261142A1
GENERAL INFORMATION:
APPLICANT: Yeaman, Timothy J.
TITLE OF INVENTION: Mutated SRC Oncogene Composition and Methods
FILE REFERENCE: USF-T136
CURRENT APPLICATION NUMBER: US/10/887,588
CURRENT FILING DATE: 2004-07-09
PRIOR APPLICATION NUMBER: US/09/444,711
PRIOR FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 536
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (1)_(536)
OTHER INFORMATION: amino acid sequence of non-receptor tyrosine kinase encoded
by the normal c-Src coding region
US-10-887-588-2

Query Match 97.2%; Score 2778.5; DB 5; Length 536;

Best Local Similarity 97.6%; Pred. No. 6.6e-172;
Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;

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QY 1 MGSNKSAPKQASQRRRSLEPSENHGA-GGAFPASQTPSKPASADGHRGSPAAPVPAAE 59
DB 1 MGSNKSAPKQASQRRRSLEPSENHGAAGGAGFPASQTPSKPASADGHRGSPAAPVPAAE 60
QY PKLPGFNSSDVTYSPORAGLAGVTTFFVALYDESRTETDLSFKKGERLOIVNNTRKV 119
DB PKLPGFNSSDVTYSPORAGLAGVTTFFVALYDESRTETDLSFKKGERLOIVNNTRKV 117
QY 120 DVREGDWWLAHSLSTGTGYIPSNYVAPSDSIQAEWYFGKITRRESERLLNENPRGT 179
DB 118 ---BGDWWLAHSLSTGTGYIPSNYVAPSDSIQAEWYFGKITRRESERLLNENPRGT 174
QY 180 FLVRESSTTGAYCLSYSDPDNAGLVKVKYIKRKLDSGGFYITSRQFNSLQOLVAYYS 239
DB 175 FLVRESSTTGAYCLSYSDPDNAGLVKVKYIKRKLDSGGFYITSRQFNSLQOLVAYYS 234
QY 240 KHADGLCHRLTTVCPSTKPTQGLAKDAMEIPRESLREVLGGCGEVMGTWGTTR 299
DB 235 KHADGLCHRLTTVCPSTKPTQGLAKDAMEIPRESLREVLGGCGEVMGTWGTTR 294
QY 300 VALKTLPGTMSPEAFLOEAQVMKKLHHEKLVOLYAVSEPIYIVTEYNSKSLDPLK 359
DB 295 VALKTLPGTMSPEAFLOEAQVMKKLHHEKLVOLYAVSEPIYIVTEYNSKSLDPLK 354
QY 360 GETSKYRLPOLVDMASQIASGMAYVERMNYVHRDLRAANILVGENLVCKVADFGLARLI 419
DB 355 GETSKYRLPOLVDMASQIASGMAYVERMNYVHRDLRAANILVGENLVCKVADFGLARLI 414
QY 420 EDNETYARQAKKEPKMTAPBAALYGRFTIKSDVMSFGILLTETTKGRVYPGVMNREV 479
DB 415 EDNETYARQAKKEPKMTAPBAALYGRFTIKSDVMSFGILLTETTKGRVYPGVMNREV 474
QY 480 LDQVERGYRMPCEPCESLHDLMCQCRKEPEERPFTEYLOAFLEDFYFSTEPQYQGE 539
DB 475 LDQVERGYRMPCEPCESLHDLMCQCRKEPEERPFTEYLOAFLEDFYFSTEPQYQGE 534
QY 540 NL 541
DB 535 NL 536
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```
RESULT 9
US-10-497-641-2
; Sequence 2, Application US/10497641
; Publication No. US20050037446A1
; GENERAL INFORMATION:
; APPLICANT: Schmitt and Stork
; TITLE OF INVENTION: AGENTS THAT RECOGNIZE SRC WHEN PHOSPHORYLATED AT SERINE 17
; FILE REFERENCE: 65064-02
; CURRENT APPLICATION NUMBER: US/10/497,641
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: PCT/US02/41564
; PRIOR FILING DATE: 2002-12-27
; PRIOR APPLICATION NUMBER: 60/345,888
; PRIOR FILING DATE: 2001-12-28
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-497-641-2
```

Query Match 97.2%; Score 2778.5; DB 5; Length 536;
Best Local Similarity 97.6%; Pred. No. 6.6e-172;
Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;

```
QY 1 MGSNKSAPKQASQRRRSLEPSENHGA-GGAFPASQTPSKPASADGHRGSPAAPVPAAE 59
DB 1 MGSNKSAPKQASQRRRSLEPSENHGAAGGAGFPASQTPSKPASADGHRGSPAAPVPAAE 60
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QY 60 PKLPGFNSSDVTYSPORAGLAGVTTFFVALYDESRTETDLSFKKGERLOIVNNTRKV 119
DB 61 PKLPGFNSSDVTYSPORAGLAGVTTFFVALYDESRTETDLSFKKGERLOIVNNTRKV 117
QY 120 DVREGDWWLAHSLSTGTGYIPSNYVAPSDSIQAEWYFGKITRRESERLLNENPRGT 179
DB 118 ---BGDWWLAHSLSTGTGYIPSNYVAPSDSIQAEWYFGKITRRESERLLNENPRGT 174
QY 180 FLVRESSTTGAYCLSYSDPDNAGLVKVKYIKRKLDSGGFYITSRQFNSLQOLVAYYS 239
DB 175 FLVRESSTTGAYCLSYSDPDNAGLVKVKYIKRKLDSGGFYITSRQFNSLQOLVAYYS 234
QY 240 KHADGLCHRLTTVCPSTKPTQGLAKDAMEIPRESLREVLGGCGEVMGTWGTTR 299
DB 235 KHADGLCHRLTTVCPSTKPTQGLAKDAMEIPRESLREVLGGCGEVMGTWGTTR 294
QY 300 VALKTLPGTMSPEAFLOEAQVMKKLHHEKLVOLYAVSEPIYIVTEYNSKSLDPLK 359
DB 295 VALKTLPGTMSPEAFLOEAQVMKKLHHEKLVOLYAVSEPIYIVTEYNSKSLDPLK 354
QY 360 GETSKYRLPOLVDMASQIASGMAYVERMNYVHRDLRAANILVGENLVCKVADFGLARLI 419
DB 355 GETSKYRLPOLVDMASQIASGMAYVERMNYVHRDLRAANILVGENLVCKVADFGLARLI 414
QY 420 EDNETYARQAKKEPKMTAPBAALYGRFTIKSDVMSFGILLTETTKGRVYPGVMNREV 479
DB 415 EDNETYARQAKKEPKMTAPBAALYGRFTIKSDVMSFGILLTETTKGRVYPGVMNREV 474
QY 480 LDQVERGYRMPCEPCESLHDLMCQCRKEPEERPFTEYLOAFLEDFYFSTEPQYQGE 539
DB 475 LDQVERGYRMPCEPCESLHDLMCQCRKEPEERPFTEYLOAFLEDFYFSTEPQYQGE 534
QY 540 NL 541
DB 535 NL 536
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```
RESULT 10
US-10-825-568-10
; Sequence 10, Application US/10825568
; Publication No. US20050069916A1
; GENERAL INFORMATION:
; APPLICANT: Brian T. Chait
; APPLICANT: Darin R. Latimer
; APPLICANT: Paul M. Lizardi
; APPLICANT: Eric R. Kershner
; APPLICANT: Jon S. Morrow
; APPLICANT: Matthew E. Roth
; APPLICANT: Martin J. Matcovich
; TITLE OF INVENTION: ULTRA-SENSITIVE DETECTION SYSTEMS
; FILE REFERENCE: 01173.000302
; CURRENT APPLICATION NUMBER: US/10/825,568
; PRIOR FILING DATE: 2004-04-14
; PRIOR APPLICATION NUMBER: US/09/929,266
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/224,939
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/283,498
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-825-568-10
```

Query Match 97.2%; Score 2778.5; DB 5; Length 536;
Best Local Similarity 97.6%; Pred. No. 6.6e-172;
Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;

QY 1 MSGNSKPKDASQRRSLSEPSENVHGA-GGAPPASQTPSKPASADHGRGSAAFVPPAAE 59
DB 1 MSGNSKPKDASQRRSLSEPSENVHGA-GGAPPASQTPSKPASADHGRGSAAFVPPAAE 60
QY 60 PKLFGFNSSDYTSFORAGALAGGTTTVALYDYESRTTDLSPFKGGERLQIVNNTTKV 119
DB 61 PKLFGFNSSDYTSFORAGALAGGTTTVALYDYESRTTDLSPFKGGERLQIVNNTTKV 117
QY 120 DVREGMMLAHSLSTGOTGYIPSNVYAPSDSIQAEEMYGKTRRESERLLNAENRGT 179
DB 118 ---EGDMMLAHSLSTGOTGYIPSNVYAPSDSIQAEEMYGKTRRESERLLNAENRGT 174
QY 180 FLVRESETTKGAACLSVSPFDNAKGLNVKHYKIRKLDGSGFYITSTRQFNSLQOLVAAYS 239
DB 175 FLVRESETTKGAACLSVSPFDNAKGLNVKHYKIRKLDGSGFYITSTRQFNSLQOLVAAYS 234
QY 240 KHAADGLCHRLTTCPTSKPQTQGLADAMEIPRESLRLEVKLQGGCFGEVWMTNGTTR 299
DB 235 KHAADGLCHRLTTCPTSKPQTQGLADAMEIPRESLRLEVKLQGGCFGEVWMTNGTTR 294
QY 300 VAIKTLKPGTMSPEALQEAQVWKLRHEKLVOLYAVSEEPYIYTEYMNKSGSLDLPLK 359
DB 295 VAIKTLKPGTMSPEALQEAQVWKLRHEKLVOLYAVSEEPYIYTEYMNKSGSLDLPLK 354
QY 360 GETGKTLRLPOLVDMASQIASGMAVYERNYVHRDLRAANILVGENLVCKVADFGIARLI 419
DB 355 GETGKTLRLPOLVDMASQIASGMAVYERNYVHRDLRAANILVGENLVCKVADFGIARLI 414
QY 420 EDNEYTARQAKFPITMTAPEALYGRFTIKSDVWSFGILLTELTTKGRVPYGMVNRREV 479
DB 415 EDNEYTARQAKFPITMTAPEALYGRFTIKSDVWSFGILLTELTTKGRVPYGMVNRREV 474
QY 480 LQOVERGYMPCPECPESLHDMCCMKREBERPFEYLOAFLEDYFTSTBPQOPGE 539
DB 475 LQOVERGYMPCPECPESLHDMCCMKREBERPFEYLOAFLEDYFTSTBPQOPGE 534
QY 540 NL 541
DB 535 NL 536

RESULT 11
US-10-821-231C-1
; Sequence 1, Application US/10821231C
; Publication No. US20050275837A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Dongmano
; APPLICANT: Ben-Amotz, Dor
; APPLICANT: Xie, Yong
; APPLICANT: Davison, Vincent J.
; APPLICANT: Mrozek, Melissa
; APPLICANT: Ortiz, Coraai
; TITLE OF INVENTION: PROCESS AND APPARATUS FOR SEGREGATION AND TESTING BY SPECTRAL
; FILE REFERENCE: 12264/17
; CURRENT APPLICATION NUMBER: US/10/821,231C
; PRIORITY FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 60/462,083
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: US 60/462,472
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: US 60/490,057
; PRIOR FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US 60/554,701
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/551,311
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 536
; TYPE: PRF
; ORGANISM: Homo sapiens

US-10-821-231C-1
Query Match 97.2%; Score 2778.5; DB 5; Length 536;
Best Local Similarity 97.6%; Pred. No. 6.6e-172;
Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;
QY 1 MSGNSKPKDASQRRSLSEPSENVHGA-GGAPPASQTPSKPASADHGRGSAAFVPPAAE 59
DB 1 MSGNSKPKDASQRRSLSEPSENVHGA-GGAPPASQTPSKPASADHGRGSAAFVPPAAE 60
QY 60 PKLFGFNSSDYTSFORAGALAGGTTTVALYDYESRTTDLSPFKGGERLQIVNNTTKV 119
DB 61 PKLFGFNSSDYTSFORAGALAGGTTTVALYDYESRTTDLSPFKGGERLQIVNNTTKV 117
QY 120 DVREGMMLAHSLSTGOTGYIPSNVYAPSDSIQAEEMYGKTRRESERLLNAENRGT 179
DB 118 ---EGDMMLAHSLSTGOTGYIPSNVYAPSDSIQAEEMYGKTRRESERLLNAENRGT 174
QY 180 FLVRESETTKGAACLSVSPFDNAKGLNVKHYKIRKLDGSGFYITSTRQFNSLQOLVAAYS 239
DB 175 FLVRESETTKGAACLSVSPFDNAKGLNVKHYKIRKLDGSGFYITSTRQFNSLQOLVAAYS 234
QY 240 KHAADGLCHRLTTCPTSKPQTQGLADAMEIPRESLRLEVKLQGGCFGEVWMTNGTTR 299
DB 235 KHAADGLCHRLTTCPTSKPQTQGLADAMEIPRESLRLEVKLQGGCFGEVWMTNGTTR 294
QY 300 VAIKTLKPGTMSPEALQEAQVWKLRHEKLVOLYAVSEEPYIYTEYMNKSGSLDLPLK 359
DB 295 VAIKTLKPGTMSPEALQEAQVWKLRHEKLVOLYAVSEEPYIYTEYMNKSGSLDLPLK 354
QY 360 GETGKTLRLPOLVDMASQIASGMAVYERNYVHRDLRAANILVGENLVCKVADFGIARLI 419
DB 355 GETGKTLRLPOLVDMASQIASGMAVYERNYVHRDLRAANILVGENLVCKVADFGIARLI 414
QY 420 EDNEYTARQAKFPITMTAPEALYGRFTIKSDVWSFGILLTELTTKGRVPYGMVNRREV 479
DB 415 EDNEYTARQAKFPITMTAPEALYGRFTIKSDVWSFGILLTELTTKGRVPYGMVNRREV 474
QY 480 LQOVERGYMPCPECPESLHDMCCMKREBERPFEYLOAFLEDYFTSTBPQOPGE 539
DB 475 LQOVERGYMPCPECPESLHDMCCMKREBERPFEYLOAFLEDYFTSTBPQOPGE 534
QY 540 NL 541
DB 535 NL 536

RESULT 12
US-10-469-469-273
; Sequence 273, Application US/10469469
; Publication No. US20060079493A1
; GENERAL INFORMATION:
; APPLICANT: FRITZ, LAWRENCE C.
; APPLICANT: BURROWS, FRANCIS J.
; TITLE OF INVENTION: METHODS FOR TREATING GENETICALLY-DEFINED PROLIFERATIVE
; FILE REFERENCE: CON-0010-USN
; CURRENT APPLICATION NUMBER: US/10/469,469
; PRIOR FILING DATE: 2003-08-27
; PRIOR APPLICATION NUMBER: PCT/US02/06518
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: 60/272,751
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 330
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 273
; LENGTH: 536
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-469-469-273
Query Match 97.2%; Score 2778.5; DB 5; Length 536;
Best Local Similarity 97.6%; Pred. No. 6.6e-172;

Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;

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Db 1 MGSNKSXPKQASQRRRLSPSEENVHGAAGGAFPASQTPSKPASADGHRGSAAPVPAAE 60
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Db 61 PKLFGFNSSDVTYVSPORAGLAGVTTFFVALYDSESTETDLSFKKGERLQIVNNT--- 117
QY 120 DVREGDWMLAHSLSGTGTGYIPSNYVAPSDSIQAEEMVFGKITRRESERLLNENPRT 179
Db 118 ---EGDWMLAHSLSGTGTGYIPSNYVAPSDSIQAEEMVFGKITRRESERLLNENPRT 174
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Db 175 FLVRESSTTGAYCYLSVDPNAGLVKVKYIKRLDSGGFYITSRTOFNSLQOLVAYYS 234
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Db 235 KHADGLCHRLTTVCPPTSKPOTQGLAKDAMEIPRESLRLVYKLGCGCFGEVMMGTWGTTR 294
QY 300 VAIKTLKPGTMSPEAFLOEAQVMKCLRHEKLVQLYAVVSEEPYIYVTEYNKSGSLDPLK 359
Db 295 VAIKTLKPGTMSPEAFLOEAQVMKCLRHEKLVQLYAVVSEEPYIYVTEYNKSGSLDPLK 354
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Db 355 GETGKYRLPOLVYMAQIASGMAVYERMYVHRDLRAANILVGENLVCKVADGLARLI 414
QY 420 EDNEYTAROGAKKFPDKMTAPPAALYGRFTIKSDVMSFGILLETTLTKGRVYVPGVNRV 479
Db 415 EDNEYTAROGAKKFPDKMTAPPAALYGRFTIKSDVMSFGILLETTLTKGRVYVPGVNRV 474
QY 480 LDQVGRGYRMPCEPCEBSLHDLMCQCRKEPESRPTFEYLQAFLEDYFTSTEPYOYGE 539
Db 475 LDQVGRGYRMPCEPCEBSLHDLMCQCRKEPESRPTFEYLQAFLEDYFTSTEPYOYGE 534
QY 540 NL 541
Db 535 NL 536
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RESULT 13

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US-11-233-510-24
; Sequence 24, Application US/11233510
; Publication No. US20060063190A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, Timothy J.
; APPLICANT: Whitehead, Clark M.
; APPLICANT: Malinowski, Douglas P.
; APPLICANT: Marcello, Raphael
; APPLICANT: Morel, Didier
; TITLE OF INVENTION: Methods and Compositions for Evaluating
; TITLE OF INVENTION: Breast Cancer Prognosis
; FILE REFERENCE: 46143/296738
; CURRENT APPLICATION NUMBER: US/11/233, 510
; PRIOR FILING DATE: 2005-09-22
; PRIOR APPLICATION NUMBER: 60/612, 073
; PRIOR FILING DATE: 2004-09-22
; PRIOR APPLICATION NUMBER: 60/611, 965
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-233-510-24
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Query Match 97.2%; Score 2778.5; DB 6; Length 536;
Best Local Similarity 97.6%; Pred. No. 6.6e-172;
Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;

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Db 1 MGSNKSXPKQASQRRRLSPSEENVHGAAGGAFPASQTPSKPASADGHRGSAAPVPAAE 60
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Db 61 PKLFGFNSSDVTYVSPORAGLAGVTTFFVALYDSESTETDLSFKKGERLQIVNNT--- 117
QY 120 DVREGDWMLAHSLSGTGTGYIPSNYVAPSDSIQAEEMVFGKITRRESERLLNENPRT 179
Db 118 ---EGDWMLAHSLSGTGTGYIPSNYVAPSDSIQAEEMVFGKITRRESERLLNENPRT 174
QY 180 FLVRESSTTGAYCYLSVDPNAGLVKVKYIKRLDSGGFYITSRTOFNSLQOLVAYYS 239
Db 175 FLVRESSTTGAYCYLSVDPNAGLVKVKYIKRLDSGGFYITSRTOFNSLQOLVAYYS 234
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Db 295 VAIKTLKPGTMSPEAFLOEAQVMKCLRHEKLVQLYAVVSEEPYIYVTEYNKSGSLDPLK 354
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Db 355 GETGKYRLPOLVYMAQIASGMAVYERMYVHRDLRAANILVGENLVCKVADGLARLI 414
QY 420 EDNEYTAROGAKKFPDKMTAPPAALYGRFTIKSDVMSFGILLETTLTKGRVYVPGVNRV 479
Db 415 EDNEYTAROGAKKFPDKMTAPPAALYGRFTIKSDVMSFGILLETTLTKGRVYVPGVNRV 474
QY 480 LDQVGRGYRMPCEPCEBSLHDLMCQCRKEPESRPTFEYLQAFLEDYFTSTEPYOYGE 539
Db 475 LDQVGRGYRMPCEPCEBSLHDLMCQCRKEPESRPTFEYLQAFLEDYFTSTEPYOYGE 534
QY 540 NL 541
Db 535 NL 536
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; Sequence 56, Application US/10394322A
; Publication No. US20030232391A1
; GENERAL INFORMATION:
; APPLICANT: Sunesis Pharmaceuticals, Inc.
; APPLICANT: Prescott, John C.
; TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
; FILE REFERENCE: 39750-0006 US
; CURRENT APPLICATION NUMBER: US/10/394, 322A
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 60/366, 892
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 535
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-394-322A-56
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Query Match 97.0%; Score 2773.5; DB 4; Length 535;
Best Local Similarity 97.6%; Pred. No. 1.4e-171;
Matches 528; Conservative 3; Mismatches 3; Indels 7; Gaps 2;

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Db 1 GSNKSXPKQASQRRRLSPSEENVHGAAGGAFPASQTPSKPASADGHRGSAAPVPAAE 60
QY 61 KLFGRFNSSDVTYVSPORAGLAGVTTFFVALYDSESTETDLSFKKGERLQIVNNTKVD 120
Db 61 KLFGRFNSSDVTYVSPORAGLAGVTTFFVALYDSESTETDLSFKKGERLQIVNNTKVD 120
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Db      61 KLFEGFNSDPTVTSPOBAGPLAGVTTFVALYDYESRTEFTDLSFKKGERLQIVNNT---- 116
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Db      117 --EGDMMLAHSLSTGQTGYIPSNYVAPSDSIQABEWTFGKITRRESERLLLNENPRGT 174
Qy      181 LVRESSETTKGAYCLSYSDFDNAGLVNKHAKIRLDSGGFYITSRTQFNSLQOLVAYYSK 240
Db      175 LVRESSETTKGAYCLSYSDFDNAGLVNKHAKIRLDSGGFYITSRTQFNSLQOLVAYYSK 234
Qy      241 HADGLCHRLTTVCPTSPKQTOGLAKDAWEIPRESLRLLEVKLGGCGFGEVMMGTWNGTTRV 300
Db      235 HADGLCHRLTTVCPTSPKQTOGLAKDAWEIPRESLRLLEVKLGGCGFGEVMMGTWNGTTRV 294
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Db      295 AITLKPGTMSPEAFLOBAQVMKKLRHEKLVOLYAVVSEEPITYITRYNKGSLDPLKG 354
Qy      361 ETGKYLRPLPOLVMSAQIASGMAYVERMNYVHRDLRAANILVGENLVCKVADFGLARLIE 420
Db      355 ETGKYLRPLPOLVMSAQIASGMAYVERMNYVHRDLRAANILVGENLVCKVADFGLARLIE 414
Qy      421 DNEYTAROGAKFPFKWTAPAEALYGRFTIKSDVMSFGILLTELTTKGRVYPGMVNRVYL 480
Db      415 DNEYTAROGAKFPFKWTAPAEALYGRFTIKSDVMSFGILLTELTTKGRVYPGMVNRVYL 474
Qy      481 DVERGYRMPCEPCEPSLHDLMCQCKRKEPBERPTEFYLOAFLEDYFTSTEBQYQGEN 540
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Qy      541 L 541
Db      535 L 535
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US-10-814-109-4
; Sequence 4, Application US/10814109
; Publication No. US20050222042A1
; GENERAL INFORMATION:
; APPLICANT: Salter, Michael
; APPLICANT: Gingrich, Jeffrey
; TITLE OF INVENTION: Method for Modification of NMDA Receptors Through Inhibition of S
; FILE REFERENCE: 2560 004
; CURRENT APPLICATION NUMBER: US/10/814,109
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 535
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-814-109-4
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Query Match      97.0%; Score 2773.5; DB 5; Length 535;
Best Local Similarity 97.6%; Pred. No. 1.4e-171;
Matches 528; Conservative 3; Mismatches 3; Indels 7; Gaps 2;
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Db      1 GSNKSKPKDASQRRRSLEPSENVHGAAGGAFPAHQTPSKPASADGHRGSPAAFPVPAAP 60
Qy      61 KLFEGFNSSPTVTSPOBAGPLAGVTTFVALYDYESRTEFTDLSFKKGERLQIVNNTAKVD 120
Db      61 KLFEGFNSSPTVTSPOBAGPLAGVTTFVALYDYESRTEFTDLSFKKGERLQIVNNT---- 116
Qy      121 VREGDMMLAHSLSTGQTGYIPSNYVAPSDSIQABEWTFGKITRRESERLLLNENPRGT 180
Db      117 --EGDMMLAHSLSTGQTGYIPSNYVAPSDSIQABEWTFGKITRRESERLLLNENPRGT 174
Qy      181 LVRESSETTKGAYCLSYSDFDNAGLVNKHAKIRLDSGGFYITSRTQFNSLQOLVAYYSK 240
Db      175 LVRESSETTKGAYCLSYSDFDNAGLVNKHAKIRLDSGGFYITSRTQFNSLQOLVAYYSK 234
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Qy      241 HADGLCHRLTTVCPTSPKQTOGLAKDAWEIPRESLRLLEVKLGGCGFGEVMMGTWNGTTRV 300
Db      235 HADGLCHRLTTVCPTSPKQTOGLAKDAWEIPRESLRLLEVKLGGCGFGEVMMGTWNGTTRV 294
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Db      295 AITLKPGTMSPEAFLOBAQVMKKLRHEKLVOLYAVVSEEPITYITRYNKGSLDPLKG 354
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Db      355 ETGKYLRPLPOLVMSAQIASGMAYVERMNYVHRDLRAANILVGENLVCKVADFGLARLIE 414
Qy      421 DNEYTAROGAKFPFKWTAPAEALYGRFTIKSDVMSFGILLTELTTKGRVYPGMVNRVYL 480
Db      415 DNEYTAROGAKFPFKWTAPAEALYGRFTIKSDVMSFGILLTELTTKGRVYPGMVNRVYL 474
Qy      481 DVERGYRMPCEPCEPSLHDLMCQCKRKEPBERPTEFYLOAFLEDYFTSTEBQYQGEN 540
Db      475 DVERGYRMPCEPCEPSLHDLMCQCKRKEPBERPTEFYLOAFLEDYFTSTEBQYQGEN 534
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Db      535 L 535
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Job time : 109.267 secs
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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 5, 2006, 17:37:49 ; Search time 7.01729 Seconds
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891.618 Million cell updates/sec

Title: US-10-691-079-3
Perfect score: 2859
Sequence: 1 MGSNKSXPDKASQRRSLRP.....AFLEDYFTSTPEYQYQENL 541

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 58871 seqs, 11565156 residues

Total number of hits satisfying chosen parameters: 58871

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.New*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1520	53.2	505	US-10-511-937-2991	Sequence 2991, Ap
2	1462.5	51.2	512	US-10-505-928-353	Sequence 353, App
3	1462.5	51.2	512	US-10-511-937-2492	Sequence 2492, Ap
4	1452	50.8	509	US-10-511-937-2467	Sequence 2467, Ap
5	832	29.1	631	US-11-312-958-60	Sequence 60, Appl
6	822	28.8	659	US-10-511-937-2593	Sequence 2593, Ap
7	795	27.8	620	US-10-511-937-2959	Sequence 2959, Ap
8	589.5	20.6	983	US-11-302-678-2	Sequence 2, Appl1
9	577	20.2	994	US-11-303-935-12	Sequence 12, Appl1
10	575	20.1	998	US-11-303-935-2	Sequence 2, Appl1
11	572.5	20.0	993	US-11-303-935-11	Sequence 11, Appl
12	556.5	19.5	1130	US-11-312-958-52	Sequence 52, Appl
13	488	17.1	894	US-11-251-465-21	Sequence 21, Appl1
14	483	16.9	943	US-11-255-147-6	Sequence 6, Appl1
15	481.5	16.8	885	US-10-505-928-432	Sequence 432, App
16	481.5	16.8	885	US-11-251-465-20	Sequence 20, Appl
17	478.5	16.7	346	US-11-255-147-4	Sequence 4, Appl1
18	478.5	16.7	348	US-11-255-147-2	Sequence 2, Appl1
19	476.5	16.7	422	US-11-251-465-67	Sequence 67, Appl1
20	476.5	16.7	422	US-11-251-465-70	Sequence 70, Appl
21	475	16.6	806	US-11-251-465-22	Sequence 22, Appl
22	470	16.4	972	US-11-255-147-8	Sequence 8, Appl1
23	457	15.8	1308	US-11-248-122-2	Sequence 2, Appl1
24	451	15.8	999	US-10-196-749-434	Sequence 434, App
25	440	15.4	391	US-11-223-945-38	Sequence 38, Appl

26	440	15.4	1259	7	US-11-223-945-40	Sequence 40, Appl
27	439	15.4	550	6	US-10-538-066-757	Sequence 757, App
28	439	15.4	1255	6	US-10-538-066-364	Sequence 364, App
29	439	15.4	1255	7	US-11-223-945-43	Sequence 43, Appl
30	434	15.2	993	6	US-10-511-937-2463	Sequence 2463, Ap
31	433	15.1	976	6	US-10-511-937-2423	Sequence 2423, Ap
32	433	15.1	1006	6	US-10-511-937-2425	Sequence 2425, Ap
33	420.5	14.7	1338	6	US-10-505-928-634	Sequence 634, App
34	420.5	14.7	1338	6	US-10-505-928-857	Sequence 857, App
35	411.5	14.4	1298	7	US-10-505-928-274	Sequence 274, App
36	407	14.2	953	7	US-11-312-958-56	Sequence 56, Appl
37	400	14.0	369	6	US-10-953-349-3910	Sequence 3909, Ap
38	400	14.0	374	6	US-10-953-349-3910	Sequence 3909, Ap
39	400	14.0	412	6	US-10-953-349-3908	Sequence 3908, Ap
40	394	13.8	344	6	US-10-511-814-2	Sequence 2, Appl1
41	394	13.8	648	6	US-10-511-814-14	Sequence 14, Appl
42	364.5	12.7	272	6	US-10-370-959-27	Sequence 27, Appl
43	364.5	12.7	278	6	US-10-370-959-17	Sequence 17, Appl
44	364.5	12.7	278	6	US-10-370-959-31	Sequence 31, Appl
45	364	12.7	247	7	US-11-251-465-75	Sequence 75, Appl

ALIGNMENTS

RESULT 1
US-10-511-937-2991
Sequence 2991, Application US/10511937
Publication No. US20060088836A1
GENERAL INFORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Wollgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
APPLICANT: Prentice, James
APPLICANT: Morris, Macdonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
FILE REFERENCE: 506612000104
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR FILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 10/325,899
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2991
LENGTH: 505
TYPE: PRT
ORGANISM: Homo sapiens
US-10-511-937-2991
Query Match 53.2%; Score 1520; DB 6; Length 505;
Best Local Similarity 55.7%; Pred. No. 2.7e-75;
Matches 299; Conservative 85; Mismatches 117; Indels 36; Gaps 6;
QY 1 MGSNKSXPDKASQRRSLRPSENVHAGAPFAPSQTPSKPASADGHRGSAFYPPAAEP 60
DB 1 MGSNKSXPDKASQRRSLRPSENVHAGAPFAPSQTPSKPASADGHRGSAFYPPAAEP 60
QY KLFGRFSSDVTYSPQAGALAGVTFV-VALVYBERSTEDLSFKKGERQIYNNTRKV 119
DB 41 ---GPNSHSNTPGIRE---AGSEDIIVVALDYEAIIHHEDLSFGQDQVVLSEES--- 90
QY 120 DVREGMWLAHSJSTGQGYIPSNVYVAPSDSIQAEWYFGKITRRESERLLTNENRGT 179
DB 91 ---GEMWKAISLATRKEGIIIPSNVYVAPSDSIQAEWYFGKITRRESERLLTNENRGT 146

[illegible]

US-10-505-928-353
 ? Sequence 353, Application US/10505928
 ? Publication No. US20060088532A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Ludwig Institute for Cancer Research et al
 ? TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
 ? FILE REFERENCE: 28967/39178
 ? CURRENT APPLICATION NUMBER: US/10/505,928
 ? CURRENT FILING DATE: 2004-08-27
 ? PRIOR APPLICATION NUMBER: US 60/363,019
 ? PRIOR FILING DATE: 2002-03-07
 ? NUMBER OF SEQ ID NOS: 866
 ? SOFTWARE: PatentIn 3.2
 ? SEQ ID NO 353
 ? LENGTH: 512
 ? TYPE: PRT
 ? ORGANISM: Homo sapiens
 ? US-10-505-928-353

Query Match	51.2%	Score 1462.5;	DB 6;	Length 512;
Best Local Similarity	53.1%	Pred. No. 3.3e-72;		
Matches 291; Conservative	86;	Mismatches 120;	Indels 51;	Gaps 10;

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QY 1 MSNSKKRPDA-----SQRBSLSESNVHAGAFAPASQTPPSKPAADCHRRPSA 51
Db 1 MGCTSKKGADSLSDGVDLKTQPVKXTEHTIIVR-----PTSKQCARP----- 44
QY 52 APVPAAEPKLPFG--FNSSDPTVTSPPRAGALAGVTTFVALYDYESRTETDLSFKKGR 109
Db 45 --VP---ESQLLPGRGFOTKD---PEEGGDIV-----VALYPDGIHPDLSLFFKKGK 89
QY 110 LQIVNNTRKAVDREGGWMVLAHSLSTGGTGYPSNVAASDSIOABEWYFGKITSREERL 169
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QY 170 LLAENPRTPLVRBSEETTKGAYCISVSDPDNAKGLNVKHYKIRKDSGGFYTSRTQFN 229
Db 143 LLAFGNSAGAFPIRESEETLKSGFSLSVDPDPVHDDVLAHKIKISLDNGGYISPRITFP 202
QY 230 SLQGLVAAYSKKADGLCHRLLTTCVPSKQPTGALAKDAMEI.PRSLSRL.EVLDGGCGGEV 289
Db 203 CISDMLTKHYQKQADGCRRLERAKCISPRQ--KPMXKDMELPRESIKLVKRLGAGCGEV 261
QY 290 WNGTANGTRVAIKTLKPGTMSPEAPLOBAQWKKLRHEKLVQLYAVVS--BEPIYIVTEY 348
Db 262 WNGYVNNSTKVAIVKTLKPGTMSVQAFLEBANIMKTLQHDKLVRYAVAVTRREPIYIITEY 321

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Qy	409	KVADFGIARLIEDNETYARQCAKFPFIKMTAPEALVGRFTIKSDVMSFGILLTELVTYKGR	468
Db	382	KIADFGIARVIEDNETYAREGAKFPFIKMTAPEALNFGFTIKSDVMSFGILLVYIIVYKGK	441
Qy	469	VVPYGMVNEBVLDDOYERGTRMPCPECESLHDLMOQWRKEPERPTFYLYLAFLDYF	528
Db	442	IPYRGATNADVMTALSQGYRMPRVENCDELDYIMKMKWEKAEERPTFDYLSGLDDFY	501
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RESULT 3
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; Sequence 2492, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2492
; LENGTH: 512
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2492

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Query Match	51.2%	Score 1462.5	DB 6	Length 512
Best Local Similarity	53.1%	Pred. No. 3.3e-72		
Matches 291	Conservative	86	Mismatches 120	Indels 51
			Gaps	10
Qy	1	MGNSKSPKDA-----SQRRLSPSENNHAGAGAPASQTPSKPASADGHRPSA	51	
Db	1	MGCIKSGKXDSLSDGDVLTQIPVRNERTITVYD-----FTSNKQORP-----	44	
Qy	52	AFVPAAPPLFEGS--FNSSPTVTPSRAGACAGVTTVALVYRESRTETDLSFFKGER	109	
Db	45	--VP---ESQLPGRQFQTKD-----PEEGQDIV-----VALVYDGIHPDLSFFKGER	89	
Qy	110	LQIVNTRKVDVREGDWMLAHSLSGTQGYIPSNVYAPSDSIQAEWYFGKTIRESERL	169	
Db	90	MKYLE-----EHGEWMAKASLTLTKEGFIPSNYVAKLTLEBEMFFKQITTKDAERQ	142	
Qy	170	LNAENRGTFLVYSEETTGAYCLASDPPMAKGLVWKYKIKLDSGGYVIRSTQFN	229	
Db	143	LNAENAGAFILRESETLKGSPSLVRDDEPYNQGVYKTKIRSLDNGGYISPIRTFP	202	
Qy	230	SLQGLVAYSKGADGLCHRLTTCVPTSKPQTQGLAKDAEIPBSRLAEVLGGQCGEIV	289	
Db	203	CISMIMHYGKQADGLCRLEKACISKPP--KPPDKDQAMEIPRESIKLVKRLAGQFQEV	261	

Qy	250	WNGTNGGTRVAIKTILPGTMSSEALOEAOVWKILRHEKLYOLUAVVS--EERIYITVEY	348
Db	252	MMGYNNSTKVAVKTLKPGTMSQALTEBEANMKTKIQHDLVRLVYNAVYTBEPPIIITTEY	322
Qy	349	MAKGSILDLPLKSETGKTYLRPLQVLVMSAQIYASGMAVYERKNYTHYRDLRAANILVGENLVC	408
Db	352	MAKGSILDLPLKSDDEGKVLPLPKLIDESAQIYASGMAVYERKNYTHYRDLRAANVTVSESLMC	383
Qy	409	KVADFGILARLIEDNENETAROGAKFPIKMTAPBEALVGRPTIKSDVMSFGILLTELTTKGR	468
Db	382	KIADFGILARVIEDNETTABEGAKFPIKMTAPBEALINOCGPIITIKSDVMSFGILLTEIYTYGK	444
Qy	469	VYPGMAVNEVLDOVERGYRMPCCPECPBSLHDLKQCMWKEBBERPTFELYLAFLDYF	528
Db	442	IYPERTADVMTALSOGYRMPREVENCPELDYIMCMWKEKABERPTFELYLSLDDFY	501
Qy	529	TSTEPQYQ	536
Db	502	TATEGOYQ	509

```

1      RESULT 4
2      US-10-511-937-2467
3      : Sequence 2467, Application US/10511937
4      : Publication No. US20060088836A1
5      : GENERAL INFORMATION:
6      : APPLICANT: EXPRESSION DIAGNOSTICS, INC.
7      : APPLICANT: Mohlgemuth, Jay
8      : APPLICANT: Fry, Kirk
9      : APPLICANT: Woodward, Robert
10     : APPLICANT: Ly, Ngoc
11     : APPLICANT: Prentice, James
12     : APPLICANT: Morris, Macdonald
13     : APPLICANT: Rosenberg, Steven
14     : TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
15     : TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
16     : FILE REFERENCE: 506612000104
17     : CURRENT APPLICATION NUMBER: US/10/511,937
18     : CURRENT FILING DATE: 2004-10-19
19     : PRIOR APPLICATION NUMBER: PCT/US2003/012946
20     : PRIOR FILING DATE: 2003-04-24
21     : PRIOR APPLICATION NUMBER: US 10/131,831
22     : PRIOR FILING DATE: 2002-04-24
23     : PRIOR APPLICATION NUMBER: US 10/325,899
24     : PRIOR FILING DATE: 2002-12-20
25     : NUMBER OF SEQ ID NOS: 3117
26     : SOFTWARE: PatentIn version 3.2
27     : SEQ ID NO 2467
28     : LENGTH: 509
29     : TYPE: PRT
30     : ORGANISM: Homo sapiens
31     : US-10-511-937-2467

```

Query Match	50.8%	Score 1452;	DB 6;	length 509;
Best Local Similarity	59.7%;	Pred. No. 1,2e-71;		
Matches	268;	Conservative	80;	Mismatches 93; Indels 8; Gaps 2

QY	89	VALVDYESTRTETDLSFKKGERLQIVNNTRKVDVREGDWMVLAHSLSTGQTGYTPSNVAPS	148
DB	67	IALSHYSESHODLDFEKGEPLRIIE-----OSGEWMAKQSLTGGCGGFIPIFNFAVKA	119
QY	149	DSIOAEKRYPGKTRRESERLTLNANENPGCTFLVASEETTKAYCICLAVSDPFINAGLANK	208
DB	120	NSLEEPFPFKULSKDARQLAAQNTYAGSLIIRSESTAGSFSLAVNDFPQNGGEVVK	179
QY	209	HYKIRKLDSGGFIYTSRTQFNSLQOLVAVYSKADGLCHRLTTVCEPYSKPQTQGLAKDAM	268
DB	180	HYKINLNGGFIYIPRIITFPGLHEILVRHYTNASGLCTRLRSPCQTQPKQ-KPMWEDHW	238
QY	269	EIPRESLILEVLDGGCGGCEVVMGMMNNTTRVAITLIKPGTMSPPAFIOEADVMKKRLR	328
DB	239	EIPRETLTKLVERLNGQGFGEVMMGTYNGHTTKAAVNSLKGGSNSPDAFLAEANLIMKOLQIQ	298

Qy	389	NYVHDELPANILVGENVCVKVADFGLARLIEDNEYTAFOGAKFPIKMTAPEALTYGRFT	448
Db	299	RLVRLYNAVVOGEPIITIEHMYENGSVDFPKTTPSGIKULINKLDDMAQIAESMATEIBER	358
Qy	329	KLVOIVYAVASEEPITIVEMYNKSGILDFLKEKETGKTYLPLQIVDMSAQIAESMAVERB	388
Db	229	RLVRLYNAVVOGEPIITIEHMYENGSVDFPKTTPSGIKULINKLDDMAQIAESMATEIBER	358
Qy	449	IKSDVWSGIIILTELTTKGVRVYPCBMAWREVLDOYBGRVMACPPECPSLHLMQOCWR	508
Db	419	IKSDVWSGIIILTELTVTGRIIPYPCMTAPEVILQNLBGRVMAWPDNCPBELYQMLRLCMK	478
Qy	509	KEPEERPFEEYLOAFLEDYFTSTPEOYOP	537
Db	479	ERPEDEPFEDYLRVLEDFTRITEGOYOP	507

```

RESULT 5
US-11-312-958-60
; Sequence 60, Application US/11312958
; Publication No. US20060100152A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Rosenfeld, Julie Bech
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 9949, 14230, 760, 62553,
; TITLE OF INVENTION: 12216, 17719, 41897, 47174, 33408, 10002, 16209, 314, 636,
; TITLE OF INVENTION: 27410, 33260, 619, 15985, 62112, 2158, 224, 615, 44373,
; TITLE OF INVENTION: 95431, 22245, 2387, 16658, 55054, 16314, 1613, 1675, 9569 OR
; TITLE OF INVENTION: 13424 MOLECULES
; FILE REFERENCE: MP102-027P1R0NANIM
; CURRENT APPLICATION NUMBER: US/11/312,958
; CURRENT FILING DATE: 2005-12-20
; PRIOR APPLICATION NUMBER: US/10/369,022
; PRIOR FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: US 60/360,495
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/370,121
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/373,010
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US 60/373,908
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/377,717
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US 60/379,949
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/382,409
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/385,280
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 60/386,879
; PRIOR FILING DATE: 2002-06-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 631
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-312-958-60

```

```
Oy Query Match      29.1% Score 632; DB 7; Length 631;  
Best Local Similarity 37.9%; Pred. No. 2.9e-38;  
Matches 186; Conservative 92; Mismatches 169; Indels 44; Gaps 13  
  
Oy 54 VPPAAERK-----LFGFNSSDVTSPQAGALAGAIVTFVALDYESRTETDLSF 104  
    :|::||  
Db 157 LPPAPERTKKRRPPIPLEEDNSEELV-----VAWYDFQAEGHDRL 200  
    ::||:  
  
Oy 105 KKGERLOLVNTRKYVDREGDMWLASHISTGCTGYPSNYA--PSDSIQAEWFYGKIT 162  
     ||::||:|||||||::|||:
```

```

Db      201 ERGGEYLL--EKRDVH---MWRAPD-KYGNBGYIPSNVYTGKSSNNLDQYEWYCRNN 253
Qy      163 RRESERLLINMENPGTFLVRESEETTKGAYCLSV-SDPDNAKGLNHYKIRKLDG--G 219
Db      254 RSKAEQ-LIRSDKXGSGFVWRBS-SQPGLYTYSLYTKFGEGSSGRHHIKETTTSPK 311
Qy      220 FYITSRTQFNSIQOLVAAYYSKHADELCHRL--TIVCPTSKPOTOGILAKDAWEI PRESLR 276
Db      312 YLAEKHAFGSIPELIIEYHKHNAAGVLTFLRNPVSKGNAPPTAAGSYEKMWINSLELT 372
Qy      277 LEVLKGOCFCGEVWNGCTNQTTRVALIKTLKPGTMSBEAFLOEAOVNMKJLHHEKLVOLYAV 336
Db      372 FMRELGSGLFGVYRLGSKMRAQYKVAIKAIRGAMCEDEFLBEAKVMKJLHPLVOLDYGV 431
Qy      337 VSEE-PIYIVTEYKNGKSLIDFLKSGETGYLRLPOLVDNSAQIASGMAVYERNVYHARDL 395
Db      432 CTQGRPIYIVTEFMRGCLINLFRQGHFSR-DVLLSNCOVDCEGMEYLERNSFIHRDL 490
Qy      396 RPAANLVGENLVCKYADAGLALIEDNETATOGAKFPIKMTAPEALYGRFPTIKSDVNS 455
Db      491 AARNCLVSEAGVAVKYSDFGMARYFLDDQYGTSSGAKFPYKMCPPFVFNYSRFSKSDVNS 550
Qy      456 FGIILLTTLTKGRVYIPGMVNRREVLDQYERGRMPCPBPCCPSBHLDMCOCKRKEBERP 515
Db      551 FGVLMVEVFTEGRMPEKXTYNEVVMYRGHRLYOPKLASNVYVEMLRCMQKEGRP 610
Qy      516 TFEVYQALFED 526
Db      611 SFEDLLRTIDE 621

```

RESULT 6
US-10-511-937-2593

```

Sequence 2593, Application US//10511937
Publication No. US20060088636A1
GENERAL INFORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Wohlgenuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
APPLICANT: Prentice, James
APPLICANT: Morris, Macdonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
FILE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
FILE REFERENCE: 506612000104
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR FILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: patentIn version 3.2
SEQ ID NO 2593
LENGTH: 659
TYPE: PRT
ORGANISM: Homo sapiens
US-10-511-937-2593

```

Query Match	28.8%	Score 822;	DB 6;	Length 659;
Best Local Similarity	36.4%	Pred. No. 1e-37;		
Matches 181; Conservative	94;	Mismatches 194;	Indels 28;	Gaps 13;

QY 33 KPSADGHRKPSAFLPPPAEPKLCFGFNSDVTYSPOAGLACAGVTTVALIYBERT 98
Db 176 KPSS--HRTKTKPLPTEEDQIL---KKLPPEPAAPVSTELKKVALIYDPMEN 221
QY 99 EPTLSFKGERLQIVNTRKVDVREEDMWLAISLSTGCGYIIPSNVAPS-DLSIAEEMV 15

[illegible]

RESULT 7
US-10-511-937-2959

```

: Sequence 2959, Application US/10511937
: Publication No. US20060088836A1
:
: GENERAL INFORMATION:
:
: APPLICANT: EXPRESSION DIAGNOSTICS, INC.
: APPLICANT: Wohlgenuth, Jay
: APPLICANT: Fry, Kirk
: APPLICANT: Woodward, Robert
: APPLICANT: Ly, Ngoc
: APPLICANT: Prentice, James
: APPLICANT: Morris, MacDonald
: APPLICANT: Rosenberg, Steven
: TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
: TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
: FILE REFERENCE: 506612000104
: CURRENT APPLICATION NUMBER: US/10/511,937
: CURRENT FILING DATE: 2004-10-19
: PRIOR APPLICATION NUMBER: PCT/US2003/012946
: PRIOR FILING DATE: 2003-04-24
: PRIOR APPLICATION NUMBER: US 10/131,831
: PRIOR FILING DATE: 2002-04-24
: PRIOR APPLICATION NUMBER: US 10/325,899
: PRIOR FILING DATE: 2002-12-20
: NUMBER OF SEQ ID NOS: 3117
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 2959
:
: LENGTH: 620
:
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-10-511-937-2959

```

Query Match	27.8%	Score 795;	DB 6;	Length 620;
Best Local Similarity	34.8%;	Pred. No. 2.7e-36;		
Matches 179;	Conservative	90;	Mismatches 181;	Indels 64;
				Gaps 15

```
OY      19  ESENVEHAGGAFPAASQTPEKRPASADHGRRSAALVPPAAEKKLFEGGRSSDVTISPOA 78
       ::::|
Db      147  DPTGN-----ASKKPLPTEPDNRR-----FLMEPE-----172
               |
OY      79  GALAGGYTFVALDYBSRTETDLSPFKKGRLQIVNNTRKYDVREGDWLWLSLSTGGNG 138
       :|||::|::|::|::|::|::|::|
```

Db 173 -----ETVIALYDQTNDFQELALRNREYCL-----LDSEIHMMRVQD-RNGHBG 219
Qy 139 YIISNVAAPS--DSIOABEYTFGKITRRESRLILNENPMTVLNRESETTKAYCLISV 196
Db 220 YPSSSYLVKSPNNLEFYEWYTKSISRDKAELLDLT-GKEGAMVWDSRTA-GTYTVSV 277
Qy 197 SDPDNA----KGLVKKYKIRKLDG--GFYTSRTQFNSLQOLVAAYSKADGICRLT 250
Db 278 --FTKAVASERNPCIKYHIKETNDNPKRYVAEKYFDSIPLLINHONGGGLVTRLR 335
Qy 251 -TVC--PTSKPQTQGLAKDAWEIPRESIRLEVKLGQCGFGEVMGTWNGTTRVAIKTLKP 307
Db 336 YPVCFGKQKAPVTAGLRYGKVVIDPSELTFQVIGSGQFGLVHLGYMLNKKOKVAIKIRRE 395
Qy 308 GTMSPEAFLOAOVMKLRHEKLVOLYAVVSE--PIYIVTEYNNKGLSLDLKSETGKYL 366
Db 396 GANSEDFEIEBAEYMWKLSHPKLVOLYGVCLQAPICLVEFEMHGCLSDLTRQGLF- 454
Qy 367 RLPOVMSAQIAGMAVVERMNVVHRDLRAANILVGENLVCKVADFGLABLIEDNEXTA 426
Db 455 AAEITLDMCLDVCGMAYLEBACVIHRDLAARNCVGENOVYIKVSDFGMTFVLDDQITS 514
Qy 427 ROGAKPFIKWTAPALYGRFTIKSDVMSFGILLTELTKGRVVPYGMVNRVLDQYERG 486
Db 515 STGKRFVVKASPEVFSFSRYSKSDVMSFGVLMMEVFPSSBKIPYENRNSVEVEDISTG 574
Qy 487 YRMPCEPCEBSLHLMCQCKRKEPERPTEYL 520
Db 575 FRLYKFLASTHYQYIMNHCKEREDRPAFSRL 608
RESULT 8
US-11-302-678-2
Sequence 2, Application US/11302678
Publication No. US20060088881A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Silos-Santiago, Immaculada
APPLICANT: Venkateswarulu, Karicheti
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING 34021, 44099, 25278,
TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559,
TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323,
TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
FILE REFERENCE: MP102-012P1NM, OMNI
CURRENT APPLICATION NUMBER: US/11/302,678
CURRENT FILING DATE: 2005-12-14
PRIOR APPLICATION NUMBER: US/10/345,680
PRIOR FILING DATE: 2003-01-16
PRIOR APPLICATION NUMBER: US 60/349,511
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/360,500
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/365,041
PRIOR FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: US 60/374,063
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/403,468
PRIOR FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: US 60/414,262
PRIOR FILING DATE: 2002-09-27
PRIOR APPLICATION NUMBER: US 60/419,986
PRIOR FILING DATE: 2002-10-21
PRIOR APPLICATION NUMBER: US 60/423,809
PRIOR FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: US 60/429,797
PRIOR FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 66
SOFTWARE: FastrSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 983
TYPE: PRT
ORGANISM: Homo Sapiens
US-11-302-678-2

Query Match 20.6%; Score 589.5; DB 7; Length 983;
Best Local Similarity 31.0%; Pred. No. 4.7e-25;
Matches 173; Conservative 82; Mismatches 166; Indels 137; Gaps 20;
Qy 49 PSAFAVPEAPAEPKLFGGNSSDVTSPQAGALAGVTTFVALYDYESRTETDLSFKKGE 108
Db 378 PNRVFL-----PRPFGILNTTVYT-----D 398
Qy 109 RLQIVNNTKRVNRESGMWMLAHSLSGTQGY----ISNVAAPSDSIOABEYTFGKITR 164
Db 399 LIAHTNTPFIDAVNG-----VSELSSPPROFAAVSITTNQAPSPVLTIKK---DRSRN 451
Qy 165 ESERLLMANPNCTFL-----VRESFTGAYCLSDPDMAGLVNK-----H 209
Db 452 SISLSWQEPHPNGIILDEYKTYEKOQETSYTL-----RANGNVTLSLKPDTIYV 506
Qy 210 YKIRKLSGCFYIYSRT-QFNS-----LQQ 233
Db 507 FQIPARTAGYGTNSKRFEPFTSPDSISGSSQVMMIAISAVAILLTVIYVILGR 566
Qy 234 LVAYSRH-AD-----GLCHRLTVCP-TSKPQTQGLAKDAWEIPRESIRL 277
Db 567 FCGYKSGHGADEKRLHFGNGLKLPGL---RTYVDPTVEDPTQAVHFAKELDATNISI 623
Qy 278 EYVLGQCGFGEVMMGTNGTTR-----VAIKTLKGTMSPEA--FLOBAQVMKLRHEKLV 331
Db 624 DKVVGAGEFGEVCSGRKLPSKKEISVAIKTLKGYTEKRRDLGERASIGQDPHPNI 683
Qy 332 QLYAVASE-PIYIVTEYNNKGLSLDLFKGETGKYLRLPOLVMSAQIAGMAVVERMNV 390
Db 684 RLBSVVTKSKEPMIVITYMENGLSDSLFKRKHDAQFYI-QLVGLRLGIASMKLSDMGY 742
Qy 391 VHRDLRAANILVGENLVCKVADFGLABLIEDN--EYTAQAKPFIKWTAPALYGRF 447
Db 743 VHRDLAARNILINSNLVCKVSDFLSRVLEDDPEAAVYTR-GGKIPIRMTSPBAIAVRKF 801
Qy 448 TISDVMSEGLITELTKGRVPPYGMVNRVLDQYERGTRMPCPEBSLHLMCQW 507
Db 802 TSASDVSYGIIVMEWVSYGERPYMENSNDYIKAVDEGYRLPPPMDCPALYQMLMDCW 861
Qy 508 RKPEPERPTEYLOAFLE 525
Db 862 QKDNNRPKEQIVSILD 879
RESULT 9
US-11-303-935-12
Sequence 12, Application US/11303935
Publication No. US20060099708A1
GENERAL INFORMATION:
APPLICANT: Ciosek, Thomas
APPLICANT: Ullauer, Axel
TITLE OF INVENTION: METHODS FOR DIAGNOSIS
AND TREATMENT OF MDKI
SIGNAL TRANSDUCTION
DISORDERS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1

QY 75 -----PORAGALAGVTTFFVAL-----YDYESRT 98
DB 358 GGRNDVTYRLICKRCSEWQECVPCGSGNIGMPOQTGLEDNYVTVMOLLAHANTFFVEA 417
QY 99 ETDLS-FKGERLQIVNNTRKVDVREGDWMLHLSLSTGQGTGYPISNVAAPS--DSIOAEB 155
DB 418 VNGVSDLSRSQRL-----FAAVSITTTQ-----AAFSQVSGWKKE- 452
QY 156 WYFKITRRESERILLNAENPRG-----TFVRESETTGACVCLASVD 198
DB 453 -----RVLQRSYQLSWQEPHEPNVITTEYEIKYEEKQDERTYSTLKXSTS-----AS 501
QY 199 FDNAGKLVNHYKTKRKLDGSGF-YITSRTQNSLQQLVAYYSKADGLCHRLTTY----- 252
DB 502 INNLKPGTVYFQIRAVTAAGYGNYSPLDVATLEE-----ASGMFEATVVSSEQN 553
QY 253 -----CPTSKPQTQ-----LAKDA 267
DB 554 PVIIVANVAVAGTIIIVFWVPGFIIGRRHCGYSKADQEGDEBELYFHKFPQTKYIIDPET 613
QY 268 WEIIPRES-----LRLEVKLGQCGFGEVWVG---TWNGTTRVAIKTLKPGTMS 311
DB 614 YEDBNRAVHQPAKELDASCIRIEKRVIGAGEFVCSGRLKLPQGRDVAVALIKLVGTYE 673
QY 312 PEA--FLQEAQVMKLAHEKLVLYAVVSE-EPYIYTEYMNKSLDPLKGETGKTLRL 368
DB 674 KORRDFICEASIMQGFPHPNVHLEGVYTRCKPMAIYIEFMENALDAFLKHDGQFVI 733
QY 369 POLVDMSAQASGAAYVERMYVHRDLRAANILVGENLYCVADFGIARLIEDNE---YT 425
DB 734 -QLVGMRLGIAAGKRYLADMGYVHRDLAARILVNSNLVCKVSDFGLSRVIEDDPEAVYT 792
QY 426 ARQAKPEPIKATBAALYGRFTIKSDVMSFGILLTELTKGAVPYPGVMNREVLDOVER 485
DB 793 T-TGKXLPVMTAEALQYRKFTSASDVMSYGIWMEMTMSYGERPYDMSNQDVIKAIIE 851
QY 486 GYRMPCEPCESLHDLMOQCKRKEPERPTEFYLOAFLE 525
DB 852 GYRLPAPMDCPAGLHQLMDCMQDRAERKFEQIVGLD 891

RESULT 11
US-11-303-935-11
; Sequence 11, Application US/11303935
; Publication No. US20060099708A1
; GENERAL INFORMATION:
; APPLICANT: Closeek, Thomas
; Ullrich, Axel
; Millauef, Birgit
; TITLE OF INVENTION: METHODS FOR DIAGNOSIS
; AND TREATMENT OF MDK1
; SIGNAL TRANSDUCTION
; DISORDERS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; STORAGE
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/303,935
; FILING DATE: 19-Dec-2005
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

Application Number: US/10/073,064
Filing Date: 12-Feb-2002
Application Number: US/08/438,265
Filing Date: May 9, 1995
Application Number: US/08/368,776
Filing Date: January 3, 1995
Application Number: <Unknown>
Filing Date: <Unknown>
Attorney/Agent Information:
Name: Waibury, Richard J.
Registration Number: 32,327
Reference/Docket Number: 208/007
Telecommunication Information:
Telephone: (213) 489-1600
Telefax: (213) 955-0440
Telex: 67-3510
Information for Seq ID No: 11:
Sequence Characteristics:
Length: 993 amino acids
Type: amino acid
Strandedness: single
Topology: linear
Molecule type: peptide
Sequence Description: SEQ ID NO: 11:
US-11-303-935-11
Query Match 20.0%; Score 572.5; DB 7; Length 993;
Best Local Similarity 28.5%; Pred. No. 3,96-24;
Matches 179; Conservative 85; Mismatches 192; Indels 171; Gaps 23;
30 AFPSAQPSKPSASDG-HRGS-----AAFPAPAEKTLFGCFNSSDTVTS----- 74
DB 300 SFSDESSRCECBDDGYRAPSDPPVYACTRPSPAPQNLII-FNINQTVVLSLMSPPADN 357
QY 75 -----PORAGALAGVTTFFVAL-----YDYESRT 98
DB 358 GGRNDVTYRLICKRCSEWQECVPCGSGNIGMPOQTGLEDNYVTVMOLLAHANTFFVEA 417
QY 99 ETDLS-FKGERLQIVNNTRKVDVREGDWMLHLSLSTGQGTGYPISNVAAPS--DSIOAEB 155
DB 418 VNGVSDLSRSQRL-----FAAVSITTTQ-----AAFSQVSGWKKE- 452
QY 156 WYFKITRRESERILLNAENPRG-----TFVRESETTGACVCLASVD 198
DB 453 -----RVLQRSYQLSWQEPHEPNVITTEYEIKYEEKQDERTYSTLKXSTS-----AS 501
QY 199 FDNAGKLVNHYKTKRKLDGSGF-YITSRTQNSLQQLVAYYSKADGLCHRLTTY--- 252
DB 502 INNLKPGTVYFQIRAVTAAGYGNYSPLDVATLEEASATRVSSQNPIIIVAVAGT 561
QY 253 -----CPTSKPQTQ-----LAKDAWEIIPRES----- 274
DB 562 IIVFWVPGFIIGRRHCGYSKADQEGDEBELYFHKFPQTKYIIDPETYEDBNRAVHQPAK 621
QY 275 -----LRLEVKLGQCGFGEVWVG---TWNGTTRVAIKTLKPGTMSPEA--FLQEAQVM 322
DB 622 ELDA SCIKIERVIGAGEFVCSGRLKLPQGRDVAVALIKLVGTYEKRQDRDFICEASIM 681
QY 323 KGLRHEKLVLYAVVSE-EPYIYTEYMNKSLDPLKGETGKTLRLPOLVDMSAQASG 381
DB 682 GQDPHPVNHLEGVYTRCKPMAIYIEFMENALDAFLKHDGQFTVI-QLVGMRLGIAAG 740
QY 382 MAYERNMYVHRDLRAANILVGENLYCVADFGIARLIEDNE---YTARQAKPEPIKTA 438
DB 741 MRYLADMGYVHRDLAARNILVNSNLVCKVSDFGLSRVIEDDPEAVYTT-TGKXLPVMTA 799
QY 439 PEAALYGRFTIKSDVMSFGILLTELTKGAVPYPGVMNREVLDOVERGYRMPCEPCEPS 498
DB 800 PEAALYGRFTIKSDVMSFGILLTELTKGAVPYPGVMNREVLDOVERGYRMPCEPCEPS 498
QY 499 LHDLMCOCKRKEPERPTEFYLOAFLE 525
DB 860 LHQMLDMCQDRAERKFEQIVGLD 886

```
RESULT 12
US-11-312-958-52
/ Sequence 52, Application US/11312958
/ Publication No. US20060100152A1
/ GENERAL INFORMATION:
/ APPLICANT: Millennium Pharmaceuticals, Inc.
/ APPLICANT: Siles-Santiago, Immaculada
/ APPLICANT: Rosenfeld, Julie Beth
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
/ TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 9949, 14230, 760, 62553,
/ TITLE OF INVENTION: 12216, 17719, 41897, 47174, 33408, 10002, 16209, 314, 636,
/ TITLE OF INVENTION: 27410, 33260, 619, 15985, 69112, 2158, 224, 615, 44373,
/ TITLE OF INVENTION: 95431, 22245, 2387, 16658, 55054, 16314, 1675, 9569 OR
/ TITLE OF INVENTION: 13424 MOLECULES
/ FILE REFERENCE: MP102-027P1RNONIM
/ CURRENT APPLICATION NUMBER: US/11/312,958
/ CURRENT FILING DATE: 2005-12-20
/ PRIOR APPLICATION NUMBER: US/10/369,022
/ PRIOR FILING DATE: 2003-02-19
/ PRIOR APPLICATION NUMBER: US 60/360,495
/ PRIOR FILING DATE: 2002-02-28
/ PRIOR APPLICATION NUMBER: US 60/370,121
/ PRIOR FILING DATE: 2002-04-04
/ PRIOR APPLICATION NUMBER: US 60/373,010
/ PRIOR FILING DATE: 2002-04-16
/ PRIOR APPLICATION NUMBER: US 60/373,908
/ PRIOR FILING DATE: 2002-04-19
/ PRIOR APPLICATION NUMBER: US 60/377,717
/ PRIOR FILING DATE: 2002-05-03
/ PRIOR APPLICATION NUMBER: US 60/379,949
/ PRIOR FILING DATE: 2002-05-13
/ PRIOR APPLICATION NUMBER: US 60/382,409
/ PRIOR FILING DATE: 2002-05-21
/ PRIOR APPLICATION NUMBER: US 60/385,280
/ PRIOR FILING DATE: 2002-06-03
/ PRIOR APPLICATION NUMBER: US 60/386,879
/ PRIOR FILING DATE: 2002-06-06
/ Remaining Prior Application data removed - See file wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 64
/ SOFTWARE: FaastSeq for Windows Version 4.0
/ SEQ ID NO 52
/ LENGTH: 1130
/ TYPE: PR1
/ ORGANISM: Homo sapiens
US-11-312-958-52

Query Match      19.5%; Score 556.5; DB 7; Length 1130;
Best Local Similarity 30.0%; Pred. No. 3,2e-23;
Matches 176; Conservative 68; Mismatches 178; Indels 165; Gaps 20;

QY 60 PRLFGFNSSDTTSQORAGALAGVTTFYALYDYSRTETDLSFKKGERLQIVNTRKY 119
DB 522 PKPF-----TAIVTTTQDAPSLIG-----VVRKDWASQNSIALS----- 556
QY 120 DVREGDWMLAHSISTGOTGYIPSNVVAAPSDSIOAEWYFGK-----ITRESERILL 171
DB 557 -----WQAPAPASNAI-----LDYEIKYKEKEHQULTYSTRSKASPVII 596
QY 172 NAEPRGTEFLVRESEETTKGAYCLVSDF-----DNAKGLNVKHYKTRKIDS---GG--- 219
DB 597 TGLKPKATKYVPHIRVATATGYSGYSQKFEFETGDETSDMAAEGQLIVATAVAGGFILL 656
QY 220 -----FYTTSRTQF-----NSLQQLVAYYSKHA---DGLCHRLTVCP---TSK 257
DB 657 VILLTFFLITGRCQWYIKAKMKSEKRRHMLQ-----NGHLRFPGI---KTYIDDTYE 707
QY 258 PQTQGLAKXAWETPRSLLEVLVGLGCGEGEVMWGTNNGTR---VAIKTLKPGTMSB 313
DB 708 DSSLAAHEBPAKEDPSRIRIERVYIGAGEGEGVCSGLKTPGKREIPALIKTLKGHMDRO 767
QY 314 A--FLQEAQVMKKLRHEKLVQLYAVVSE----- 339
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DB 768 RRDFLREASIMGFDPHPIIRLEGVTKRSFPAIGVEAFCPFLRAGFLNSIOAPHVPVG 827
QY 340 -----BEIYIVTEYMNKGSLLDLKSTGTXYLLPQIVDMSAQIAGMAVERM 388
DB 828 GGSLLPPIRIPAGRWVMTVVEWMENGSIDSFRLRKIDGHFTYI---QIVGLMRGLASCMKTLSDM 886
QY 389 NYVHRDLRANILVGENLVCKVADFGIARLIEDNEYTA---ROGAKFPPIKWTAPREALYGR 446
DB 887 GYVHRDLARNILVNSNLVCKVSDPGLSKVLDEDPBAATTGGKIPIMTAPREALYGR 946
QY 447 FTIKSDVMSFGILLTELTKGRVPYGVNREVLQVBERGYRMPCEPCEPSIHDIMCQC 506
DB 947 FSSASDAMSXYGIWMEVMSGERPYWEMGNQVILSIEEGYRLPAPMGCPASIHQLMLHC 1006
QY 507 WRKEPEREPFETLOAF-----EDYFSTNEPQVRGE 539
DB 1007 WQERNHRPRKFTDIVSFLDKLIRNPSALHTLVEDIILWPE---SPGE 1050
```

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RESULT 13
US-11-251-465-21
/ Sequence 21, Application US/11251465
/ Publication No. US20060094061A1
/ GENERAL INFORMATION:
/ APPLICANT: Beye, Reginald
/ APPLICANT: Vandeghinste, Nick
/ APPLICANT: Tonne, Peter
/ APPLICANT: Klaassen, Hubertus
/ TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The
/ TITLE OF INVENTION: Same, Useful In The Treatment Of Joint Degenerative And
/ FILE REFERENCE: P30, 172-A USA
/ CURRENT APPLICATION NUMBER: US/11/251,465
/ CURRENT FILING DATE: 2005-10-14
/ PRIOR APPLICATION NUMBER: 60/619,384
/ PRIOR FILING DATE: 2004-10-15
/ NUMBER OF SEQ ID NOS: 880
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 21
/ LENGTH: 894
/ TYPE: PR1
/ ORGANISM: Homo sapiens
US-11-251-465-21

Query Match      17.1%; Score 488; DB 7; Length 894;
Best Local Similarity 28.4%; Pred. No. 1.2e-19;
Matches 170; Conservative 71; Mismatches 215; Indels 142; Gaps 23;
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QY 14 RRRSLRPSENVAGAGAFPASQTPSK-----PASADGHRGSAAFV--- 54
DB 295 RLGSLHPIHPYH---IRVACTSSQGPSWTHMLEVETREPGVPLGPPEPISATRNGSQAFVIM 353
QY 55 -PPAA--EPKLFQ--GFNSSDT-----VTSFORAGALAGVTTFYALYDES 96
DB 354 QEPRAPLQGTLLGYRLAYGQDTPREVLIDGRQEVTTLELQDGSVSNLTVCAAY----- 409
QY 97 RTETDLSFKKGERLQIVNTRKYVDVREGDWMLAHSISTGOTGYI---PSNVVAASDSIOABE 155
DB 410 -----TAAGDGPWSLPVPLEAWRPOQAPVHQLVKEPSTPAPS 447
QY 156 W-----YFGKTRRESERILLNAENPRGTFV---RESEETTKGAYCLVSDFPNKGLVNYK 208
DB 448 WPMWYVLGAVVAACVLL-----ALFLVHRKKKEIRYQ---EVEFPEYVERGELVYV 496
QY 209 HYKIRLDSGFGFYITSRTQFNSLQQLVAYYSKHADGLCHRLTTVCPPTSXPQTQGLAKXAM 268
DB 497 RYRVKRSYSRR---TTBATLNSL-----GISEELK 523
QY 269 E-----IPRESLRLEVLKLGCGCGEGEVMWGTN---GTTTVAIKTLKPG---TMSB-EATL 316
DB 524 EKLRDVMDVRHKKVVALGKTLGEGEFGAVMEGQINODDSLKVAVVTKMKIAICTRSBLEDFL 583
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QY      317  SEAGYMKLRHKKLVOLYAVV---SEEPYI---ITYEYNNKSGLLDPL----KGEGRKX 365
Db      564  SEAVCMKEDEHNMYMKLIVCGQGESERESFPAAVVLTPFKHGDLSFLYSLGQOPY 633
QY      366  LRLPOLVDMSAQIAGSMAYVERBNYVHRDLRANILVGENLYCKVADFGIARLIBENEYT 425
Db      644  LPTQMLVFKMADIASGMEYLSLTKRFIHRDLAARNCMLNEMSVCAVDFGLSKITVNGDY- 702
QY      426  ARQG--AKFPYKTAPEALYGRFTTKSDVWSGILLTELTTKGRVPYGMVRREVLDQY 483
Db      703  YRQGRIAKMPVKMIAIESLADRYTTSKSDVWSFGVTMWEIATGTQTPYPEVENSEIYDYL 762
QY      484  BGRGYMPCPEPCPEBSLHDMCOCKMRKEPERPFXYLOAFLEBYFTSTBQYQYQGENL 541
Db      763  RQGNRIKQPADCLDGLIYALMSRCHMEINPODRBSFTLRREDLENTLKALPPAQEDETIL 820

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RESULT 14

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US-11-255-147-6
; Sequence 6, Application US/11255147
; Publication No. US20060094081A1
; GENERAL INFORMATION:
; APPLICANT: SCHUBERT, CARSTEN
; APPLICANT: SPRINGER, BARRY A.
; APPLICANT: DECKMAN, INGRID
; APPLICANT: PATCH, RAYMOND J.
; APPLICANT: STRUBLE, GEOFFREY T.
; APPLICANT: MA, HONGCHANG
; APPLICANT: SCHALK-HIHI, CELINE
; APPLICANT: BRANDT, BENJAMIN M.
; APPLICANT: PETROUNIA, IOANNA
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF THE C-FMS KINASE DOMAIN:
; TITLE OF INVENTION: APPLICATIONS AND USE OF HETEROLOGOUS SUBSTITUTIONS OF
; TITLE OF INVENTION: KINASE INSERT DOMAINS FOR CRYSTALLIZATION
; FILE REFERENCE: PRD2389USNP
; CURRENT APPLICATION NUMBER: US/11/255,147
; CURRENT FILING DATE: 2005-10-20
; PRIOR APPLICATION NUMBER: 60/620,698
; PRIOR FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 6
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-255-147-6

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Query Match	16.9%	Score 483	DB 7	Length 343
Best Local Similarity	35.9%	Pred No. 8.2e-20		
Matches	107	Conservative	60	Mismatches 105
			Indels	26
			Gaps	8

QY	250	TTVCPTSKPQTGSLAKDAWEIPRESLRLEVKLGQSCFSEV-----MMGTNGTTRVAIK	303
DB	41	TFIDTOLPY-----NEKEFERNRLQFGKTLGAGAFGKVVATATFGJGKEDAVLKVAVK	95
QY	304	TLKPGTWS--PEAFLOEAOVMKKL-RHEKLVOLY-AVVSBEPIYATVETMNGKSLDFLK	359
DB	96	MUKSTRHADKREALMSCLKIMHLOHEHIVVLLACHTGGGVVVITTECCGDDLNTLFR	155
QY	360	GET-----GKYLRLPOLVDMSAQIASGMAYERNNTYHRLDPAANILVGENLVCKY	410
DB	156	RKSLRPEAENNNGRPPTRDILLHFSSOVAOGAFASLRKCHIRDVAAARVLLTNGHVAKI	215
QY	411	ADFGIAR-LIEDNEVTAQGAKEPKIMTAPAEALVGRPFITKIDWSFGILLTELTTKGRV	469
DB	216	GDFGIARIDMDSNTIVKGNARLPLVXMAFPESIPFCVYTVQSDVWSXYGLIMEIFSLGIN	275
QY	470	PYRG-MVNRVULDOYRGTRMCPPECESLHLMCCCKRKPESRPFFETVQATLED	526
DB	276	PYPGLIVNSKFKVLVDGYOMAOPEAFAPKNITISIMQCAALPEPTRPFFQOICSTLOE	333

RESULT 15

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US-10-505-928-432
; Sequence 432, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 432
; LENGTH: 885
; TYPE: prt
; ORGANISM: Homo sapiens
US-10-505-928-432

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Query Match Similarity      16.8%: Score 481.5; DB 6; Length 885;
Best Local Similarity      28.5%: Pred. No. 2,6e-19;
Matches 169; Conservative   71; Mismatches 211; Indels 143; Gaps 23

OY      14 RRRSLPESENHVGAGAPASQTPSK-----PASADGHRGSAAFV-- 54
DB      295 RLGSILHPTPYH-IRVACTSSQGPSMTHTMLPVEPREGVPLGPPENISATRNQSCQAFVH 353
OY      55 -PPAA--EPKIFG---GFNSSDT-----VTSQPRAGALAGATTFFALVDYS 96
DB      354 QEPRAPILOGTLLGRYLAQGGDTPETVLMDIGRQVETLELQDGSYSNLTCVAAY---- 409
OY      97 RTEPDLSEKKEERLQIVNTRKVDREDDWMLAHSLSGTQGTGYPISNYVAPSPDSIQAEW 156
DB      410 -----TAAGDPMSLPVPLBAMRPVKEPS-----TPAFSMPMW 442
OY      157 Y-FGKITRRESERLLLAENPRGTFVY--KSEFTTKGAYCLISVSDFDNAKGLNVGHYKI 212
DB      443 YVLGAVVAACVLL-----ALFLVHRKKETRYG---EVEPPTVERGELVYRYRV 491
OY      213 RKLDSGGFYIISRTQFNSLQOLVAYYSKHADGLCHRLTVCPTSKQTOGLADAW----- 269
DB      492 RKYSISR--TTEATLSL-----GISEBLKEKLR 518
OY      270 --IPRESLRLEVKLGQSCFGEVWNGTWN--GTTTVAIKTLKPG--TWSP-EAFLQEAQ 320
DB      519 DVMDVRHKVVALGKTGLGEGEFGAVNEGQINODDSILKVAIKTKMIAICTSRELEDFLSEAV 578
OY      321 VMKTLRHEKLVQVLVAV--SEEPFY----VTEFMNKGSLDLF----KGETGKTLRLP 369
DB      579 CMKEPDHNVNWLKIGVCFQSGSRESFPAVPVLLPMPKKGDDLSFLYSRLGQDPVLLPQ 638
OY      370 QLVMSAQIAGSMAVVERMNVYHRLPRAANILVGENLVCKVADFGIARLIEDNEYARQ 429
DB      639 MLVFMFMADIASGMETLSKTRFIHRDLAARNCLNENMSCVADFGLSKTIYNGDY-YRQG 697
OY      430 --AKFPIWTADEAALYGRFTTKSDVMSFGILLTELTKGARVPYRGMVNRREVLDQVERGY 487
DB      698 RIAKMPVFMIAIESLADRVYTSKSDVMSFGVMMIAIRGQPPYRDEVENSRIYDYLROGN 757
OY      488 RMPCEPECEPSLHDMQCCKRKEPEERPTFEYLOAFLEDYFSTSEQVYQGENUL 541
DB      758 RLKQPADCLDGLYALMSKCMELNPDQRSFTLELRDLENTLKALPPAGPBDILL 811

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